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90	42	9.9	67	15	Q9J194	Q9J194 human immun	163	40.5	9.6	69	2	Q9ZEU9	Q9zeu9 lactobacill
91	42	9.9	67	15	Q9J172	Q9J172 human immun	164	40.5	9.6	69	15	Q9WMR4	Q9wmr4 human immun
92	42	9.9	67	15	Q9J163	Q9J163 human immun	165	40.5	9.6	69	15	Q9WMO5	Q9wmq5 human immun
93	42	9.9	67	15	Q9J142	Q9J142 human immun	166	40.5	9.6	69	16	Q9KY84	Q9ky84 streptomyc
94	42	9.9	67	15	Q9J160	Q9J160 human immun	167	40.5	9.6	70	7	Q46870	Q46870 homo sapien
95	42	9.9	68	15	Q9J150	Q9J150 human immun	168	40.5	9.6	70	14	Q99IX6	Q99ix6 uncultured
96	42	9.9	68	15	Q9J146	Q9J146 human immun	169	40.5	9.6	70	16	P71998	P71998 mycobacteri
97	42	9.9	68	15	Q9J145	Q9J145 human immun	170	40.5	9.6	74	12	Q66059	Q66059 canine herp
98	42	9.9	68	15	Q9J143	Q9J143 human immun	171	40.5	9.6	76	2	Q8VN33	Q8vn33 helicobacte
99	42	9.9	68	15	Q9J608	Q9J608 human immun	172	40.5	9.6	77	15	Q38442	Q38442 human immun
100	42	9.9	69	16	Q8XNS4	Q8xns4 clostridium	173	40.5	9.6	77	16	Q8YF42	Q8yf42 brucella me
101	42	9.9	72	2	Q48506	Q48506 lactococcus	174	40.5	9.6	78	4	Q96T74	Q96t74 homo sapien
102	42	9.9	72	2	Q07693	Q07693 mycobacteri	175	40.5	9.6	79	2	Q936T5	Q936t5 pseudomonas
103	42	9.9	72	5	Q9VGM8	Q9vgm8 drosophila	176	40.5	9.6	79	17	Q8TUT4	Q8tut4 methanopyru
104	42	9.9	72	5	Q27513	Q27513 methanobact	177	40.5	9.6	81	2	Q9EUC0	Q9euc0 pseudomonas
105	42	9.9	75	4	Q9UGQ6	Q9ugq6 homo sapien	178	40.5	9.6	86	15	Q38069	Q38069 human immun
106	42	9.9	76	12	Q64944	Q64944 avian infec	179	40.5	9.6	86	15	Q38245	Q38245 human immun
107	42	9.9	76	12	Q64947	Q64947 avian infec	180	40.5	9.6	86	15	Q38246	Q38246 human immun
108	42	9.9	79	16	Q928X5	Q928x5 chlamydia p	181	40.5	9.6	86	15	Q38247	Q38247 human immun
109	42	9.9	79	16	Q9JSH8	Q9jsh8 chlamydia p	182	40.5	9.6	86	15	Q38249	Q38249 human immun
110	42	9.9	81	6	Q28836	Q28836 ovis artes	183	40.5	9.6	86	15	Q38250	Q38250 human immun
111	42	9.9	81	16	Q9K247	Q9k247 chlamydia p	184	40.5	9.6	86	15	Q38252	Q38252 human immun
112	42	9.9	85	16	Q9R9D7	Q8r9d7 thermoanaer	185	40.5	9.6	86	15	Q38253	Q38253 human immun
113	42	9.9	86	16	Q92CF9	Q92cf9 listeria in	186	40.5	9.6	86	15	Q38254	Q38254 human immun
114	42	9.9	86	16	Q8Y7M9	Q8y7m9 listeria mo	187	40.5	9.6	86	15	Q38255	Q38255 human immun
115	42	9.9	88	5	Q9S532	Q9s532 drosophila	188	40.5	9.6	86	15	Q38256	Q38256 human immun
116	42	9.9	89	2	Q9AKH7	Q9akh7 rickettsia	189	40.5	9.6	86	15	Q38258	Q38258 human immun
117	42	9.9	89	10	Q8RX10	Q8rx10 arabidopsis	190	40.5	9.6	86	15	Q38259	Q38259 human immun
118	42	9.9	89	16	Q9K781	Q9k781 bacillus ha	191	40.5	9.6	86	15	Q38260	Q38260 human immun
119	42	9.9	90	2	P72094	P72094 neisseria m	192	40.5	9.6	86	15	Q38261	Q38261 human immun
120	42	9.9	90	15	Q41594	Q41594 human immun	193	40.5	9.6	86	15	Q38262	Q38262 human immun
121	41.5	9.8	63	11	Q9CT35	Q9ctj5 mus musculo	194	40.5	9.6	86	15	Q38263	Q38263 human immun
122	41.5	9.8	66	5	Q9VE14	Q9ve14 drosophila	195	40.5	9.6	86	15	Q38264	Q38264 human immun
123	41.5	9.8	66	15	Q9J127	Q9j127 human immun	196	40.5	9.6	86	15	Q38265	Q38265 human immun
124	41.5	9.8	70	14	Q9J178	Q9j178 uncultured	197	40.5	9.6	86	15	Q38267	Q38267 human immun
125	41.5	9.8	70	15	Q9J602	Q9j602 human immun	198	40.5	9.6	86	15	Q38268	Q38268 human immun
126	41.5	9.8	72	15	Q9THU4	Q9thu4 clostridium	199	40.5	9.6	86	15	Q38271	Q38271 human immun
127	41.5	9.8	72	15	Q9H273	Q9h273 human immun	200	40.5	9.6	86	15	Q38274	Q38274 human immun
128	41.5	9.8	88	15	Q9B204	Q9b204 rhizobium l	201	40.5	9.6	86	15	Q38275	Q38275 human immun
129	41.5	9.8	88	16	Q9G229	Q9g229 leishmania	202	40.5	9.6	86	15	Q38276	Q38276 human immun
130	41.5	9.8	89	5	Q9G239	Q9g239 oryza sativ	203	40.5	9.6	86	15	Q38277	Q38277 human immun
131	41.5	9.8	89	16	Q9JGWH	Q9jgwh streptomyce	204	40.5	9.6	86	15	Q38278	Q38278 human immun
132	41.5	9.8	89	16	Q9JGJ7	Q9jg7 streptomyce	205	40.5	9.6	86	15	Q38279	Q38279 human immun
133	41	9.7	63	9	Q9S060	Q9s060 mycobacteri	206	40.5	9.6	86	15	Q38280	Q38280 human immun
134	41	9.7	63	10	Q9K590	Q9k590 nicotiana t	207	40.5	9.6	86	15	Q38281	Q38281 human immun
135	41	9.7	65	10	Q9S056	Q9s056 zea mays (m	208	40.5	9.6	86	15	Q38283	Q38283 human immun
136	41	9.7	65	15	Q9J115	Q9j115 human immun	209	40.5	9.6	86	15	Q38284	Q38284 human immun
137	41	9.7	66	12	Q9V9T5	Q9v9t5 african swi	210	40.5	9.6	86	15	Q38287	Q38287 human immun
138	41	9.7	66	15	Q9J598	Q9j598 human immun	211	40.5	9.6	86	15	Q38288	Q38288 human immun
139	41	9.7	67	15	Q9J141	Q9j141 human immun	212	40.5	9.6	86	15	Q38289	Q38289 human immun
140	41	9.7	67	15	Q9J590	Q9j590 human immun	213	40.5	9.6	86	15	Q38290	Q38290 human immun
141	41	9.7	68	2	Q46605	Q46605 desulfovibr	214	40.5	9.6	86	15	Q38293	Q38293 human immun
142	41	9.7	69	10	Q41693	Q41693 vigna radia	215	40.5	9.6	86	15	Q38296	Q38296 human immun
143	41	9.7	70	5	Q9VV37	Q9vv37 drosophila	216	40.5	9.6	86	15	Q38297	Q38297 human immun
144	41	9.7	71	12	Q91ET4	Q91et4 cydia pomon	217	40.5	9.6	86	15	Q38298	Q38298 human immun
145	41	9.7	71	15	Q9J585	Q9j585 human immun	218	40.5	9.6	86	15	Q38301	Q38301 human immun
146	41	9.7	72	15	Q9J591	Q9j591 human immun	219	40.5	9.6	86	15	Q38302	Q38302 human immun
147	41	9.7	75	15	Q76056	Q76056 human immun	220	40.5	9.6	86	15	Q38303	Q38303 human immun
148	41	9.7	76	6	Q8WMJ9	Q8wmj9 macaca mula	221	40.5	9.6	86	15	Q38304	Q38304 human immun
149	41	9.7	78	12	Q9PX51	Q9px51 shope fibro	222	40.5	9.6	86	15	Q38305	Q38305 human immun
150	41	9.7	79	4	Q9XRP2	Q9xrp2 homo sapien	223	40.5	9.6	86	15	Q38306	Q38306 human immun
151	41	9.7	85	2	Q9WKP2	Q9wkp2 xanthomonas	224	40.5	9.6	86	15	Q38307	Q38307 human immun
152	41	9.7	86	4	Q9KJ23	Q9kj23 homo sapien	225	40.5	9.6	86	15	Q38308	Q38308 human immun
153	41	9.7	86	16	Q9JZ77	Q9jzt7 neisseria m	226	40.5	9.6	86	15	Q38309	Q38309 human immun
154	41	9.7	87	17	Q9RK24	Q9rk24 methanosarc	227	40.5	9.6	86	15	Q38310	Q38310 human immun
155	41	9.7	88	10	Q42092	Q42092 arabidopsis	228	40.5	9.6	86	15	Q38311	Q38311 human immun
156	41	9.7	88	2	Q9AM06	Q9am06 plectonema	229	40.5	9.6	86	15	Q38312	Q38312 human immun
157	40.5	9.6	52	4	Q9G6J3	Q9g6j3 homo sapien	230	40.5	9.6	86	15	Q38313	Q38313 human immun
158	40.5	9.6	66	15	Q9J186	Q9j186 human immun	231	40.5	9.6	86	15	Q38314	Q38314 human immun
159	40.5	9.6	66	15	Q38432	Q38432 human immun	232	40.5	9.6	86	15	Q38315	Q38315 human immun
160	40.5	9.6	67	15	Q9J176	Q9j176 human immun	233	40.5	9.6	86	15	Q38316	Q38316 human immun
161	40.5	9.6	68	2	Q50886	Q50886 myxococcus	234	40.5	9.6	86	15	Q38317	Q38317 human immun
162	40.5	9.6	68	15	Q74620	Q74620 human immun	235	40.5	9.6	86	15	Q38319	Q38319 human immun

236	40.5	9.6	86	15	038320	human	immun	038320	309	40	9.5	67	15	097599	human	immun
237	40.5	9.6	86	15	038321	human	immun	038321	310	40	9.5	67	15	097607	human	immun
238	40.5	9.6	86	15	038322	human	immun	038322	311	40	9.5	67	16	097157	clostridium	
239	40.5	9.6	86	15	038323	human	immun	038323	312	40	9.5	68	15	097196	human	immun
240	40.5	9.6	86	15	038324	human	immun	038324	313	40	9.5	68	15	097191	human	immun
241	40.5	9.6	86	15	038325	human	immun	038325	314	40	9.5	68	15	097180	human	immun
242	40.5	9.6	86	15	038326	human	immun	038326	315	40	9.5	68	15	097179	human	immun
243	40.5	9.6	86	15	038327	human	immun	038327	316	40	9.5	68	15	097165	human	immun
244	40.5	9.6	86	15	038328	human	immun	038328	317	40	9.5	68	15	097164	human	immun
245	40.5	9.6	86	15	038330	human	immun	038330	318	40	9.5	68	15	097149	human	immun
246	40.5	9.6	86	15	038331	human	immun	038331	319	40	9.5	68	15	097146	human	immun
247	40.5	9.6	86	15	038333	human	immun	038333	320	40	9.5	68	15	097057	human	immun
248	40.5	9.6	86	15	038334	human	immun	038334	321	40	9.5	69	15	097134	human	immun
249	40.5	9.6	86	15	038451	human	immun	038451	322	40	9.5	69	15	097119	human	immun
250	40.5	9.6	86	15	038452	human	immun	038452	323	40	9.5	70	5	094857	drosophila	
251	40.5	9.6	86	15	038453	human	immun	038453	324	40	9.5	70	5	094871	drosophila	
252	40.5	9.6	86	15	038454	human	immun	038454	325	40	9.5	70	5	094937	drosophila	
253	40.5	9.6	86	15	038455	human	immun	038455	326	40	9.5	70	5	094951	drosophila	
254	40.5	9.6	86	15	038456	human	immun	038456	327	40	9.5	70	5	076263	human	immun
255	40.5	9.6	86	15	038457	human	immun	038457	328	40	9.5	71	15	076263	human	immun
256	40.5	9.6	86	15	038239	human	immun	038239	329	40	9.5	71	15	097611	human	immun
257	40.5	9.6	86	15	097128	human	immun	097128	330	40	9.5	72	15	097157	human	immun
258	40.5	9.6	86	15	097621	human	immun	097621	331	40	9.5	72	15	097157	human	immun
259	40.5	9.6	86	15	038050	human	immun	038050	332	40	9.5	72	15	076045	human	immun
260	40.5	9.6	86	15	038063	human	immun	038063	333	40	9.5	73	3	097599	human	immun
261	40.5	9.6	86	15	038064	human	immun	038064	334	40	9.5	73	3	097178	human	immun
262	40.5	9.6	86	15	038346	human	immun	038346	335	40	9.5	73	15	076058	human	immun
263	40.5	9.6	86	15	038347	human	immun	038347	336	40	9.5	74	15	076265	human	immun
264	40.5	9.6	86	15	038348	human	immun	038348	337	40	9.5	74	15	076061	human	immun
265	40.5	9.6	86	15	038350	human	immun	038350	338	40	9.5	74	15	076063	human	





528	38	9.0	76	12	064950	064950 avian infec	601	37.5	8.9	68	15	074261	human immun
529	38	9.0	76	15	009529	009529 human immun	602	37.5	8.9	68	15	074263	human immun
530	38	9.0	76	12	040608	040608 hepatitis c	603	37.5	8.9	68	15	074265	human immun
531	38	9.0	76	12	040609	040609 hepatitis c	604	37.5	8.9	68	15	074267	human immun
532	38	9.0	79	2	092467	092467 escherichia	605	37.5	8.9	68	15	074269	human immun
533	38	9.0	80	6	09TSE2	09TSE2 sus scrofa	606	37.5	8.9	68	15	074271	human immun
534	38	9.0	80	10	09TSE5	09TSE5 zea mays (m	607	37.5	8.9	69	4	Q9BU94	Q9BU94 homo sapien
535	38	9.0	80	10	08S0N7	08S0N7 oryza sativ	608	37.5	8.9	69	12	Q8QWQ3	Q8QWQ3 human coxsa
536	38	9.0	81	06	09S0N7	09S0N7 streptomyce	609	37.5	8.9	69	15	Q9WMD2	Q9WMD2 human immun
537	38	9.0	81	06	09S0N7	09S0N7 rhizobium m	610	37.5	8.9	69	15	Q9WMT1	Q9WMT1 human immun
538	38	9.0	82	15	092254	092254 strongyloid	611	37.5	8.9	69	15	Q9WNR5	Q9WNR5 human immun
539	38	9.0	84	5	018505	018505 mus musculu	612	37.5	8.9	71	1	Q977L2	Q977L2 uncultured
540	38	9.0	85	11	08VDD4	08VDD4 mus musculu	613	37.5	8.9	72	15	Q9WFE1	Q9WFE1 human immun
541	38	9.0	85	16	09LJF4	09LJF4 rhizobium l	614	37.5	8.9	74	5	Q9NLX4	Q9NLX4 leishmania
542	38	9.0	86	9	Q9B057	Q9B057 mycobacteri	615	37.5	8.9	74	10	Q9LZP5	Q9LZP5 arabidopsis
543	38	9.0	88	6	062851	062851 ovis aries	616	37.5	8.9	74	15	Q91F12	Q91F12 human immun
544	38	9.0	90	10	094H52	094H52 oryza sativ	617	37.5	8.9	74	16	053491	053491 mycobacteri
545	38	9.0	90	16	08XSC5	08XSC5 ralstonia s	618	37.5	8.9	76	2	Q8VNR3	Q8VNR3 helicobacte
546	37.5	8.9	47	15	073724	073724 human immun	619	37.5	8.9	77	6	Q9GMR8	Q9GMR8 macaca fasc
547	37.5	8.9	47	15	073726	073726 human immun	620	37.5	8.9	77	10	Q9XTX4	Q9XTX4 oryza sativ
548	37.5	8.9	47	15	073728	073728 human immun	621	37.5	8.9	77	15	Q38436	Q38436 human immun
549	37.5	8.9	47	15	073729	073729 human immun	622	37.5	8.9	78	2	Q8RVC1	Q8RVC1 escherichia
550	37.5	8.9	47	15	073731	073731 human immun	623	37.5	8.9	78	15	Q38440	Q38440 human immun
551	37.5	8.9	47	15	073733	073733 human immun	624	37.5	8.9	78	15	Q38450	Q38450 human immun
552	37.5	8.9	47	15	073737	073737 human immun	625	37.5	8.9	79	15	Q38435	Q38435 human immun
553	37.5	8.9	47	15	073765	073765 human immun	626	37.5	8.9	79	15	Q38441	Q38441 human immun
554	37.5	8.9	47	15	073767	073767 human immun	627	37.5	8.9	80	3	Q38448	Q38448 human immun
555	37.5	8.9	47	15	073769	073769 human immun	628	37.5	8.9	80	3	Q9HGR0	Q9HGR0 poltrasia c
556	37.5	8.9	47	15	073771	073771 human immun	629	37.5	8.9	80	11	Q62503	Q62503 mus musculu
557	37.5	8.9	47	15	073773	073773 human immun	630	37.5	8.9	80	15	Q90VQ1	Q90VQ1 human immun
558	37.5	8.9	49	15	073811	073811 human immun	631	37.5	8.9	82	5	Q95T21	Q95T21 drosophila
559	37.5	8.9	49	15	073813	073813 human immun	632	37.5	8.9	82	11	Q922V7	Q922V7 mus musculu
560	37.5	8.9	49	15	073815	073815 human immun	633	37.5	8.9	82	15	Q38456	Q38456 human immun
561	37.5	8.9	49	15	073817	073817 human immun	634	37.5	8.9	82	16	Q8VKP2	Q8VKP2 mycobacteri
562	37.5	8.9	49	15	073827	073827 human immun	635	37.5	8.9	83	5	Q95PS6	Q95PS6 leishmania
563	37.5	8.9	50	4	Q43666	Q43666 homo sapien	636	37.5	8.9	83	15	Q905F4	Q905F4 human immun
564	37.5	8.9	57	15	037615	037615 mus musculu	637	37.5	8.9	85	10	Q8S511	Q8S511 cucumis mel
565	37.5	8.9	58	11	Q912N0	Q912N0 human immun	638	37.5	8.9	86	15	Q38035	Q38035 human immun
566	37.5	8.9	58	12	Q96874	Q96874 hepatitis c	639	37.5	8.9	86	15	Q38037	Q38037 human immun
567	37.5	8.9	61	5	Q967U2	Q967U2 brachyosteo	640	37.5	8.9	86	15	Q38038	Q38038 human immun
568	37.5	8.9	65	15	Q905A4	Q905A4 human immun	641	37.5	8.9	86	15	Q38039	Q38039 human immun
569	37.5	8.9	65	16	P72917	P72917 synecocyst	642	37.5	8.9	86	15	Q38270	Q38270 human immun
570	37.5	8.9	66	12	0801V2	0801V2 hepatitis c	643	37.5	8.9	86	15	Q38443	Q38443 human immun
571	37.5	8.9	66	16	08VHC3	Q8VHC3 bruceella me	644	37.5	8.9	86	15	Q38446	Q38446 human immun
572	37.5	8.9	67	2	Q8VNR3	Q8VNR3 helicobacte	645	37.5	8.9	86	15	Q38454	Q38454 human immun
573	37.5	8.9	67	16	Q9L0X3	Q9L0X3 streptomyce	646	37.5	8.9	86	15	Q38454	Q38454 human immun
574	37.5	8.9	68	15	Q69617	Q69617 human immun	647	37.5	8.9	86	15	Q38462	Q38462 human immun
575	37.5	8.9	68	15	Q69619	Q69619 human immun	648	37.5	8.9	86	15	Q38463	Q38463 human immun
576	37.5	8.9	68	15	Q69619	Q69619 human immun	649	37.5	8.9	86	15	Q38489	Q38489 human immun
577	37.5	8.9	68	15	Q69649	Q69649 human immun	650	37.5	8.9	86	15	Q38490	Q38490 human immun
578	37.5	8.9	68	15	Q74091	Q74091 human immun	651	37.5	8.9	86	15	Q38497	Q38497 human immun
579	37.5	8.9	68	15	Q74249	Q74249 human immun	652	37.5	8.9	86	15	Q38505	Q38505 human immun
580	37.5	8.9	68	15	Q74256	Q74256 human immun	653	37.5	8.9	86	15	Q38517	Q38517 human immun
581	37.5	8.9	68	15	Q74258	Q74258 human immun	654	37.5	8.9	86	15	Q38519	Q38519 human immun
582	37.5	8.9	68	15	Q74258	Q74258 human immun	655	37.5	8.9	86	15	Q38531	Q38531 human immun
583	37.5	8.9	68	15	Q74296	Q74296 human immun	656	37.5	8.9	86	15	Q38532	Q38532 human immun
584	37.5	8.9	68	15	Q74296	Q74296 human immun	657	37.5	8.9	86	15	Q38535	Q38535 human immun
585	37.5	8.9	68	15	Q74296	Q74296 human immun	658	37.5	8.9	86	16	Q928H4	Q928H4 rhizobium m
586	37.5	8.9	68	15	Q74296	Q74296 human immun	659	37.5	8.9	87	1	Q05705	Q05705 sulfolobus
587	37.5	8.9	68	15	Q74103	Q74103 human immun	660	37.5	8.9	87	2	Q32894	Q32894 mycobacteri
588	37.5	8.9	68	15	Q74294	Q74294 human immun	661	37.5	8.9	87	11	Q99KN4	Q99KN4 porcellio s
589	37.5	8.9	68	15	Q74247	Q74247 human immun	662	37.5	8.9	87	15	Q38482	Q38482 mus musculu
590	37.5	8.9	68	15	Q74616	Q74616 human immun	663	37.5	8.9	87	15	Q38493	Q38493 human immun
591	37.5	8.9	68	15	Q74628	Q74628 human immun	664	37.5	8.9	89	5	Q964V3	Q964V3 procambur
592	37.5	8.9	68	15	Q74632	Q74632 human immun	665	37.5	8.9	89	15	Q9WFE3	Q9WFE3 human immun
593	37.5	8.9	68	15	Q74638	Q74638 human immun	666	37.5	8.9	89	15	Q38025	Q38025 human immun
594	37.5	8.9	68	15	Q74640	Q74640 human immun	667	37.5	8.9	89	15	Q38026	Q38026 human immun
595	37.5	8.9	68	15	Q74643	Q74643 human immun	668	37.5	8.9	89	15	Q38028	Q38028 human immun
596	37.5	8.9	68	15	Q74647	Q74647 human immun	669	37.5	8.9	89	15	Q38033	Q38033 human immun
597	37.5	8.9	68	15	Q74649	Q74649 human immun	670	37.5	8.9	89	15	Q38066	Q38066 human immun
598	37.5	8.9	68	15	Q74670	Q74670 human immun	671	37.5	8.9	89	17	Q8U1N6	Q8U1N6 pyrococcus
599	37.5	8.9	68	15	Q74672	Q74672 human immun	672	37.5	8.9	90	5	Q97102	Q97102 drosophila
600	37.5	8.9	68	15	Q74672	Q74672 human immun	673	37.5	8.9	90	15	Q41561	Q41561 human immun

674	37	8.7	42	2	P82555	P82555 streptococc	747	37	8.7	79	15	038467	038467 human immun
675	37	8.7	44	15	O89363	O89363 human immun	748	37	8.7	79	15	038471	038471 human immun
676	37	8.7	45	2	O47202	O47202 escherichia	749	37	8.7	79	16	O9PH12	O9PH12 xylella fas
677	37	8.7	45	12	O9DSS2	O9DSS2 salmireline	750	37	8.7	80	2	O51000	O51000 neisseria g
678	37	8.7	50	2	O9RAD1	O9RAD1 rhodofexer	751	37	8.7	80	5	O8STA4	O8STA4 penaeus jap
679	37	8.7	50	16	O98D00	O98D00 rhizobium l	752	37	8.7	80	9	O64261	O64261 mycobacteri
680	37	8.7	52	16	O92NN7	O92NN7 rhizobium m	753	37	8.7	80	10	O38439	O38439 human immun
681	37	8.7	53	2	O2RL85	O2RL85 rhizobium m	754	37	8.7	81	15	O38439	O38439 human immun
682	37	8.7	53	5	O9U7L0	O9U7L0 plasmodium	755	37	8.7	81	10	O04814	O04814 sporobolus
683	37	8.7	53	15	O87399	O87399 chimpanzee	756	37	8.7	81	12	O9YPK9	O9YPK9 encephalomy
684	37	8.7	53	15	O87405	O87405 chimpanzee	757	37	8.7	81	12	O8VAP4	O8VAP4 white spot
685	37	8.7	53	15	O87414	O87414 chimpanzee	758	37	8.7	81	12	O9W8J1	O9W8J1 encephalomy
686	37	8.7	53	16	O8U422	O8U422 agrobacteri	759	37	8.7	82	10	O9FP81	O9FP81 oryza sativ
687	37	8.7	53	17	O96XV5	O96XV5 sulfolobus	760	37	8.7	82	10	O8T960	O8T960 drosophila
688	37	8.7	57	5	O8T7Y9	O8T7Y9 caenorhabdi	761	37	8.7	83	5	O8T960	O8T960 drosophila
689	37	8.7	58	15	O87420	O87420 chimpanzee	762	37	8.7	83	12	O9YPK3	O9YPK3 porcine enc
690	37	8.7	59	12	O39817	O39817 encephalomy	763	37	8.7	83	12	O9YPL3	O9YPL3 encephalomy
691	37	8.7	62	7	O98149	O98149 papio hamad	764	37	8.7	83	12	O9YPL3	O9YPL3 encephalomy
692	37	8.7	62	7	O9XRX3	O9XRX3 papio cynoc	765	37	8.7	83	12	O9YPL3	O9YPL3 encephalomy
693	37	8.7	62	7	O30881	O30881 papio hamad	766	37	8.7	84	16	O9FPA8	O9FPA8 oryza sativ
694	37	8.7	62	7	O30591	O30591 macaca mula	767	37	8.7	84	16	O9KAV4	O9KAV4 bacillus ha
695	37	8.7	62	15	O87395	O87395 chimpanzee	768	37	8.7	84	16	O8Y190	O8Y190 synechocyst
696	37	8.7	62	16	O9PHB7	O9PHB7 xylella fas	769	37	8.7	84	16	O9XAG7	O9XAG7 streptomyce
697	37	8.7	63	2	O9Z431	O9Z431 pseudomonas	770	37	8.7	85	5	O9VDM5	O9VDM5 drosophila
698	37	8.7	63	2	O9R3T3	O9R3T3 pseudomonas	771	37	8.7	85	6	O13114	O13114 isooden mac
699	37	8.7	63	11	O99MY4	O99MY4 mus musculu	772	37	8.7	85	6	O13114	O13114 isooden mac
700	37	8.7	64	15	O9J167	O9J167 human immun	773	37	8.7	85	6	O02795	O02795 ornithorhyn
701	37	8.7	64	15	O9J155	O9J155 human immun	774	37	8.7	85	6	O02798	O02798 petaurus br
702	37	8.7	64	16	O8RCK5	O8RCK5 agrobacteri	775	37	8.7	85	6	O13104	O13104 cercarctus
703	37	8.7	65	2	O07265	O07265 mycobacteri	776	37	8.7	85	6	O02803	O02803 trichosurus
704	37	8.7	65	15	O9J147	O9J147 human immun	777	37	8.7	85	6	O02792	O02792 notoryctes
705	37	8.7	65	15	O9J139	O9J139 human immun	778	37	8.7	85	6	O02790	O02790 macropus ru
706	37	8.7	65	15	O97584	O97584 human immun	779	37	8.7	85	6	O13105	O13105 dasyruroides
707	37	8.7	66	15	O9J185	O9J185 human immun	780	37	8.7	85	6	O02801	O02801 tachyglossu
708	37	8.7	66	16	O8ZCY3	O8ZCY3 yersinia pe	781	37	8.7	86	11	O9JIK6	O9JIK6 mus musculu
709	37	8.7	66	17	O9VEZ2	O9VEZ2 aeropyrum p	782	37	8.7	86	15	O38459	O38459 human immun
710	37	8.7	67	15	O97609	O97609 human immun	783	37	8.7	87	15	O38425	O38425 human immun
711	37	8.7	67	15	O38429	O38429 human immun	784	37	8.7	87	15	O38426	O38426 human immun
712	37	8.7	67	15	O38431	O38431 human immun	785	37	8.7	87	15	O38427	O38427 human immun
713	37	8.7	68	15	O9J166	O9J166 human immun	786	37	8.7	87	15	O38444	O38444 human immun
714	37	8.7	68	15	O97603	O97603 human immun	787	37	8.7	87	15	O38445	O38445 human immun
715	37	8.7	68	15	O38430	O38430 human immun	788	37	8.7	87	15	O38465	O38465 human immun
716	37	8.7	69	12	O8QMD8	O8QMD8 human echov	789	37	8.7	87	15	O38470	O38470 human immun
717	37	8.7	69	15	O90540	O90540 human immun	790	37	8.7	87	15	O38473	O38473 human immun
718	37	8.7	69	15	O97613	O97613 human immun	791	37	8.7	87	15	O38474	O38474 human immun
719	37	8.7	71	10	O9XGY3	O9XGY3 malus domes	792	37	8.7	87	15	O38475	O38475 human immun
720	37	8.7	71	10	O90584	O90584 human immun	793	37	8.7	87	15	O38478	O38478 human immun
721	37	8.7	72	11	O91X84	O91X84 mus musculu	794	37	8.7	87	15	O38479	O38479 human immun
722	37	8.7	72	17	O8Z257	O8Z257 pyrobaculum	795	37	8.7	87	15	O38480	O38480 human immun
723	37	8.7	73	10	O9FL96	O9FL96 arabidopsis	796	37	8.7	87	15	O38481	O38481 human immun
724	37	8.7	73	11	O8R4G4	O8R4G4 rattus norv	797	37	8.7	87	15	O38484	O38484 human immun
725	37	8.7	73	11	O8R1H0	O8R1H0 mus musculu	798	37	8.7	87	15	O38485	O38485 human immun
726	37	8.7	73	15	O9J170	O9J170 human immun	799	37	8.7	87	15	O38486	O38486 human immun
727	37	8.7	73	15	O38428	O38428 human immun	800	37	8.7	87	15	O38488	O38488 human immun
728	37	8.7	73	16	O8ZEP2	O8ZEP2 yersinia pe	801	37	8.7	87	15	O38494	O38494 human immun
729	37	8.7	74	8	O35301	O35301 oryza sativ	802	37	8.7	87	15	O38496	O38496 human immun
730	37	8.7	74	12	O9W8B2	O9W8B2 encephalomy	803	37	8.7	87	15	O38500	O38500 human immun
731	37	8.7	75	6	O95LM4	O95LM4 macaca fasc	804	37	8.7	87	15	O38502	O38502 human immun
732	37	8.7	75	11	O8R043	O8R043 mus musculu	805	37	8.7	87	15	O38503	O38503 human immun
733	37	8.7	75	12	O9WK35	O9WK35 encephalomy	806	37	8.7	87	15	O38504	O38504 human immun
734	37	8.7	75	15	O38438	O38438 human immun	807	37	8.7	87	15	O38507	O38507 human immun
735	37	8.7	75	15	O38491	O38491 human immun	808	37	8.7	87	15	O38508	O38508 human immun
736	37	8.7	76	12	O64943	O64943 avian infec	809	37	8.7	87	15	O38512	O38512 human immun
737	37	8.7	76	12	O68828	O68828 human cytom	810	37	8.7	87	15	O38513	O38513 human immun
738	37	8.7	78	2	O9AF88	O9AF88 anaplasma m	811	37	8.7	87	15	O38515	O38515 human immun
739	37	8.7	78	15	O38433	O38433 human immun	812	37	8.7	87	15	O38516	O38516 human immun
740	37	8.7	78	15	O38434	O38434 human immun	813	37	8.7	87	15	O38518	O38518 human immun
741	37	8.7	78	15	O38437	O38437 human immun	814	37	8.7	87	15	O38528	O38528 human immun
742	37	8.7	78	15	O38449	O38449 human immun	815	37	8.7	87	15	O38538	O38538 human immun
743	37	8.7	78	15	O38468	O38468 human immun	816	37	8.7	87	16	O92Y16	O92Y16 rhizobium m
744	37	8.7	78	15	O38469	O38469 human immun	817	37	8.7	88	5	O95857	O95857 drosophila
745	37	8.7	78	16	O9PRY1	O9PRY1 xylella fas	818	37	8.7	88	5	O9W109	O9W109 drosophila
746	37	8.7	78	16	O9PBM4	O9PBM4 xylella fas	819	37	8.7	88	15	O38476	O38476 human immun

820	37	8.7	88	15	Q38487	Q38487 human immun	893	36.5	8.6	85	9	Q9A204	Q9A204 bacterioph
821	37	8.7	88	15	Q38495	Q38495 human immun	894	36.5	8.6	86	15	Q90V10	Q90V10 human immun
822	37	8.7	88	15	Q38498	Q38498 human immun	895	36.5	8.6	86	15	Q38533	Q38533 human immun
823	37	8.7	88	15	Q38506	Q38506 human immun	896	36.5	8.6	86	16	Q9CHT9	Q9CHT9 lactococcus
824	37	8.7	88	16	Q9P17	Q9P17 xylella fas	897	36.5	8.6	87	2	Q9F125	Q9F125 bacillus ci
825	37	8.7	88	16	Q9A679	Q9A679 thermoanaer	898	36.5	8.6	87	2	Q9F125	Q9F125 pseudomonas
826	37	8.7	88	17	Q8U0X6	Q8U0X6 pseudomonas	899	36.5	8.6	87	2	Q9B311	Q9B311 homo sapien
827	37	8.7	89	16	Q9A016	Q9A016 pseudomonas	900	36.5	8.6	87	4	Q9A008	Q9A008 caulobacter
828	37	8.7	89	16	Q9A016	Q9A016 pseudomonas	901	36.5	8.6	88	2	Q52509	Q52509 pseudomonas
829	37	8.7	90	16	Q9A016	Q9A016 pseudomonas	902	36.5	8.6	88	4	Q9UDK0	Q9UDK0 homo sapien
830	37	8.7	90	15	Q72819	Q72819 human immun	903	36.5	8.6	88	5	Q9VUN4	Q9VUN4 drosophila
831	37	8.7	90	15	Q72819	Q72819 human immun	904	36.5	8.6	88	8	Q34242	Q34242 calyptogena
832	37	8.7	90	15	Q72819	Q72819 human immun	905	36.5	8.6	88	8	Q34244	Q34244 calyptogena
833	36.5	8.6	43	16	Q9CHS4	Q9CHS4 lactococcus	906	36.5	8.6	89	15	Q9YV33	Q9YV33 human immun
834	36.5	8.6	47	5	Q9VBF3	Q9VBF3 drosophila	907	36.5	8.6	89	15	Q9YV33	Q9YV33 human immun
835	36.5	8.6	50	15	Q9B372	Q9B372 human immun	908	36.5	8.6	89	15	Q9YV33	Q9YV33 human immun
836	36.5	8.6	53	16	Q4165	Q4165 streptomyce	909	36.5	8.6	89	15	Q9YV31	Q9YV31 human immun
837	36.5	8.6	58	10	Q9X14	Q9X14 oryza sativ	910	36.5	8.6	89	15	Q9YV29	Q9YV29 human immun
838	36.5	8.6	58	16	Q9KAY9	Q9KAY9 bacillus ha	911	36.5	8.6	89	15	Q9YV26	Q9YV26 human immun
839	36.5	8.6	59	5	Q9NCR6	Q9NCR6 cryptospori	912	36.5	8.6	89	15	Q38040	Q38040 human immun
840	36.5	8.6	61	16	Q8VKNO	Q8VKNO mycobacteri	913	36.5	8.6	89	15	Q38041	Q38041 human immun
841	36.5	8.6	62	4	Q96DC3	Q96DC3 homo sapien	914	36.5	8.6	89	15	Q38042	Q38042 human immun
842	36.5	8.6	62	17	Q73988	Q73988 pyrococcus	915	36.5	8.6	89	15	Q38043	Q38043 human immun
843	36.5	8.6	63	6	Q8S081	Q8S081 pengo pygma	916	36.5	8.6	89	15	Q38044	Q38044 human immun
844	36.5	8.6	63	9	Q9FZV8	Q9FZV8 bacterioph	917	36.5	8.6	89	15	Q38045	Q38045 human immun
845	36.5	8.6	64	13	Q31950	Q31950 gallus gall	918	36.5	8.6	89	15	Q38046	Q38046 human immun
846	36.5	8.6	66	9	Q47322	Q47322 bacterioph	919	36.5	8.6	89	15	Q38047	Q38047 human immun
847	36.5	8.6	66	16	Q9X044	Q9X044 ralstonia s	920	36.5	8.6	89	15	Q38048	Q38048 human immun
848	36.5	8.6	67	2	Q8VW06	Q8VW06 helicobacte	921	36.5	8.6	89	15	Q38049	Q38049 human immun
849	36.5	8.6	68	2	Q8VW06	Q8VW06 helicobacte	922	36.5	8.6	89	15	Q38052	Q38052 human immun
850	36.5	8.6	68	15	Q74306	Q74306 human immun	923	36.5	8.6	89	15	Q38054	Q38054 human immun
851	36.5	8.6	68	16	Q8VJH4	Q8VJH4 mycobacteri	924	36.5	8.6	89	15	Q38055	Q38055 human immun
852	36.5	8.6	69	15	Q9WU00	Q9WU00 human immun	925	36.5	8.6	89	15	Q38056	Q38056 human immun
853	36.5	8.6	70	4	Q9H363	Q9H363 homo sapien	926	36.5	8.6	89	15	Q38057	Q38057 human immun
854	36.5	8.6	71	16	Q99SP6	Q99SP6 staphylococ	927	36.5	8.6	89	15	Q38058	Q38058 human immun
855	36.5	8.6	72	3	Q8WZU1	Q8WZU1 neurospora	928	36.5	8.6	89	15	Q38059	Q38059 human immun
856	36.5	8.6	72	6	Q18889	Q18889 ateles belz	929	36.5	8.6	89	15	Q38060	Q38060 human immun
857	36.5	8.6	72	6	Q18889	Q18889 ateles belz	930	36.5	8.6	89	15	Q38061	Q38061 human immun
858	36.5	8.6	72	6	Q18889	Q18889 ateles belz	931	36.5	8.6	89	15	Q38062	Q38062 human immun
859	36.5	8.6	72	11	Q9C2U1	Q9C2U1 mus muscullu	932	36.5	8.6	89	15	Q38065	Q38065 human immun
860	36.5	8.6	72	11	Q9C2U1	Q9C2U1 mus muscullu	933	36.5	8.6	89	15	Q38067	Q38067 human immun
861	36.5	8.6	74	4	Q9CR64	Q9CR64 mus muscullu	934	36.5	8.6	89	15	Q38068	Q38068 human immun
862	36.5	8.6	75	12	Q41955	Q41955 murid herpe	935	36.5	8.6	89	15	Q9W13	Q9W13 human immun
863	36.5	8.6	75	16	Q8X167	Q8X167 clostridium	936	36.5	8.6	89	16	Q9F7F9	Q9F7F9 rhizobium l
864	36.5	8.6	76	12	Q64949	Q64949 avian infec	937	36.5	8.6	90	16	Q9PFH0	Q9PFH0 xylella fas
865	36.5	8.6	78	2	Q9K114	Q9K114 streptomyce	938	36	8.5	40	13	Q9PV59	Q9PV59 acipenser s
866	36.5	8.6	78	17	Q30275	Q30275 archaeoglob	939	36	8.5	42	16	Q8X034	Q8X034 ralstonia s
867	36.5	8.6	79	15	Q93389	Q93389 human immun	940	36	8.5	44	2	Q9EX07	Q9EX07 clostridium
868	36.5	8.6	79	15	Q93389	Q93389 human immun	941	36	8.5	47	15	Q87252	Q87252 chimpanzee
869	36.5	8.6	79	15	Q93389	Q93389 human immun	942	36	8.5	47	16	Q97L29	Q97L29 clostridium
870	36.5	8.6	79	17	Q98X06	Q98X06 streptomyce	943	36	8.5	48	10	Q9W370	Q9W370 betula verr
871	36.5	8.6	80	12	Q8QX7	Q8QX7 halobacteri	944	36	8.5	48	10	Q91942	Q91942 xiphophorus
872	36.5	8.6	80	12	Q8QX7	Q8QX7 white spot	945	36	8.5	50	3	Q20195	Q20195 caenorhabdi
873	36.5	8.6	80	15	Q90V64	Q90V64 human immun	946	36	8.5	50	3	Q20195	Q20195 caenorhabdi
874	36.5	8.6	80	15	Q90V64	Q90V64 human immun	947	36	8.5	52	15	Q87372	Q87372 chimpanzee
875	36.5	8.6	80	15	Q90V64	Q90V64 human immun	948	36	8.5	52	16	Q9PGQ3	Q9PGQ3 xylella fas
876	36.5	8.6	81	12	Q36600	Q36600 hepatitis e	949	36	8.5	53	15	Q87347	Q87347 chimpanzee
877	36.5	8.6	81	12	Q36601	Q36601 hepatitis e	950	36	8.5	53	15	Q87402	Q87402 chimpanzee
878	36.5	8.6	81	12	Q36602	Q36602 hepatitis e	951	36	8.5	53	16	Q8U5R8	Q8U5R8 agrobacteri
879	36.5	8.6	81	12	Q36603	Q36603 hepatitis e	952	36	8.5	55	4	Q15281	Q15281 homo sapien
880	36.5	8.6	81	15	Q91893	Q91893 human immun	953	36	8.5	55	12	Q8V0G5	Q8V0G5 asinine her
881	36.5	8.6	81	15	Q930E4	Q930E4 human immun	954	36	8.5	55	12	Q8V0G4	Q8V0G4 asinine her
882	36.5	8.6	81	15	Q98ZV4	Q98ZV4 human immun	955	36	8.5	55	12	Q8V0G3	Q8V0G3 asinine her
883	36.5	8.6	81	15	Q8UPP8	Q8UPP8 human immun	956	36	8.5	56	4	Q9NVE3	Q9NVE3 streptomyce
884	36.5	8.6	81	15	Q8UPN1	Q8UPN1 human immun	957	36	8.5	56	4	Q96HT7	Q96HT7 homo sapien
885	36.5	8.6	81	15	Q8UPM2	Q8UPM2 human immun	958	36	8.5	56	4	Q95J69	Q95J69 pan troglod
886	36.5	8.6	82	15	Q8UPM2	Q8UPM2 human immun	959	36	8.5	56	12	Q9WPH2	Q9WPH2 equine herp
887	36.5	8.6	82	15	Q8UPM2	Q8UPM2 human immun	960	36	8.5	56	12	Q8V0G2	Q8V0G2 asinine her
888	36.5	8.6	83	11	Q63174	Q63174 rattus norv	961	36	8.5	56	12	Q8V0G1	Q8V0G1 asinine her
889	36.5	8.6	83	11	Q63174	Q63174 rattus norv	962	36	8.5	56	12	Q8V0G0	Q8V0G0 asinine her
890	36.5	8.6	83	16	Q9YKZ3	Q9YKZ3 human immun	963	36	8.5	56	12	Q8V0F9	Q8V0F9 asinine her
891	36.5	8.6	84	9	Q9YTR3	Q9YTR3 staphylococ	964	36	8.5	56	16	Q9ECK2	Q9ECK2 xylella fas
892	36.5	8.6	84	17	Q9W6P6	Q9W6P6 bacterioph	965	36	8.5	56	16	Q97RW6	Q97RW6 streptococ



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RA  SEQUENCE FROM N.A.
RT  "Studies on the tail region of the temperate coliphage 186 genome.";
RL  Thesis (1993), University of Adelaide.
RN  [2]

RP  SEQUENCE FROM N.A.
RX  MEDLINE-983711265; PubMed-9705261;
RA  Portelli R., Dodd I.B., Xue Q., Egan J.B.;
RT  "The late-expressed region of the temperate coliphage 186 genome.";
RL  Virology 248:117-130(1998)
DR  EMBL; U32222; AAC34169.1;
FT  NON_TER 1 1
FT  VARIANT 15 15 S -> *
FT  VARIANT 51 51 O -> *
SQ  SEQUENCE 58 AA; 6491 MW; 1199113D8CDEB8E6 CRC64;

Query Match 13.2%; Score 56; DB 9; Length 58;
Best Local Similarity 38.5%; Pred. No. 35;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 38 PTEALSVAVEEGLAWRKKGCLRLGTH 63
Db 31 PSELYSLSTELITWREKALQSRGNH 56

RESULT 4
ID Q23341 PRELIMINARY; PRT; 80 AA.
AC Q23341;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypothetical 8.5 kDa protein.
GN ZC477.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Du 2.;
RT "The sequence of C. elegans cosmid ZC477.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U40802; AAK19010.1; -.
KW Hypothetical protein.
SQ SEQUENCE 80 AA; 8481 MW; AE43A8268EB6C423 CRC64;

Query Match 12.8%; Score 54; DB 5; Length 80;
Best Local Similarity 28.4%; Pred. No. 89;
Matches 23; Conservative 9; Mismatches 35; Indels 14; Gaps 2;

QY 6 CSSOSISPMBSISNSLVAMDSGOKSRVNPTEALSVAVEEGLAWRKKGCLRLGTHGS 65
Db 4 CSPKILPAGSSSSSTT-----SSQIRPPLSLASLSEELRVEECSPRVGAKES 56
QY 66 -----PTASSOSSATNMAI 79
Db 57 SFYCTEQPAQSSYSREDKLC 77

RESULT 5
ID Q9JMT2 PRELIMINARY; PRT; 84 AA.
AC Q9JMT2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE YbgA protein.
DE YbgA protein.
GN YbgA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX Shmizu H., Saitoh Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.;
RT "Complete nucleotide sequence of the F plasmid: Its implications for
organization and diversification of plasmid genomes.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-90317835; PubMed-2164585;
RA Yoshida Y., Fujita Y., Ohnubo E.;
RT "Nucleotide sequence of the promoter-distal region of the tra operon
of plasmid R100, including traI (DNA helicase I) and traD genes.";
RL J. Mol. Biol. 214:39-53(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-87194554; PubMed-3032897;
RA Saadi S., Maas W.K., Hill D.F., Bergquist P.L.;
RT "Nucleotide sequence analysis of RepFIC, a basic replicon present in
IncFII plasmids P307 and F, and its relation to the RepA replicon of
IncFII plasmids.";
RL J. Bacteriol. 169:1836-1846(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-95337425; PubMed-7612932;
RA Broom J.E., Hill D.F., Hughes G., Jones W.A., McNaughton J.C.,
RA Stockwell P.A., Petersen G.B.;
RT "Sequence of a transposon identified as Tn1000 (gamma delta).";
RL DNA Seq. 5:185-189(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Eichenlaub R.;
RT "F plasmid DNA complete mini-F region (F coordinates 40.301F to
49.869F).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-86139669; PubMed-3949712;
RA Helsenberg M., Eichenlaub R.;
RT "Twelve 43-base-pair repeats map in a cis-acting region essential for
partition of plasmid mini-F.";
RL J. Bacteriol. 165:1043-1045(1986).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE-99296678; PubMed-10366527;
RA Manwaring N.P., Skurray R.A., Firth N.;
RT "Nucleotide sequence of the F plasmid leading region.";
RL Plasmid 41:219-225(1999).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE-94359430; PubMed-7915817;
RA Frost L.S., Ippen-Ihler K., Skurray R.A.;
RT "An analysis of the sequence and gene products of the transfer region
of the F sex factor.";
RL Microbiol. Rev. 58:162-210(1994).
DR EMBL; AP001918; BAA97888.1; -.
KW Plasmid; Complete proteome.
SQ SEQUENCE 84 AA; 9265 MW; 183C60CAF87121F7 CRC64;

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Query Match      12.5%; Score 53; DB 12; Length 80;
Best Local Similarity 25.6%; Pred. NO. 1.2e+02;
Matches 20; Conservative 12; Mismatches 28; Indels 18; Gaps 2;
QY 13 PMRSISSENSIVAMDFSGKSRV-----IENPTAALSVAAVEEGLAWRKKGLRLGTG 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 PVARSGPSHVGELADPGDFLEWVGRGNLYISPPGOARISISRGTA-----KHT 55

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QY      65 SPYASSOASATMIAHRS 82
      I : : : I I I
Db      56 SSSSSSSSSSQPELIORS 73

RESULT 7
OS7347 PRELIMINARY; PRT; 88 AA.
AC OS7347;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Beta Bl-crystallin (Fragment).
OS xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCHI_TaxID=8355;
RN [1] RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97312614; PubMed=9169055;
RT Alnemati C.R., Chow P.L., Laog R.A., Hemmati-Brivanlou A.;
RN "Lens induction by Pax-6 in Xenopus laevis.";
RL Dev. Biol. 185:110-123 (1997).
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF
CC THE VERTEBRATE EYE LENS (BY SIMILARITY).
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY
CC -1- SIMILAR GREEK KEY MOTIFS (BY SIMILARITY).
CC EMBL: AF035363; AAB87702.1;
DR HSSP; P26775; IBD7.
DR InterPro: IPR001064; Crystallin.
DR Pfam; PF00300; crystall; 2.
DR SMART; SM00247; XTALbg; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR Duplication; Eye lens protein.
KW NON_TER 1
KW NON_TER 1
FT NON_TER 88
FT NON_TER 88
SQ SEQUENCE 88 AA; 10461 MW; A9164E3275EE0E1E CRC64;

Query Match 12.1%; Score 51; DB 13; Length 88;
Best Local Similarity 26.6%; Pred. No. 2.2e+02;
Matches 17; Conservative 10; Mismatches 23; Indels 14; Gaps
QY 3 RSGCGSSQSTSPMRKSTENSELVAM----DFSGQKSRVIENTPEALSAVEGLAWRKKGCL 58
Db 14 RSDC-FMSARPIRMDNQEHKIFLECTDFKGNKMEIIDDVPSL-----WAYGFCD 63
QY 59 RLGT 62
Db 64 RVGS 67

RESULT 8
Q9NFC8 PRELIMINARY; PRT; 65 AA.
AC Q9NFC8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG18844 protein.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Gallie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-Y., Andrews-Pfannkuch C., Baldwin D.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Beasley E.M.,  
 RA Borkova D., Botchan M.R., Beck J., Butler H., Bhandari P., Bolshakov S.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evansgela C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glueck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,  
 RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003423; AAG22397.1;  
 DR Flybase; FBgn0042164; CG18844.  
 DR InterPro; IPR001395; Aldo/ket\_red.  
 DR PROSITE; PS00063; ALDOXETO\_REDUCTASE\_3; UNKNOWN 1.  
 SQ SEQUENCE 65 AA; 7223 MW; 5E84BC8FEDC92DFD CRC64;  
 Query Match 11.5%; Score 48.5; DB 5; Length 65;  
 Best Local Similarity 37.5%; Pred. No. 3e+02;  
 Matches 15; Conservative 4; Mismatches 12; Indels 9; Gaps 2;  
 QY 3 RSGCS-----SOSISPMR-SISENSLVAMDFSGOKSR 33  
 DB 12 RRGCCATSSKMLARSVSPNRFSSANFIQVTFSGPNSR 51  
 RESULT 9  
 Q9BD73 PRELIMINARY; PRT; 90 AA.  
 AC Q9BD73  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DE MHC class II antigen beta chain (Fragment).  
 GN DLA-DRA1.  
 OS Canis lupus (Gray wolf).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9612;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kennedy L.J., Angles J.M.;  
 RT "Nomenclature for the DLA system, 2000: Second report of the ISAG DLA  
 RT Nomenclature Committee";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF343738; AAK13509.1;  
 FT NON\_TER 1  
 FT NON\_TER 90  
 SQ SEQUENCE 90 AA; 9600 MW; D4F5E19F28AD13AF CRC64;  
 Query Match 11.5%; Score 48.5; DB 7; Length 90;  
 Best Local Similarity 29.08; Pred. No. 4.4e+02;  
 Matches 20; Conservative 8; Mismatches 34; Indels 7; Gaps 2;  
 QY 2 GRSGCSQSISPMRSISENSLVAMDFSGOKSRVIENTEALSVAVEGLAWKKGCLRLG 61  
 DB 16 GRSGCSQKMDTSITGRCTASTWGTGRSRSSGGPT--LSPGTRRRSSWSGR-----G 68  
 QY 62 THCSPTASS 70  
 DB 69 PRWTPADT 77  
 RESULT 10  
 Q9R6C9 PRELIMINARY; PRT; 89 AA.  
 AC Q9R6C9  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE TIORF132 protein (Hypothetical protein At06153).  
 DE TIORF132 OR AT06153 OR AGR\_PTI\_BX147.  
 GN Agrobacterium tumefaciens, and  
 OS Agrobacterium tumefaciens, (strain C58 / ATCC 33970).  
 OC Plasmid pTI-SAKURA and Plasmid pTIC58.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 NCBI\_TaxID=358, 176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=A.tumefaciens; STRAIN=MAFF301001; PLASMID=PTI-SAKURA;  
 RX MEDLINE=20184752; PubMed=10721727;  
 RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,  
 RA "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid";  
 RT Gene 242:331-336(2000).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=A.tumefaciens; STRAIN=MAFF301001; PLASMID=PTI-SAKURA;  
 RX MEDLINE=98193120; PubMed=9524202;  
 RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;  
 RT "Novel structural difference between nopaline- and octopine-type trbJ  
 RT gene: construction of genetic and physical map and sequencing of  
 RT trbJ/traI and rep gene clusters of a new Ti plasmid pTI-SAKURA";  
 RL Biochim. Biophys. Acta 1396:1-7(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=A.tumefaciens; STRAIN=MAFF301001; PLASMID=PTI-SAKURA;  
 RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;  
 RT "Genome structure of pTI-SAKURA(I): Strategy for DNA sequencing of a  
 RT Japanese cherry-ti plasmid";  
 RL Nucleic Acids Symp. Ser. 37:159-160(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=A.tumefaciens; STRAIN=MAFF301001; PLASMID=PTI-SAKURA;  
 RA Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;  
 RT "Genome structure of pTI-SAKURA (III): Characteristics of T-DNA";  
 RL Nucleic Acids Symp. Ser. 39:185-186(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=A.tumefaciens; STRAIN=MAFF301001; PLASMID=PTI-SAKURA;  
 RA Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;



"Genome structure of pTi-SAKURA (IV): Characteristics of tra region." ; Nucleic Acids Symp. Ser. 39:187-188(1998).

[16] Nucleic Acids Symp. Ser. 39:163-166(1996).

RP SEQUENCE FROM N.A.

RC SPECIES=A.tumefaciens; STRAIN=MAFF301001; PLASMID=PRI-SAKURA;

RC Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;

RT Genome structure of pri-SAKURA (V): Complete nucleotide sequence of

RT plasmid pri-SAKURA's vir region in Agrobacterium tumefaciens.;

RT Nucleic Acids Symp. Ser. 39:265-266(1998).

RT [17]

RP SEQUENCE FROM N.A.

RP SPECIES=A.tumefaciens (strain C58 / ATCC 33970); PLASMID=PTIC58;

RP MEDLINE=2160850; PubMed=1174319;

RC Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida M.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,

RA Chapman P., Clendinning T., Deatherage G., Gillet W., Grant C.,

RA Kutyavyn T., Levy R., Li M.-J., McClelland E., Palmeri A.,

RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.F., Gordon M.P., Olson M.V.,

RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

RT C58.;"

RT Sci. 294:2317-2323(2001).

RL	Science 294:2317-2323(2001).
RN	[8].
RN	SEQUENCE FROM N.A.
RP	SPECIES-A tumefaciens (strain C58 / ATCC 33970); PLASMID-PTTC58;
RC	MEDLINE-Z1608351; Pubmed-11741394;
RC	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA	Quorillo B., Goldman B.-S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA	Houmel K., Gordon J., Vaudin M., Dartchouk O., Epp A., Liu F.,
RA	Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA	Fianagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA	Cielo C., Slater S.
RT	Genome sequence of the plant pathogen and biotechnology agent
RT	<i>Agrobacterium tumefaciens</i> C58.*
RT	Agrobacterium tumefaciens C58.*
RT	Science 294:2323-2328(2001).
DR	EMBL; AB016260; BAA87757.1; -
DR	EMBL; AB009434; AAL46389.1; -
DR	EMBL; AE007941; AAK91116.1; -
DR	EMBL; AE007941; AAK91116.1; -
DR	Hypothetical protein; Plasmid; Complete proteome.
SK	SEQUENCE 89 AA; 9939 MW; 913CC000126DBE9C CRC64;
QW	

Query Match 11.3%; Score 48; DB 16; Length 89;  
Best Local Similarity 41.2%; Pred. No. 5e+02;  
Matches 14; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

**Qy** 28 SGQSRVIENTEALSVAVEEGLAWRKKGCRLRG 61  
- : ||||| - : ||| : |||  
**Dd** 29 SQRKSRV-----PCSLAVTSSMLHRQKGAVRLG 56

RESULT 11		Q93D08	
ID	Q93D08	PRELIMINARY:	PRT; 90 AA.
DC	Q93D08; 2001 (TReMBUrel. 19, Created)		
DT	01-DEC-2001 (TReMBUrel. 19, Last sequence update)		
DT	01-DEC-2001 (TReMBUrel. 19, Last annotation update)		
DE	Hypothetical 9.9 kDa protein.		
OS	Unidentified bacterium.		
OC	Bacteria; environmental samples.		
OX	NCBI_TaxID=2338;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2136188; PubMed=11679351;		
RA	Stokes H.W., Holmes A.J., Nield B.S., Holley M.P., Nevalainen K.M.H.,		
RB	Mabbitt B.C., Gillings M.R.;		
RT	"Gene Cassette PCR: Sequence-Independent Recovery of Entire Genes from		
RA	Environmental DNA.,"		
RL	Appl. Environ. Microbiol. 67:5240-5246(2001).		

DR EMBL; AF378539; AAK56383.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 90 AA; 9906 MW; 281676BA0DAEA28A CRC64;

Query Match 11.3%; Score 48; DB 2; Length 90;  
Best Local Similarity 28.1%; Pred. No. 5.1e+02;  
Matches 18; Conservative 14; Mismatches 26; Indels 6; Gaps 3;

QY . 5 GCSSQSIS:PMRSISENSLVAMDFSGOKSRVIENPTAELSVAVEGLAWRKKC--LRLG 61  
| : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 22 GVADQAMSAEFRSLDDCLSGIKESSGKELKIITNEPEVSGLSNGKF---GCQEKRSRG 78

Qy	62	THGS	65
		:	
Db	79	TKGT	82

RESULT 12	
Q9J125	
ID	PRELIMINARY; PR7; 66 AA.
Q9J125	
AC	Q9J125
AD	01-OCT-2000 (TREMBLrel. 15, Created)
AT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 15, Last annotation update)
DE	Gag protein (Fragment).
DN	GAG.
OS	Human immunodeficiency virus type 1.
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11676;
ON	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=FIN9399;
RA	Liltsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkontio H.,
RA	Leinikki P., Salminen M.O.;
RT	"Analysis of HIV-1 genetic subtypes in Finland reveals good
RT	correlation between molecular and epidemiological data.";
RL	Scand. J. Infect. Dis. 0:0-0(2000).
RL	EMBL; AF219348; AAF30254.1; "
DR	HSSP; P05888; 1AAF.
DT	NON_TER 1
FT	NON_TER 1
FT	66
FT	66
SO	SEQUENCE 66 AA; 7236 MW; F74F42FF9F24AD6E CRC64:

Query Match	11.28;	Score 47.5;	DB 15;	Length 66;
Best Local Similarity	35.98;	Pred. No. 4e+02;		
Matches 14;	Conservative 4;	Mismatches 20;	Indels 1;	Gaps 1;

QY	26	DFSGKSRVIENPT	TEALSVAVEEGL	AWRRKKGCLRLG	THG	64
		: ↓ ↓ :	: ↓ ↓ :	: ↓ ↓ ↓ :	: ↓ ↓ ↓ :	
Db	28	NFKGOR-RXLSA	STVAEGHILARN	CRAPRKKGCKKEG	65	

[illegible]

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
 RA Yeh K.-C., Davis R.W., Federapfel N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire  
 RT Sinorhizobium meliloti pSymA megaplasmid.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
 DR EMBL: AE007230; AAK05048.1; -;  
 KW Hypothetical protein; plasmid; Complete proteome.  
 SQ SEQUENCE 90 AA; 9914 MW; CC9E8095982DD1D5 CRC64;

Query Match 11.2%; Score 47.5; DB 16; Length 90;  
 Best Local Similarity 22.1%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 15; Mismatches 19; Indels 19; Gaps 3;  
 QY 11 ISPMRSISNSLVAMDFSGOKSRVIENTEALSVAVVEGLAW-----BKKGLRL-CT 62  
 DB 11 VAPKDLDDTMSAADFA-----QLFGVYTOGSMWETFYERGQADGIFRLSGT 59  
 QY 63 HGSPTASS 70  
 DB 60 RKTNPSS 67

RESULT 14  
 Q8ROX3  
 ID Q8ROX3 PRELIMINARY; PRT; 79 AA.  
 AC Q8ROX3;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Similar to LOC164714.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=THYMUS GLAND;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC026208; AAK26208.1; -;  
 SQ SEQUENCE 79 AA; 8632 MW; 806C30C3455C10BE CRC64;

Query Match 11.1%; Score 47; DB 11; Length 79;  
 Best Local Similarity 28.0%; Pred. No. 5.7e+02;  
 Matches 14; Conservative 5; Mismatches 11; Indels 20; Gaps 2;  
 QY 37 NPTALSVAVEEG-----LAWRKGC-----LRLGTHGSP 66  
 DB 16 HPERLCFSATOGIHAGSLNRRPCTGLQTIEFSROYLHGERLCTRGAP 65

RESULT 15  
 Q30681  
 ID Q30681 PRELIMINARY; PRT; 86 AA.  
 AC Q30681;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Plasmid pFAJ2600 putative plasmid multimer resolution  
 DE putative DNA-binding replication protein (repB), putative replication  
 DE protein (repA), and putative plasmid partitioning protein (para)  
 DE genes.  
 OS Rhodococcus erythropolis.  
 OG Plasmid pFAJ2600.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=1833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NI86721;  
 RA MEDLINE=98015402; PubMed=9353918;  
 RA De Mot R., Nagy I., De Schrijver A., Pattanapitpaisal P.,  
 RA Schoofs G., Vanderleyden J.;

RT "Structural analysis of the 6-kb cryptic plasmid pFAJ2600 from  
 RT Rhodococcus erythropolis NI86/21 and construction of Escherichia coli-  
 RT Rhodococcus shuttle vectors.";  
 RL Microbiology 143:3137-3147(1997).  
 DR EMBL: AP013088; AAC45810.1; -;  
 KW Plasmid.  
 SQ SEQUENCE 86 AA; 9140 MW; CB240A7B86386B18 CRC64;

Query Match 11.1%; Score 47; DB 2; Length 86;  
 Best Local Similarity 22.0%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 18; Mismatches 40; Indels 6; Gaps 3;  
 QY 3 RSCGSSQSSISPMRSISNSLVAMDFSGOKSRVIENTEALSVAVVEGLAWRKKGCLRLG- 61  
 DB 4 RSGTSHPVPRPTGLGVAELA-VQMNHPGAGGDC--DLTRRMQIWHVHGSSMLRRGGGOMAW 60  
 QY 62 --THGSPATASSOSSATNMAIHR 81  
 DB 61 RVAHVHTLAEGVNTAAGGVHR 82

RESULT 16  
 Q9RCDA  
 ID Q9RCDA PRELIMINARY; PRT; 79 AA.  
 AC Q9RCDA;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical 8.6 kDa protein.  
 OS Xanthomonas campestris.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xanthomonas.  
 OX NCBI\_TaxID=339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TAP44-3; TRANSPOSON=TN5044;  
 RX MEDLINE=99406912; PubMed=10476039;  
 RA Minakhina S., Kholodii G., Mindlin S., Yurieva O., Nikiforov V.;  
 RT "Tn5053 family transposons are res site hunters sensing plasmid res  
 RT sites occupied by cognate resolvases.";  
 RL Mol. Microbiol. 33:1059-1068(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TAP44-3; TRANSPOSON=TN5044;  
 RA Kholodii G., Yurieva O., Mindlin S., Gorlenko Z., Rybochkin V.,  
 RT "Tn5044, a novel Tn3 family transposon coding for temperature  
 RT sensitive mercury resistance.";  
 RL Res. Microbiol. 151:1-12(2000).  
 DR EMBL: Y17691; CAB65713.1; -;  
 KW Hypothetical protein; Plasmid.  
 SQ SEQUENCE 79 AA; 8626 MW; 1639B3E026E36706 CRC64;

Query Match 11.0%; Score 46.5; DB 2; Length 79;  
 Best Local Similarity 31.0%; Pred. No. 6.5e+02;  
 Matches 18; Conservative 14; Mismatches 15; Indels 11; Gaps 4;  
 QY 2 GRSCGSSQSSISPMRSISNSLVAMDFSGOKSRVIB-NPTEA-LSVAVVEGLAWRK 55  
 DB 28 GRKGLSRFI-----EEAVRAHILELSAQKAVNAHLSEALTDVADEALAWASK 78

RESULT 17  
 Q96U90  
 ID Q96U90 PRELIMINARY; PRT; 80 AA.  
 AC Q96U90;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Probable ribosomal protein S19, mitochondrial.  
 GN BII09.070.  
 OS Neurospora crassa.

OC Eukaryota; Fungi; ASCOMYCOTA; Pezizomycotina; Sordariomycetes;  
 OC Sordariales; Sordariaceae; Neurospora.  
 OC NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schnite U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL513409; CAD11378.1; -  
 DR InterPro; IPR002222; Ribosomal\_S19.  
 DR Pfam; PF00203; Ribosomal\_S19; 1.  
 DR ProDom; PD001012; Ribosomal\_S19; 1.  
 KW Ribosomal protein.  
 SQ SEQUENCE 80 AA; 9018 MW; DA38F8D77C20E041 CRC64;  
 Query Match 11.0%; Score 46.5; DB 3; Length 80;  
 Best Local Similarity 25.0%; Pred. No. 6.6e+02;  
 Matches 12; Conservative 14; Mismatches 21; Indels 1; Gaps 1;  
 QY 9 OSISPMRSISENSLVAMDFSGOKSRVIENTPEALSVAVEEGLAWRKKG 56  
 DB 30 KKIAPIRQARSAILPNFVGLKQVQV-HNGKDYIDLTVTEEMVGHKLK 76  
 RESULT 18  
 QY 098K26 PRELIMINARY; PRT; 88 AA.  
 AC 098K26;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein msr1249.  
 GN MSR1249.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OC NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Iidosawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP002997; BAB48667.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 88 AA; 9552 MW; DA4EE5FE549D2D2C CRC64;  
 Query Match 11.0%; Score 46.5; DB 16; Length 88;  
 Best Local Similarity 22.0%; Pred. No. 7.4e+02;  
 Matches 11; Conservative 13; Mismatches 25; Indels 1; Gaps 1;  
 QY 14 MRSISENSLVAMDFSGOKSRV-IENTPEALSVAVEEGLAWRKKGLRGT 62  
 DB 28 WSLSLGRITATEAARSARYOTERAIRSLPIELQKDIOWPEASDFKTKT 77  
 RESULT 19  
 QY 093KW8 PRELIMINARY; PRT; 90 AA.  
 AC 093KW8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Cysteine proteinase (Fragment).  
 OS Narcissus pseudonarcissus (Daifodil).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;  
 OC Narcissus.  
 OC NCBI\_TaxID=39639;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. DUTCH MASTER; TISSUE=SENESCING TEPALS OF 4-DAY OLD FLOWERS;  
 RA Hunter D.A., Yi M., Reid M.S.;  
 RT "Role of Ethylene and ABA in Perianth Senescence of Daffodil  
 (Narcissus pseudonarcissus L. Dutch Master).";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF420011; AAL16903.1; -  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR Pfam; PF00112; Peptidase\_C1; 1.  
 DR ProDom; PD000158; Peptidase\_C1; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; UNKNOWN\_1.  
 FT NON\_TER 1 90  
 FT NON\_TER 90 90  
 SQ SEQUENCE 90 AA; 9346 MW; 5B7C407359B3A658 CRC64;  
 Query Match 11.0%; Score 46.5; DB 10; Length 90;  
 Best Local Similarity 33.3%; Pred. No. 7.6e+02;  
 Matches 24; Conservative 13; Mismatches 22; Indels 13; Gaps 7;  
 QY 1 QCRSGCSQSISPMRSISENSLVAMDFSGOKSRVIENTPEALSVAVEEGLAWR--KKG 57  
 DB 19 QGR--CSSKK--SPVISIDGYNVPVNEAALMKAVAN--QPVSAIEASGNAPQFYSEGV 73  
 QY 58 L--RLGT---HG 64  
 DB 74 FTGRCGTLDHG 85  
 RESULT 20  
 QY 08VY75 PRELIMINARY; PRT; 54 AA.  
 AC 08VY75;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Putative MYB family transcription factor.  
 GN AT2G16720.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY072387; AAL62379.1; -  
 SQ SEQUENCE 54 AA; 6078 MW; 2A9B672F34B7BEDA CRC64;  
 Query Match 10.9%; Score 46; DB 10; Length 54;  
 Best Local Similarity 31.7%; Pred. No. 4.6e+02;  
 Matches 13; Conservative 9; Mismatches 9; Indels 10; Gaps 2;  
 QY 6 CSSQSI-----SPMRSENSL-----VAMDFSGOKSRVIE 36  
 DB 7 CSSETVKQCTENSSSISSYSSIDISSNVGYDFLGLKTRILD 47  
 RESULT 21  
 QY 076048

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ID Q76048 PRELIMINARY; PRT; 77 AA.
AC Q76048;
AT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE P24/p25/p7 (Fragment).
DN GAG.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;.
RN [1]
RP SEQUENCE FROM N.A.
RA Salminen M.O.;
RT "Rapid and simple characterization of in vivo HIV-1 sequences using
RT solid phase direct sequencing.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93090493; PubMed=1457219;
RA Salminen M.;
RT "Rapid and simple characterization of in vivo HIV-1 sequences using
RT solid-phase direct sequencing.";
RL AIDS Res. Hum. Retroviruses 8:1733-1742(1992).
DR EMBL; Z11145; CAA77496.1;
DR HSSP; P05888; 1AAF
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00096; Zf-CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 2.
FT NON_TER 1
FT CHAIN 1
FT SEQUENCE 77 AA; 77
SQ.
Query Match 10.9%; Score 46; DB 15; Length 77;
Best Local Similarity 23.4%; Pred. No. 7.2e+02;
Matches 15; Conservative 7; Mismatches 14; Indels 28; Gaps:
Qy 29 GKSRLV-----ENPTSLSVAVEEG-----LAWRKKGCLRL 60
Db 1 GHKRLVLAQAAMSKATNAATIMMGRNFRNQRKTVKFCNGKGCHIARNCRAPRKKGCKW 60
Qy 61 GTHG 64
Db 61 GKEG 64
RESULT 22
Q8WMF9 PRELIMINARY; PRT; 86 AA.
ID Q8WMF9
AC Q8WMF9;
AT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE Peptidoglycan recognition protein (Fragment).
DN PGLYRP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=ADIPOSE TISSUE;
RT Kappeler S.R.;
RT "The peptidoglycan recognition protein, PGRP, is expressed in the
RT lactating mammary gland of camels.";
RL submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ310355; CAC83647.1;
FT NON_TER 1
FT CHAIN 1
FT SEQUENCE 86 AA; 9517 MW; BFC5DC02AF1CB25 CRC64;
SQ.
Query Match 10.9%; Score 46; DB 6; Length 86;

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09PCX0	PRELIMINARY;	PRT;	65 AA.
ID	Q9PCX0		
AC	Q9PCX0		
CD	01-OCT-2000 (TRENBUrel. 15, Created)		
DDT	01-OCT-2000 (TRENBUrel. 15, Last sequence update)		
DE	01-MAR-2002 (TRENBUrel. 20, Last annotation update)		
DE	Hypothetical protein Xf1634.		
GN	Xf1634.		
GN	Xylella fastidiosa.		
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;		
OC	Xylella.		
OX	NCBI_TaxID=2371;		
NRN	[1]		
RRP	SEQUENCE FROM N.A.		
RRP	STRAIN=9A5C;		
RRX	MEDLINE=20365717; PubMed=10910347;		
RA	Simpson A.J.G., Reinach P.C., Arruda P., Abreu F.A., Acencio M.,		
RA	Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,		
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,		
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,		
RA	Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,		
RA	Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,		
RA	Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferri J.A.,		
RA	Francia J.S., Francia S.C., Franco M.C., Frohme M., Furlan L.R.,		
RA	Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,		
RA	Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,		
RA	Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,		
RA	Lemos E.G.M., Lemus M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,		
RA	Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,		
RA	Marques C.F.M., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,		
RA	Maneck C.F.M., Maracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,		
RA	Moon D.H., Nagai M.R., Nascimento A.L.T.O., Netto L.E.S.,		
RA	Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,		

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OM protein ~ protein search, using sw model

Run on: March 28, 2003, 08:56:00 ; Search time 18.5197 Seconds  
(without alignments)  
188.125 Million cell updates

188.125 Million cell updates/sec

100

Sequence: 1 QGRSGCSQSISPMRSEN.....SPTASSQSATNMAIHRSQP 84  
 PerfectScore: 4236  
 Evalue: 9.36e-97  
 PercentIdent: 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 7863

Minimum DB	seq length: 40
Maximum DB	seq length: 90

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	12.2	51.5	73	1	RPON_METJ4
2	47	11.1	71	1	Y16K_BP44
3	46.5	11.0	62	1	Y205_METJ4
4	45	10.6	76	1	CD24_RAT
5	45	10.6	79	1	MT2_MALDO
6	45	10.6	82	1	RADC_STA4U
7	44.5	10.5	68	1	GNGL_HUMAN
8	43	10.2	82	1	Y567_METJ4
9	42.5	10.0	67	1	HFO2_METFO
10	42.5	10.0	88	1	RS19_CHLTR
11	42	9.9	45	1	AT12_HSV4
12	42	9.9	78	1	YHG6_ECOLI
13	42	9.9	83	1	THOB_PSPME
14	41.5	9.8	67	1	HPOB_MEFRO
15	41.5	9.8	87	1	RS19_MYCGA
16	41.5	9.8	88	1	C552_MAFYB
17	41.5	9.8	88	1	RS19_CHLPN
18	41	9.7	66	1	RPON_SULSO
19	40.5	9.6	43	1	C03_CACRN
20	40.5	9.6	68	1	GG65_HUMAN
21	40	9.5	41	1	BXAC_HUMAN
22	40	9.5	56	1	H52M_LTCES
23	40	9.5	72	1	RPON_THEAC
24	40	9.5	72	1	RPON_THEVO
25	39.5	9.3	83	1	V18T_BP77
26	39	9.2	43	1	CC4_CACRN
27	39	9.2	43	1	R522_ECOLI
28	39	9.2	85	1	R37A_MYXGL
29	38.5	9.1	54	1	BAF_BORBR
30	38.5	9.1	67	1	CSPF_STRCO
31	38.5	9.1	72	1	Y003_ARCFU
32	38.5	9.1	74	1	C05A_BOVIN
33	38.5	9.1	74	1	NIFI_NOSSN

107	34.5	8.2	89	1	RS14_STRPN	O97sv0 streptococc	180	32.5	7.7	78	1	GVPA_HALME	P23761 halobacteri
108	34.5	8.2	89	1	RS19_XLPA	O9pe72 xylella fas	181	32.5	7.7	78	1	GVPA_NATW	O33397 natronobact
109	34.5	8.2	90	1	RS19_BRAJA	P10335 bradyrhizob	182	32.5	7.7	79	1	MT2_ACTCH	O43390 actinidia c
110	34	8.0	46	1	V11_BPT3	P20833 bacterioph	183	32.5	7.7	79	1	AFB3_RAPSA	O24332 raphanus sa
111	34	8.0	50	1	RS30_AERPE	O9v9t9 aeropyrum p	184	32.5	7.7	80	1	Y906_TREPA	O83876 treponema p
112	34	8.0	51	1	VG62_BPMO2	O64254 mycobacteri	185	32.5	7.7	81	1	VP0_HVILJR	P20882 human immun
113	34	8.0	52	1	RL40_TREYB	P21899 typanosoma	186	32.5	7.7	81	1	VP0_HVILJR	P19554 human immun
114	34	8.0	52	1	RL40_TREYB	P14795 typanosoma	187	32.5	7.7	83	1	C554_PARSF	P00105 paracoccus
115	34	8.0	52	1	Y07K_PNV	P20954 papaya mosa	188	32.5	7.7	83	1	EX7S_BRUME	O8y17 bruceella me
116	34	8.0	71	1	NXLA_BUNMU	O93y74 streptococc	189	32.5	7.7	83	1	Y285_ARCFU	O29984 archaeoglob
117	34	8.0	74	1	Y82C_SSV1	P01378 streptococc	190	32.5	7.7	87	1	Y898_MYCTU	O10566 mycobacteri
118	34	8.0	77	1	Y82C_SSV1	P20994 vaccinia vi	191	32.5	7.7	87	1	YFJM_ECCLI	P52128 escherichia
119	34	8.0	79	1	YH65_SVNY3	P72913 synecocyst	192	32.5	7.7	87	1	HG17_CHICK	P02314 gallus gall
120	34	8.0	86	1	VPW_OMVVS	P19510 ovine lentil	193	32.5	7.7	89	1	RS20_HELPJ	O9zmz1 helicobacte
121	34	8.0	86	1	YH65_SVNY3	P81290 bacillus st	194	32.5	7.7	89	1	PTSO_ECCLI	P36027 escherichia
122	34	8.0	88	1	RS16_BACST	P33801 bacterioph	195	32.5	7.7	90	1	RHT3_RHOTO	P33996 rhodospirid
123	34	8.0	88	1	Y12E_BPT7	P33084 bacterioph	196	32.5	7.7	90	1	RHT3_RHOTO	O28197 archaeoglob
124	34	8.0	89	1	Y12E_BPT7	O92ct1 rickettsia	197	32.5	7.7	90	1	RHT3_RHOTO	P36388 akodon azar
125	34	8.0	90	1	RS20_RICPR	O48425 bacterioph	198	32.5	7.7	90	1	RHT3_RHOTO	P36388 akodon azar
126	33.5	7.9	58	1	NINP_BEH19	O95705 hylobates l	199	32.5	7.7	54	1	SRV_AKOAZ	P05558 rhea americ
127	33.5	7.9	68	1	ATP8_HYLLA	P01522 conus geogr	200	32.5	7.7	54	1	Y058_NPVAC	P41462 autographa
128	33.5	7.9	73	1	Y165_SVNP6	P05676 synecococc	201	32.5	7.7	57	1	RS21_CLOPE	O8xiu0 clostridium
129	33.5	7.9	77	1	PSAC_SRECO	O96804 skeletonema	202	32.5	7.7	58	1	NAS1_ASTST	P01438 astrotia st
130	33.5	7.9	80	1	DEF8_MOUSE	P50706 mus musculu	203	32.5	7.7	62	1	V452_BPT4	P07878 bacterioph
131	33.5	7.9	81	1	PSAC_ODOSI	P49477 odontella s	204	32.5	7.7	63	1	YDIE_ECCLI	P40721 escherichia
132	33.5	7.9	82	1	DEF8_MOUSE	O64016 mus musculu	205	32.5	7.7	64	1	PHYE_PHYBI	P81565 phylomedusa
133	33.5	7.9	82	1	YFTD_METFE	P56509 methanother	206	32.5	7.7	64	1	YEEW_ECCLI	P76366 escherichia
134	33.5	7.9	83	1	RT19_PLASU	P50893 platyomonas	207	32.5	7.7	65	1	RK33_MAIZE	P25461 zea mays (m
135	33.5	7.9	83	1	NER_HUMAN	O00479 homo sapien	208	32.5	7.7	66	1	CADO_BUNCA	P81783 bungarus ca
136	33.5	7.9	89	1	YH73_HUMAN	P46496 haemophilus	209	32.5	7.7	66	1	HST_YERKR	P31518 yersinia kr
137	33.5	7.9	89	1	YH73_HUMAN	P03785 bacterioph	210	32.5	7.7	66	1	HST_YERKR	P38040 drosophila
138	33.5	7.9	89	1	YH73_HUMAN	P58924 conus geogr	211	32.5	7.7	70	1	YVAK_VACCC	P20520 vaccinia vi
139	33	7.8	42	1	YH73_HUMAN	P81244 proclosporid	212	32.5	7.7	71	1	ICIA_SOLTU	P01052 solanum tub
140	33	7.8	45	1	YH73_HUMAN	P81244 proclosporid	213	32.5	7.7	71	1	YVAK_VACCC	P46878 escherichia
141	33	7.8	52	1	YH73_HUMAN	P81244 proclosporid	214	32.5	7.7	71	1	YVAK_VACCC	P33872 variola vir
142	33	7.8	52	1	YH73_HUMAN	P81244 proclosporid	215	32.5	7.7	73	1	YVAK_VACCC	P33872 variola vir
143	33	7.8	56	1	YH73_HUMAN	P81244 proclosporid	216	32.5	7.7	75	1	YH73_HUMAN	P33872 variola vir
144	33	7.8	61	1	YH73_HUMAN	P81244 proclosporid	217	32.5	7.7	75	1	YH73_HUMAN	P33872 variola vir
145	33	7.8	61	1	YH73_HUMAN	P81244 proclosporid	218	32.5	7.7	75	1	YH73_HUMAN	P33872 variola vir
146	33	7.8	62	1	YH73_HUMAN	P81244 proclosporid	219	32.5	7.7	76	1	YH73_HUMAN	P33872 variola vir
147	33	7.8	62	1	YH73_HUMAN	P81244 proclosporid	220	32.5	7.7	76	1	YH73_HUMAN	P33872 variola vir
148	33	7.8	72	1	YH73_HUMAN	P81244 proclosporid	221	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
149	33	7.8	72	1	YH73_HUMAN	P81244 proclosporid	222	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
150	33	7.8	72	1	YH73_HUMAN	P81244 proclosporid	223	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
151	33	7.8	73	1	YH73_HUMAN	P81244 proclosporid	224	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
152	33	7.8	73	1	YH73_HUMAN	P81244 proclosporid	225	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
153	33	7.8	75	1	YH73_HUMAN	P81244 proclosporid	226	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
154	33	7.8	75	1	YH73_HUMAN	P81244 proclosporid	227	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
155	33	7.8	78	1	YH73_HUMAN	P81244 proclosporid	228	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
156	33	7.8	78	1	YH73_HUMAN	P81244 proclosporid	229	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
157	33	7.8	78	1	YH73_HUMAN	P81244 proclosporid	230	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
158	33	7.8	81	1	YH73_HUMAN	P81244 proclosporid	231	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
159	33	7.8	81	1	YH73_HUMAN	P81244 proclosporid	232	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
160	33	7.8	82	1	YH73_HUMAN	P81244 proclosporid	233	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
161	33	7.8	82	1	YH73_HUMAN	P81244 proclosporid	234	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
162	33	7.8	83	1	YH73_HUMAN	P81244 proclosporid	235	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
163	33	7.8	83	1	YH73_HUMAN	P81244 proclosporid	236	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
164	33	7.8	84	1	YH73_HUMAN	P81244 proclosporid	237	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
165	33	7.8	85	1	YH73_HUMAN	P81244 proclosporid	238	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
166	33	7.8	85	1	YH73_HUMAN	P81244 proclosporid	239	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
167	33	7.8	89	1	YH73_HUMAN	P81244 proclosporid	240	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
168	33	7.8	90	1	YH73_HUMAN	P81244 proclosporid	241	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
169	32.5	7.7	45	1	YH73_HUMAN	P81244 proclosporid	242	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
170	32.5	7.7	47	1	YH73_HUMAN	P81244 proclosporid	243	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
171	32.5	7.7	52	1	YH73_HUMAN	P81244 proclosporid	244	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
172	32.5	7.7	52	1	YH73_HUMAN	P81244 proclosporid	245	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
173	32.5	7.7	55	1	YH73_HUMAN	P81244 proclosporid	246	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
174	32.5	7.7	55	1	YH73_HUMAN	P81244 proclosporid	247	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
175	32.5	7.7	58	1	YH73_HUMAN	P81244 proclosporid	248	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
176	32.5	7.7	61	1	YH73_HUMAN	P81244 proclosporid	249	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
177	32.5	7.7	67	1	YH73_HUMAN	P81244 proclosporid	250	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
178	32.5	7.7	77	1	YH73_HUMAN	P81244 proclosporid	251	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir
179	32.5	7.7	78	1	YH73_HUMAN	P81244 proclosporid	252	32.5	7.7	77	1	YH73_HUMAN	P33872 variola vir

253	31.5	7.4	80	1	FRL1_METJA	Q60368 methanococc	326	30.5	7.2	47	1	RL33_STAAN	Q9ags7 staphylococ
254	31.5	7.4	80	1	PSAC_ANTSP	Q6439 antithamnio	327	30.5	7.2	54	1	PM11_LOCM1	P80059 locusta miq
255	31.5	7.4	80	1	YMCV_HSV62	Q13916 schizosacch	328	30.5	7.2	57	1	V3A_IBVP3	P30238 avian infec
256	31.5	7.4	81	1	ULIL_HSV62	P52459 human herpe	329	30.5	7.2	58	1	FER_METTE	Q01700 methanosarc
257	31.5	7.4	81	1	YLOC_BACSU	Q31738 bacillus su	330	30.5	7.2	59	1	PART_HUMAN	Q9npd0 homo sapien
258	31.5	7.4	82	1	MTZB_LYCES	Q40158 lycopersico	331	30.5	7.2	60	1	NXSL_MICNI	P80548 micrurus ni
259	31.5	7.4	84	1	VPU_HVIBN	P20212 human immu	332	30.5	7.2	60	1	Y05L_BPT4	P39237 bacterioph
260	31.5	7.4	84	1	Y101_SSV1	P20212 sulfolobus	333	30.5	7.2	62	1	RHT1_RHOTO	P07907 rhodospirid
261	31.5	7.4	86	1	Y009_BHPH1	P51710 bacterioph	334	30.5	7.2	63	1	CSRA_HAETN	Q9J5a4 haemophilus
262	31.5	7.4	87	1	DEFA_RAT	Q62713 rattus norv	335	30.5	7.2	63	1	RS09_FOHPV	Q9w25 burkholderi
263	31.5	7.4	87	1	DEFB_RAT	Q921f1 rattus norv	336	30.5	7.2	63	1	RS21_BURMA	P93663 macropus ro
264	31.5	7.4	87	1	IM13_ARATH	Q9xh48 arabidopsis	337	30.5	7.2	69	1	NPB8_MACRO	P93669 aeromonas h
265	31.5	7.4	88	1	RS20_CLOAB	Q971k0 clostridium	338	30.5	7.2	70	1	FRFL_AERHI	P82943 bos taurus
266	31.5	7.4	89	1	HG17_HUMAN	P05204 homo sapien	339	30.5	7.2	70	1	REG1_BOVIN	P70943 burkholderi
267	31.5	7.4	89	1	YHLA_BACSU	P39798 bacillus su	340	30.5	7.2	70	1	RS21_BURPS	P41433 autographa
268	31.5	7.4	90	1	REV_HV1W2	P05866 human immu	341	30.5	7.2	71	1	Y029_NPVAC	P41433 autographa
269	31	7.3	43	1	CC2_CARCN	P32955 carlica cand	342	30.5	7.2	74	1	CBQ_CHRVI	P65440 chromatium
270	31	7.3	46	1	VIT_ANAPL	P56530 anas platyr	343	30.5	7.2	74	1	CSMB_CHLVI	Q46473 chlorobium
271	31	7.3	48	1	RL40_METTH	Q26653 methanobact	344	30.5	7.2	75	1	GVAL_HALNI	P08958 halobacteri
272	31	7.3	54	1	GALA_CANFA	P33710 catfish faml	345	30.5	7.2	77	1	TACL_TACTR	P14213 tachyleus
273	31	7.3	55	1	LECA_LATSA	P23208 lathyrus sa	346	30.5	7.2	77	1	YOR2_FIVSD	Q14781 feline immu
274	31	7.3	56	1	VG36_BMD2	O22001 mycobacteri	347	30.5	7.2	78	1	CBX2_HUMAN	P19033 chlamydomon
275	31	7.3	60	1	TAP_ORNO	PA7726 ornithodor	348	30.5	7.2	80	1	PSAC_CHLRE	Q00914 chlamydomon
276	31	7.3	62	1	UCRX_BOVIN	P00130 bos taurus	349	30.5	7.2	80	1	PSAC_CVACA	Q19905 cyanidium c
277	31	7.3	63	1	JHEB_TRINI	P30810 trichoplusi	350	30.5	7.2	80	1	PSAC_PINTH	P1649 pinus thum
278	31	7.3	63	1	YALA_ECOLI	P08366 escherichia	351	30.5	7.2	81	1	SPR6_RABIT	P12517 human immu
279	31	7.3	63	1	RAK35_CVACA	Q9t1r9 cyanidium c	352	30.5	7.2	81	1	R27A_YEAST	O18776 oryctolagus
280	31	7.3	66	1	COPP_HELPJ	Q9zm70 helicobacte	353	30.5	7.2	82	1	R27B_YEAST	P35997 saccharomyc
281	31	7.3	66	1	DMS5_PACDA	O93455 pachymedusa	354	30.5	7.2	82	1	RL27_STRCO	Q91111 streptomyce
282	31	7.3	66	1	RPN0_SULAC	P39472 sulfolobus	355	30.5	7.2	84	1	RS20_BORBU	Q95394 borrelia bu
283	31	7.3	67	1	ATP8_MOUSE	P03930 mus musculu	356	30.5	7.2	85	1	SCXX_CENSC	Q26287 drosophila
284	31	7.3	67	1	IF1A_MOUSE	Q60872 mus musculu	357	30.5	7.2	85	1	PER_DROTE	P52000 mycobacteri
285	31	7.3	68	1	YHGB_KLEPN	P11160 klebsiella	358	30.5	7.2	86	1	RS12_MYCGO	Q8u1h2 agrobacteri
286	31	7.3	69	1	RL28_AQUAE	O66492 aquifex seo	359	30.5	7.2	88	1	RS20_AGRT5	P02313 bos taurus
287	31	7.3	70	1	RL31_HAEDU	O59450 haemophilus	360	30.5	7.2	88	1	HG17_BOVIN	P80272 sus scrofa
288	31	7.3	72	1	Y541_BORBU	O51491 borrelia bu	361	30.5	7.2	89	1	YG17_PIG	Q11116 caenorhabd1
289	31	7.3	73	1	BP4C_BRANA	P41506 brassica na	362	30.5	7.2	89	1	YC36_METTH	P11697 staphylococ
290	31	7.3	73	1	YB76_HAEN	P44120 haemophilus	363	30.5	7.2	89	1	GG11_STAHA	O19912 cyanidium c
291	31	7.3	75	1	MT1_CICAR	Q39458 cicier ariet	364	30.5	7.2	89	1	RG33_CVACA	Q9cdv5 lactococcus
292	31	7.3	75	1	YH11_CLOPE	Q8xjps clostridium	365	30.5	7.2	89	1	IPR_SOLME	P01078 solanum mel
293	31	7.3	76	1	SECG_MYCPN	Q9exd0 mycoplasma	366	30.5	7.2	89	1	IOVO_GRUCA	P52239 balearica p
294	31	7.3	76	1	TXP6_APTSC	P49270 apocostichus	367	30.5	7.2	89	1	IOVO_HALIN	P05577 hallastur i
295	31	7.3	77	1	RL28_HAEN	P4364 haemophilus	368	30.5	7.2	89	1	VG36_BPMLS	Q05246 mycobacteri
296	31	7.3	77	1	SECG_MYCGE	P58061 mycoplasma	369	30.5	7.2	89	1	CSRA_BUCAI	P05246 mycobacteri
297	31	7.3	77	1	Y125_HUMAN	Q14138 homo sapien	370	30.5	7.2	89	1	YCU5_CAEEL	O22702 caenorhabd1
298	31	7.3	77	1	Y4D0_HRISN	P55409 rhizobium s	371	30.5	7.2	89	1	CXV1_CONIM	P57017 bacterioph
299	31	7.3	78	1	M6_LILHE	Q40189 lilium henr	372	30.5	7.2	89	1	Y6K4_BBP22	O29178 archaeoglob
300	31	7.3	78	1	MULI_PROMI	P09461 proteus mir	373	30.5	7.2	89	1	YA87_ARCFU	P31803 escherichia
301	31	7.3	78	1	YD80_METJA	Q58775 methanococc	374	30.5	7.2	89	1	CSRA_ECOLI	Q47620 erwinia car
302	31	7.3	80	1	AKA7_MOUSE	O55074 mus musculu	375	30.5	7.2	89	1	TX12_DIGCA	P55817 diquelia ca
303	31	7.3	80	1	MT2_FRAAN	P93134 fragaria an	376	30.5	7.2	89	1	Y667_ARCFU	Q29590 haemophilus
304	31	7.3	81	1	NX52_AIPLA	P19959 alpysurus l	377	30.5	7.2	89	1	Y704_HAEN	P44040 haemophilus
305	31	7.3	81	1	RS16_CLOPE	O8xjp4 clostridium	378	30.5	7.2	89	1	DMPL_PSESP	P49172 pseudomonas
306	31	7.3	82	1	YF76_ARCFU	O28696 archaeoglob	379	30.5	7.2	89	1	HPIT_RHOTE	P33678 rhodocycylus
307	31	7.3	83	1	EXTS_RHIME	Q921r9 rhizobium m	380	30.5	7.2	89	1	UCRX_HUMAN	Q9udw1 homo sapien
308	31	7.3	83	1	IM45_ECOLI	P13476 escherichia	381	30.5	7.2	89	1	XYLH_PSEPU	Q01468 pseudomonas
309	31	7.3	83	1	IM45_ECOLI	Q57300 escherichia	382	30.5	7.2	89	1	ITR2_ASCSU	P81492 hirtudinaria
310	31	7.3	84	1	MULI_PSEAE	P11221 pseudomonas	383	30.5	7.2	89	1	YBFL_ECOLI	Q9kuh3 vibrio chol
311	31	7.3	84	1	RNS_GIRCA	O29535 giraffa cam	384	30.5	7.2	89	1	ITR2_ASCSU	P80341 thermus the
312	31	7.3	84	1	RS16_RALSO	Q8y0w0 ralstonia s	385	30.5	7.2	89	1	YBFL_ECOLI	P39901 escherichia
313	31	7.3	85	1	V10_METJA	O57755 methanococc	386	30.5	7.2	89	1	ITR2_ASCSU	P01049 ascaris suu
314	31	7.3	85	1	TAT_HV1B7	P04608 bacterioph	387	30.5	7.2	89	1	HJAL_METJA	O57632 methanococc
315	31	7.3	86	1	ANPE_MACAM	P19605 macrozoarce	388	30.5	7.2	89	1	HJAL_METJA	O58342 methanococc
316	31	7.3	87	1	RS16_FUSNN	Q8rv8 fusobacteri	389	30.5	7.2	89	1	GEPE_BACCE	O68684 bacillus ce
317	31	7.3	87	1	EXTS_STRCO	Q9fms4 streptomyce	390	30.5	7.2	89	1	CSRA_SERMA	O85735 serratia ma
318	31	7.3	88	1	YF76_ARCFU	P74891 salmonelella	391	30.5	7.2	89	1	Y375_TREPA	O83390 treponema p
319	31	7.3	88	1	SSAS_SALTY	O64224 mycobacteri	392	30.5	7.2	89	1	FLC2_ECOLI	P23367 escherichia
320	31	7.3	88	1	VG30_BPMO2	Q46971 escherichia	393	30.5	7.2	89	1	BDM_ECO57	Q8xat7 escherichia
321	31	7.3	90	1	MTFS_ECOLI	Q02918 glycine max	394	30.5	7.2	89	1		
322	31	7.3	90	1	Y36A_SOYEN	Q9knm3 vibrio chol	395	30.5	7.2	89	1		
323	31	7.3	90	1	POZ_VIBCH	P08804 human immu	396	30.5	7.2	89	1		
324	31	7.3	90	1	VPU_HV1N5		397	30.5	7.2	89	1		
325	30.5	7.2	45	1			398	30.5	7.2	89	1		



399	7.1	71	1	BDM_ECOLI	P76127	escherichia	472	29.5	7.0	80	1	PSAC_FREDI	P23810	fremyella d
400	30	7.1	1	NTB2_XENLA	P19011	xenopus lae	473	29.5	7.0	80	1	PSAC_PORPU	P51374	porphyra pu
401	30	7.1	72	NTK4_OPNHA	P80156	ophiophagus	474	29.5	7.0	80	1	PSAC_SINY3	P32422	synochocyst
402	30	7.1	71	NXL5_OPNHA	P80965	ophiophagus	475	29.5	7.0	80	1	S61G_YEAST	P35179	saccharomyc
403	30	7.1	72	SAS5_BACME	P04835	bacillus me	476	29.5	7.0	81	1	TXFB_DENAN	P01404	dendrosapi
404	30	7.1	74	COLE_ZOPAT	P80032	zophobas at	477	29.5	7.0	81	1	VPU_HVLY2	P35966	huma immun
405	30	7.1	74	TXPL_APTSC	P49267	apostichus	478	29.5	7.0	82	1	NKSB_NAJAT	P80958	naja atra (
406	30	7.1	75	YH56_CLOAB	P97196	ciostriidum	479	29.5	7.0	82	1	YFDX_PLEBO	P46043	pletonema
407	30	7.1	76	SPY1_CHICK	Q97411	gallus gall	480	29.5	7.0	84	1	TAC2_HUMAN	P20155	homo sapien
408	30	7.1	76	TEC_BFPI	Q06561	bacteriophia	481	29.5	7.0	84	1	RL24_SULAC	O05613	sulfolobus
409	30	7.1	77	CSME_CHLTE	Q88986	chlorobium	482	29.5	7.0	86	1	PAK1_CENSC	P72712	synochocyst
410	30	7.1	77	LEA2_PIG	Q95104	sus scrofa	483	29.5	7.0	86	1	SCX1_CENSC	P01491	centruroid
411	30	7.1	77	YF67_XYLFA	Q99813	xyella fas	484	29.5	7.0	87	1	SSS1_SCICA	P31275	scyllorhinu
412	30	7.1	77	YHR2_VACCV	P17358	vaccinia vi	485	29.5	7.0	88	1	PHHP_LISMO	Q31148	lystertia mo
413	30	7.1	78	DLTC_STAAM	Q53663	staphylococ	486	29.5	7.0	88	1	YPER_NPVLD	P36868	lymantria d
414	30	7.1	78	DLTC_STAAX	Q9x2n6	staphylococ	487	29.5	7.0	88	1	PERC_ECO27	P43475	escherichia
415	30	7.1	78	R28B_STRCO	Q9x8k8	streptomyce	488	29.5	7.0	90	1	LITP_PHYSA	P08947	phyliomedus
416	30	7.1	79	EX7S_LACLA	Q9x8k3	lactococcus	489	29.5	7.0	90	1	R37A_OSTOS	O61598	ostertagia
417	30	7.1	80	MT2_BRARP	Q42494	brassica ra	490	29.5	7.0	90	1	RS16_LACLA	Q9c1b2	lactococcus
418	30	7.1	80	MT2_BRARP	Q39269	brassica ra	491	29.5	6.9	43	1	CC1_CARN	P32954	carica cand
419	30	7.1	80	MT2_RICCO	P30564	ricinus com	492	29.5	6.9	44	1	DERM_PIG	P45846	sus scrofa
420	30	7.1	80	XJBE_ECOLI	P32686	escherichia	493	29.5	6.9	46	1	RL34_PSEAO	O86448	pseudanabae
421	30	7.1	80	YV6A_VIBCH	P58093	vibrio chol	494	29.5	6.9	47	1	RL40_METJA	P54058	methanococ
422	30	7.1	81	ATPH_PRA	P08212	pisum sativ	495	29.5	6.9	48	1	RR32_VICFA	P15820	vicia faba
423	30	7.1	81	PER_BAGST	P00843	spinacia ol	496	29.5	6.9	49	1	YLDH_MYCHY	P46188	mycoplasma
424	30	7.1	81	RS16_YERPE	P00212	baginellus st	497	29.5	6.9	50	1	INS_PROGU	P01331	proechimys
425	30	7.1	82	CNCG_SFEIR	O82b07	yersinia pe	498	29.5	6.9	50	1	RS14_METH	O36125	methanobact
426	30	7.1	83	ELAC_MACEU	O53175	speromphili	499	29.5	6.9	51	1	LOVO_RHYFU	P52251	rhynchobact
427	30	7.1	83	RS14_MACEU	O82845	macropus eu	500	29.5	6.9	51	1	LHB2_ECTHA	P80105	ectothiorho
428	30	7.1	83	VF19_BRAPS	P421q3	bacteriophis	501	29.5	6.9	54	1	TOVO_MACEU	P81041	macropus eu
429	30	7.1	84	GLRL_ECOLI	P24036	arabidopsis	502	29.5	6.9	54	1	TOVO_HALAL	P05578	syds coprot
430	30	7.1	85	IATP_YEAST	P00277	escherichia	503	29.5	6.9	54	1	TOVO_MACEU	P52268	hallaetetus
431	30	7.1	85	YME3_THIFE	P01097	saccharomyc	504	29.5	6.9	55	1	ELAG_ADE05	P06438	humandeno
432	30	7.1	86	ACP_CYACA	P22904	thiobacilli	505	29.5	6.9	55	1	RR32_SPIOL	P38404	spinacia ol
433	30	7.1	86	RS18_CAMJE	O19921	cyanidum c	506	29.5	6.9	57	1	BB1_HUMAN	P02020	homo sapien
434	30	7.1	86	SCX1_CENNO	P69301	campylobact	507	29.5	6.9	58	1	FER_DESCI	Q00401	caenorhabdi
435	30	7.1	86	SCX1_CENNO	P51223	centruroid	508	29.5	6.9	58	1	YRD5_CABEL	Q85559	archaeoglob
436	30	7.1	86	YABA_ESCAPE	P45665	centruroid	509	29.5	6.9	60	1	YH14_ARCFU	P07215	saccharomyc
437	30	7.1	86	YABA_ESCAPE	P28243	escherichia	510	29.5	6.9	61	1	MYC_YEAST	O83797	treponema p
438	30	7.1	87	SELW_MOUSE	P51414	arabidopsis	511	29.5	6.9	61	1	Y825_TREPA	O29173	archaeoglob
439	30	7.1	88	Y27A_AERPE	P49904	mus musculus	512	29.5	6.9	61	1	YA92_ARCFU	P08820	vicia faba
440	30	7.1	88	RL31_METAC	Q88q97	mycoplasma	513	29.5	6.9	62	1	ICIS_VICFA	P15113	candida gla
441	30	7.1	89	Y27A_AERPE	P21474	bacillus su	514	29.5	6.9	62	1	MT1_CANGA	P10458	laticauda c
442	30	7.1	89	Y27A_AERPE	P58322	aeropyrum p	515	29.5	6.9	62	1	MXSC_LATCR	P10460	laticauda l
443	30	7.1	89	Y27A_AERPE	Q08600	klebsiella	516	29.5	6.9	63	1	YPTA_BACSU	P34521	caenorhabdi
444	30	7.1	90	AF1Q_MOUSE	P97783	mus musculus	517	29.5	6.9	63	1	ANP2_MACAM	P19608	macrozoarce
445	30	7.1	90	ASIA_BPT4	P32267	bacteriophia	518	29.5	6.9	64	1	RL35_CHLTR	P03773	bacteriophia
446	30	7.1	90	YVPM_BPPD	P27389	bacteriophia	519	29.5	6.9	64	1	Y64_LAMBD	P24333	crotalus du
447	30	7.1	90	YVPM_BPPD	Q10189	schizosacch	520	29.5	6.9	64	1	MX1_CRODU	P24333	crotalus du
448	30	7.1	90	YVPM_BPPD	Q09680	bos taurus	521	29.5	6.9	65	1	MX3_CRODU	P25669	thermococcu
449	29.5	7.0	47	GIP_BOVIN	Q08079	synechococ	522	29.5	6.9	66	1	HANA_THEZI	Q17313	ceratitidis c
450	29.5	7.0	47	UCR3_DROME	Q9XV35	drosophila	523	29.5	6.9	66	1	CERC_CERCA	Q17313	haemophilus
451	29.5	7.0	55	CD52_MACFA	P32763	macaca fasc	524	29.5	6.9	67	1	YEO2_HAEIN	Q04646	mus musculus
452	29.5	7.0	61	CD52_MACFA	P31398	homo sapien	525	29.5	6.9	70	1	ATNG_MOUSE	P16221	rattus norv
453	29.5	7.0	61	YW98_PYRAB	Q9uz10	pyrococcus	526	29.5	6.9	71	1	HSIB_FEREN	P78699	kluyveromyc
454	29.5	7.0	61	YW98_PYRAB	P46066	centruroid	527	29.5	6.9	71	1	SOMI_KLULA	Q09005	xenopus lae
455	29.5	7.0	63	SCXV_CENSC	P42543	bacteriophia	528	29.5	6.9	71	1	STIB_XENLA	P19009	xenopus lae
456	29.5	7.0	63	Y008_BPL2	P35074	caenorhabdi	529	29.5	6.9	71	1	IF1_XYLFA	Q9pdd4	xyella fas
457	29.5	7.0	66	Y008_BPL2	Q88556	archaeoglob	530	29.5	6.9	72	1	RPOZ_CLOAB	Q971c9	ciostriidum
458	29.5	7.0	66	Y008_BPL2	Q9y812	pyrococcus	531	29.5	6.9	72	1	VG18_BPMOB	Q38625	bacteriophia
459	29.5	7.0	67	HMTB_METH	P50484	methanobact	532	29.5	6.9	72	1	NG11_NAJOX	P01382	naja oxiata
460	29.5	7.0	67	YVAV_VACCV	P20528	vaccinia vi	533	29.5	6.9	72	1	RL24_HELPJ	Q9zjs3	helicobacte
461	29.5	7.0	68	YB10_HALNI	P17104	halobacteri	534	29.5	6.9	73	1	DNBI_POVBA	P14998	polymaviru
462	29.5	7.0	68	YB10_HALNI	O14610	homo sapien	535	29.5	6.9	73	1	VIAL_MYCTU	P19771	mycobacteri
463	29.5	7.0	73	YB10_HALNI	P11256	yersinia ps	536	29.5	6.9	74	1	Z123_HUMAN	P35273	homo sapien
464	29.5	7.0	73	YB10_HALNI	Q97bc2	listeria mo	537	29.5	6.9	74	1	GBG4_MOUSE	P50150	homo sapien
465	29.5	7.0	75	EX7S_LISMO	O8y7c3	listeria mo	538	29.5	6.9	75	1	Y13H_BPT4	P39501	bacteriophia
466	29.5	7.0	75	EX7S_LISMO	P20087	thiobacilli	539	29.5	6.9	75	1	YB7F_SCHPO	O14330	schizosacch
467	29.5	7.0	76	YML1_THIFE	O78423	quillardia	540	29.5	6.9	75	1			
468	29.5	7.0	76	YML1_THIFE	O78423	quillardia	541	29.5	6.9	75	1			
469	29.5	7.0	77	YVFB_VACCV	P20560	vaccinia vi	542	29.5	6.9	75	1			
470	29.5	7.0	77	YVFB_VACCV	P20560	vaccinia vi	543	29.5	6.9	75	1			
471	29.5	7.0	80	C550_THAWE	O98448	thalassiosi	544	29.5	6.9	75	1			

545	29	6.9	75	1	YE69_MPTJJA	Q58864	methanococc
546	29	6.9	75	1	YEED_ECOLI	P33014	escherichia
547	29	6.9	76	1	ETL1_MACFA	Q28469	macaca fasc
548	29	6.9	76	1	RUXG_HUMAN	P15357	homo sapien
549	29	6.9	76	1	YNCJ_ECOLI	P76105	escherichia
550	29	6.9	77	1	YQAF_BACSU	P45903	bacillus su
551	29	6.9	77	1	LEA2_MACMU	Q95m25	macaca mula
552	29	6.9	77	1	YDCE_ECOLI	P31992	escherichia
553	29	6.9	77	1	YG17_ARCFU	Q28656	archaeoglob
554	29	6.9	78	1	MT2_NICGU	Q40396	nicotiana p
555	29	6.9	78	1	RL28_TREPA	P96131	treponema p
556	29	6.9	78	1	RL19_ACACA	P46762	acanthamoeb
557	29	6.9	79	1	AFB3_BRANA	Q39313	brassica na
558	29	6.9	79	1	YF71_HAEIN	P44260	haemophilus
559	29	6.9	80	1	ATPD_PIG	Q95312	sus scrofa
560	29	6.9	80	1	VPY_BIV27	P24035	bovine immu
561	29	6.9	80	1	YK09_MYCRU	Q10848	mycobacteri
562	29	6.9	82	1	ATPH_CHLRE	Q37304	chlamydomon
563	29	6.9	82	1	MT21_ORLYA	P94029	oryza sativ
564	29	6.9	83	1	RL23_HALNI	Q06842	halobacteri
565	29	6.9	83	1	RL17_PORPU	P51305	porphyra pu
566	29	6.9	83	1	RS27_HUMAN	P42677	homo sapien
567	29	6.9	83	1	RS27_RAT	P24051	ratu mus norv
568	29	6.9	83	1	RS27_XENLA	P47904	xenopus lae
569	29	6.9	83	1	Y46S_SYNT3	P73882	synecocyst
570	29	6.9	84	1	IM13_ORYSA	Q94975	oryza sativ
571	29	6.9	84	1	SC13_MESNA	Q94975	oryza sativ
572	29	6.9	85	1	HLK5_MAIZE	P56683	zea mays (m
573	29	6.9	85	1	HLG3_MAIZE	P56683	zea mays (m
574	29	6.9	85	1	PSY1_PREDI	P11397	fremyella d
575	29	6.9	85	1	RS17_MYCE	P47406	mycoplasma
576	29	6.9	85	1	SCX8_CENGE	Q95wd1	centruoide
577	29	6.9	86	1	ACPX_STRGN	Q02570	streptomyce
578	29	6.9	86	1	MYSF_PDI	P54695	dictyosteli
579	29	6.9	86	1	YFUE_HAEIN	P44746	haemophilus
580	29	6.9	87	1	ANP5_MACAM	P19607	macrozoarc
581	29	6.9	87	1	ANPD_MACAM	P19604	macrozoarc
582	29	6.9	87	1	RS70_CANAB	Q9pm64	campylobact
583	29	6.9	87	1	RS70_CLOPE	Q8x1s2	clostridium
584	29	6.9	87	1	SCX1_CENGE	P01492	centruoide
585	29	6.9	87	1	SCX6_CENNO	P45664	centruoide
586	29	6.9	87	1	Y230_METJA	Q57683	methanococ
587	29	6.9	87	1	Y230_METJA	Q57683	methanococ
588	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
589	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
590	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
591	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
592	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
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594	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
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614	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
615	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
616	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst
617	29	6.9	88	1	Y434_SYNT3	P58235	synecocyst

691	28	6.6	57	1	IVBK_DENPO	P00981 dendroaspis	764	28	6.6	80	1	PSAC_MESVI	Q9mum9 mesostigma
692	28	6.6	57	1	NIND_LAMED	P03767 bacterioph	765	28	6.6	80	1	PSAC_NEPOL	Q9tkv9 nephroselmi
693	28	6.6	58	1	RHO_THIFE	P52158 thioacacillu	766	28	6.6	80	1	RS16_MYCGA	Q9rdv4 mycoplasma
694	28	6.6	58	1	TX50_DENJA	P01419 dendroaspis	767	28	6.6	81	1	ATPH_ARATH	P56760 arabidopsis
695	28	6.6	58	1	V3A_IBVB	P30237 avian infec	768	28	6.6	82	1	ATPH_GUITH	O78479 guillardia
696	28	6.6	59	1	Y0AH_SALRY	P56505 salmonella	769	28	6.6	82	1	CTXA_BACSU	Q45336 bacillus su
697	28	6.6	60	1	MERC_SHIFL	P04337 shigella fl	770	28	6.6	82	1	CX06_CONST	Q9x2k5 conus stria
698	28	6.6	60	1	NXS1_ENHSC	P25492 enhydrina s	771	28	6.6	82	1	IACP_SALTI	Q82495 salmonella
699	28	6.6	60	1	NXS1_HYDCY	P25494 enhydrina s	772	28	6.6	82	1	IMCL_SALTI	P18643 salmoneilla
700	28	6.6	60	1	NXS2_ENHSC	P25493 enhydrina s	773	28	6.6	82	1	SASG_BACST	P07785 bacillus st
701	28	6.6	61	1	NXS3_NAJHA	P01420 naja haje a	774	28	6.6	82	1	TX5A_PIG	O76199 phenetria
702	28	6.6	61	1	RL34_MYCTU	P95065 mycobacteri	775	28	6.6	82	1	U2AG_PIG	Q29350 sus scrofa
703	28	6.6	62	1	IT13_MOMCH	P09407 momordica c	776	28	6.6	82	1	YAS7_VIBCH	Q9k448 vibrio chol
704	28	6.6	62	1	SCX2_BUTCU	P15221 buthus eupe	777	28	6.6	82	1	YCXL_VICFA	P08889 victia faba
705	28	6.6	62	1	YPPE_BACSU	P50834 bacillus su	778	28	6.6	83	1	NSGL_RAT	P02883 rattus norv
706	28	6.6	63	1	COXO_MOUSE	P17665 mus musculu	779	28	6.6	83	1	RS28_SULTO	Q97328 sulfotobius
707	28	6.6	63	1	LANN_SPMU	P22287 cladosporiu	780	28	6.6	83	1	RUXX_THEAC	P57670 thermoplas
708	28	6.6	63	1	YL33_DROME	Q68586 streptococc	781	28	6.6	83	1	TATA_MYCTU	Q10703 mycobacteri
709	28	6.6	63	1	YH13_RHOCA	O9vr-93 rhodobacter	782	28	6.6	83	1	RUXX_BPML5	Q05242 mycobacteri
710	28	6.6	64	1	YL35_CHLNP	P30791 rhodobacter	783	28	6.6	83	1	VG03_BPML5	P27391 bacterioph
711	28	6.6	64	1	Y00A_ARCFU	Q9z6r8 chlamydia p	784	28	6.6	83	1	Y098_RICPR	Q9ze49 rickettsia
712	28	6.6	64	1	KED2_ECOLI	P58024 archaeoglob	785	28	6.6	84	1	YEXA_BACSU	Q9x7l3 rhizobium m
713	28	6.6	66	1	KIN2_ARATH	P13967 escherichia	786	28	6.6	84	1	MINE_XYLFA	P12049 bacillus su
714	28	6.6	66	1	YK15_CAEEL	P13967 escherichia	787	28	6.6	85	1	RS17_MYCPN	Q9pdq9 xylella fas
715	28	6.6	66	1	YK15_CAEEL	P13967 escherichia	788	28	6.6	85	1	OAGL_VIBCH	Q50309 mycoplasma
716	28	6.6	66	1	SM64_HUMAN	P31169 arabidopsis	789	28	6.6	86	1	RL3E_ARCFU	Q28389 archaeoglob
717	28	6.6	66	1	YAP8_TALEU	P93377 nicotiana t	790	28	6.6	86	1	RL3E_ARCFU	Q919c8 thioacacillu
718	28	6.6	66	1	ATP8_TALEU	P52099 escherichia	791	28	6.6	86	1	RS16_THIFE	P03793 bacterioph
719	28	6.6	67	1	GONI_MACMU	Q9mjb2 talpa europ	792	28	6.6	86	1	V16_BPT7	P26217 erwina chr
720	28	6.6	67	1	RL35_SYNY3	P48959 synechocyst	793	28	6.6	87	1	YIEC_ERWCH	Q9qu57 conus glori
721	28	6.6	67	1	YJUX_ENTCL	P39431 enterobacte	794	28	6.6	88	1	YK16_ERWCH	P79729 brachydanio
722	28	6.6	67	1	YK15_CAEEL	P42172 caenorhabdi	795	28	6.6	88	1	YK16_ERWCH	O96033 homo sapien
723	28	6.6	68	1	YK15_CAEEL	P41953 caenorhabdi	796	28	6.6	88	1	YK16_ERWCH	P02907 staphylococ
724	28	6.6	68	1	YK15_CAEEL	P41314 didelphis m	797	28	6.6	88	1	YK16_ERWCH	P49197 caenorhabdi
725	28	6.6	69	1	YK15_CAEEL	P41314 didelphis m	798	28	6.6	88	1	YK16_ERWCH	P43937 staphylococ
726	28	6.6	69	1	YK15_CAEEL	P41314 didelphis m	799	28	6.6	88	1	YK16_ERWCH	P49197 caenorhabdi
727	28	6.6	69	1	YK15_CAEEL	P41314 didelphis m	800	28	6.6	88	1	YK16_ERWCH	Q919c8 thioacacillu
728	28	6.6	70	1	YK15_CAEEL	P41314 didelphis m	801	28	6.6	88	1	YK16_ERWCH	Q919c8 thioacacillu
729	28	6.6	70	1	YK15_CAEEL	P41314 didelphis m	802	28	6.6	89	1	YK16_ERWCH	P26217 erwina chr
730	28	6.6	71	1	YK15_CAEEL	P41314 didelphis m	803	28	6.6	89	1	YK16_ERWCH	P36217 erwina chr
731	28	6.6	72	1	YK15_CAEEL	P41314 didelphis m	804	28	6.6	89	1	YK16_ERWCH	Q9qu57 conus glori
732	28	6.6	72	1	YK15_CAEEL	P41314 didelphis m	805	28	6.6	90	1	YK16_ERWCH	P79729 brachydanio
733	28	6.6	72	1	YK15_CAEEL	P41314 didelphis m	806	28	6.6	90	1	YK16_ERWCH	O96033 homo sapien
734	28	6.6	73	1	YK15_CAEEL	P41314 didelphis m	807	28	6.6	90	1	YK16_ERWCH	P02907 staphylococ
735	28	6.6	73	1	YK15_CAEEL	P41314 didelphis m	808	28	6.6	90	1	YK16_ERWCH	P49197 caenorhabdi
736	28	6.6	73	1	YK15_CAEEL	P41314 didelphis m	809	28	6.6	90	1	YK16_ERWCH	P43937 staphylococ
737	28	6.6	74	1	YK15_CAEEL	P41314 didelphis m	810	28	6.6	90	1	YK16_ERWCH	P49197 caenorhabdi
738	28	6.6	74	1	YK15_CAEEL	P41314 didelphis m	811	28	6.6	90	1	YK16_ERWCH	Q919c8 thioacacillu
739	28	6.6	74	1	YK15_CAEEL	P41314 didelphis m	812	28	6.6	90	1	YK16_ERWCH	Q919c8 thioacacillu
740	28	6.6	75	1	YK15_CAEEL	P41314 didelphis m	813	28	6.6	90	1	YK16_ERWCH	P26217 erwina chr
741	28	6.6	75	1	YK15_CAEEL	P41314 didelphis m	814	28	6.6	90	1	YK16_ERWCH	Q9qu57 conus glori
742	28	6.6	75	1	YK15_CAEEL	P41314 didelphis m	815	28	6.6	90	1	YK16_ERWCH	P79729 brachydanio
743	28	6.6	76	1	YK15_CAEEL	P41314 didelphis m	816	28	6.6	90	1	YK16_ERWCH	O96033 homo sapien
744	28	6.6	76	1	YK15_CAEEL	P41314 didelphis m	817	28	6.6	90	1	YK16_ERWCH	P02907 staphylococ
745	28	6.6	76	1	YK15_CAEEL	P41314 didelphis m	818	28	6.6	90	1	YK16_ERWCH	P49197 caenorhabdi
746	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	819	28	6.6	90	1	YK16_ERWCH	P43937 staphylococ
747	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	820	28	6.6	90	1	YK16_ERWCH	P49197 caenorhabdi
748	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	821	28	6.6	90	1	YK16_ERWCH	Q919c8 thioacacillu
749	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	822	28	6.6	90	1	YK16_ERWCH	Q919c8 thioacacillu
750	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	823	28	6.6	90	1	YK16_ERWCH	P26217 erwina chr
751	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	824	28	6.6	90	1	YK16_ERWCH	Q9qu57 conus glori
752	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	825	28	6.6	90	1	YK16_ERWCH	P79729 brachydanio
753	28	6.6	77	1	YK15_CAEEL	P41314 didelphis m	826	28	6.6	90	1	YK16_ERWCH	O96033 homo sapien
754	28	6.6	78	1	YK15_CAEEL	P41314 didelphis m	827	28	6.6	90	1	YK16_ERWCH	P02907 staphylococ
755	28	6.6	78	1	YK15_CAEEL	P41314 didelphis m	828	28	6.6	90	1	YK16_ERWCH	P49197 caenorhabdi
756	28	6.6	78	1	YK15_CAEEL	P41314 didelphis m	829	28	6.6	90	1	YK16_ERWCH	P43937 staphylococ
757	28	6.6	78	1	YK15_CAEEL	P41314 didelphis m	830	28	6.6	90	1	YK16_ERWCH	P49197 caenorhabdi
758	28	6.6	78	1	YK15_CAEEL	P41314 didelphis m	831	28	6.6	90	1	YK16_ERWCH	Q919c8 thioacacillu
759	28	6.6	79	1	YK15_CAEEL	P41314 didelphis m	832	28	6.6	90	1	YK16_ERWCH	P26217 erwina chr
760	28	6.6	79	1	YK15_CAEEL	P41314 didelphis m	833	28	6.6	90	1	YK16_ERWCH	Q9qu57 conus glori
761	28	6.6	79	1	YK15_CAEEL	P41314 didelphis m	834	28	6.6	90	1	YK16_ERWCH	P79729 brachydanio
762	28	6.6	80	1	YK15_CAEEL	P41314 didelphis m	835	28	6.6	90	1	YK16_ERWCH	O96033 homo sapien
763	28	6.6	80	1	YK15_CAEEL	P41314 didelphis m	836	28	6.6	90	1	YK16_ERWCH	P02907 staphylococ



## RESULT 2

## RESULT 2

OS *Methanococcus jannaschii*.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP. SEQUENCE FROM N.A.

```

CC SIGNAL TRANSDUCER CAN PLAY VERY DIFFERENT ROLES IN DIFFERENT CELL
CC TYPES AS A DIRECT CONSEQUENCE OF ITS GLYCOSYLATION.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM, IN
CC POSTMITOTIC CELLS OF SPINAL CORD, HINDBRAIN, MIDBRAIN AND
CC FOREBRAIN. EXPRESSED IN EPITHELIUM DURING THE DEVELOPMENT OF NON-
CC NEURAL TISSUES. EXPRESSED IN TOOTH DEVELOPMENT, SPECIFICALLY IN
CC MESENCHYMAL CELLS DIFFERENTIATING INTO ODONTOBLAST IN DENTAL
CC PAPILLA, AS WELL AS IN THE DEVELOPING EYE AND HAIR FOLLICLE.
CC -!- DEVELOPMENTAL STAGE: DETECTED IN PRIMITIVE ECTODERM, MESODERM AND
CC -!- VENTRAL ENDODERM; DOWN-REGULATED WHEN ORGANOGENESIS IS COMPLETED.
CC -!- PTM: EXTENSIVELY O-GLYCOSYLATED (BY SIMILARITY). THE CARBOHYDRATE
CC STRUCTURE MAY BE REGULATED IN A TISSUE SPECIFIC AND DEVELOPMENTAL
CC STAGE SPECIFIC MANNER.
CC -!- SIMILARITY: TO OTHER MAMMALIAN SPECIES CD24.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: Z11663; CAA77731.1; -
CC GENE: CD24;
CC EMBL: U49062; AAG91470.1; -
CC GLYCOPROTEIN; GPI-anchor; Membrane; Signal; Differentiation.
CC FT SIGNAL 1 26 POTENTIAL.
CC FT CHAIN 27 56 SIGNAL TRANSDUCER CD24.
CC FT PROPEP 57 76 REMOVED IN MATURE FORM (BY SIMILARITY).
CC FT CARBOHYD 27 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 37 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT LIPID 56 56 GPI-ANCHOR (POTENTIAL).
CC FT SEQUENCE 76 AA; 7862 MW; 42845E70EC39D958 CRC64;
CC -----
CC Query Match 10.6%; Score 45; DB 1; Length 76;
CC Best Local Similarity 24.4%; Pred. No. 1.7e+02;
CC Matches 19; Conservative 10; Mismatches 15; Indels 34; Gaps 4;
CC -----
CC QY 6 CSSQSPMSRISNSLVAMDFSGOKS-RVIENTEALSVAVLEGIAWKKGLRLQTHG 64
CC I: I::I III:I III:I
CC 26 CNOTSVAP-----FSGNOSIAAPNPTNAT-----RSGC----- 55
CC -----
CC QY 65 SPTASSQSASATNMAIHS 82
CC I: II::I :I: I
CC DB 56 ---SSLQSTAGLLALSLS 70
CC -----
CC RESULT 5
CC WT2_MALDO
CC ID WT2_MALDO STANDARD; PRT; 79 AA.
CC AC Q34058;
CC OS 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DT Metallothionein-like protein type 2.
CC GN MTL.
CC OS Malus domestica (Apple) (Malus sylvestris).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC OC eurosid I; Rosales; Rosaceae; Maloideae; Malus.
CC NCBI_TaxID:3750;
CC NRN [1]
CC NRN SEQUENCE FROM N.A.
CC TISSUE=Fruit cortical tissue;
CC ORA Reid S.J., Ross G.S.;
CC RA "Up-regulation of two cDNA clones encoding metallothionein-like
CC RT proteins in apple fruit during cool storage.";
CC RT Physiol. Plantarum 100:183-189,(1997).
CC CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY: FAMILY 15

```





OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / AFCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;  
 RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kierlavage R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Glodek A.,  
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii";  
 RT Science 273:1058-1073(1996).  
 RL  
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 CC  
 DR EMBL; U67505; AAB98558.1; -  
 DR TIGR; MJ0567; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 82 AA; 8766 MW; 3F3810EEFC9F81CE CRC64;  
 Query Match 10.2%; Score 43; DB 1; Length 82;  
 Best Local Similarity 25.9%; Pred. No. 3.1e+02;  
 Matches 15; Conservative 10; Mismatches 15; Indels 18; Gaps 3;  
 QY 4 GSSQSSISPMRSISLVMDFSGOKSRVJEN-----PTLSVAVEGLAWR 53  
 DB 20 AGCCAG-----QRLVSGINGISGLKLVIRNONGPVILSTKGSNIAIGRLANK 67  
 RESULT 9  
 ID HFO2\_METFO STANDARD; PRT; 67 AA.  
 AC P48783;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Archaeal histone A2.  
 GN HFOA2.  
 OS Methanobacterium formicicum.  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanobacterium.  
 OX NCBI\_TaxID=2162;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JF-1;  
 RX MEDLINE=95138058; PubMed=7836329;  
 RA Darcy T.J., Sandman K.M., Reeve J.N.;  
 RT "Methanobacterium formicicum, a mesophilic methanogen, contains three  
 RT Hfo histones";  
 RL J. Bacteriol. 177:858-860(1995).  
 RL  
 CC PARTIAL SEQUENCE.  
 RX MEDLINE=95138058; PubMed=7836329;  
 RA Sandman K.M., Grayling R.A., Reeve J.N.;  
 RL Unpublished results, cited by:  
 RL Darcy T.J., Sandman K.M., Reeve J.N.;  
 RL J. Bacteriol. 177:858-860(1995).  
 CC  
 CC -!- FUNCTION: BINDS AND COMPACT DNA (95 TO 150 BASE PAIRS) TO FORM  
 CC NUCLEOSOME-LIKE STRUCTURES THAT CONTAIN POSITIVE DNA SUPERCOILS.  
 CC  
 CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).

CC  
 CC -!- SIMILARITY: BELONGS TO THE HMF FAMILY OF ARCHAEAL HISTONES  
 CC  
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 CC  
 DR EMBL; U12931; AAA67722.1; -  
 DR HSP; P48781; 1567;  
 DR InterPro; IPR003958; CBFA\_NFYB\_domain.  
 DR InterPro; IPR004822; Histone\_core.  
 DR Pfam; PF00808; CBFD\_NFYB\_HMF; 1.  
 KW DNA-binding; Multigene family.  
 FT INIT\_MET 0  
 FT MET 0  
 SQ SEQUENCE 67 AA; 7064 MW; 0AAFCAC535BF2E10 CRC64;  
 Query Match 10.0%; Score 42.5; DB 1; Length 67;  
 Best Local Similarity 25.8%; Pred. No. 2.8e+02;  
 Matches 16; Conservative 12; Mismatches 25; Indels 9; Gaps 2;  
 QY 11 ISPMRSISLVMDFSGOKSRVJENPTLSVAVEGLAWRKGCRLRGLTH-GSPTAS 69  
 DB 5 IAPVGRILKNA-----CAQRISDDAKEALAKALENGEELAKKAVELAKHGRKTVK 56  
 QY 70 SQ 71  
 DB 57 AE 58  
 RESULT 10  
 ID RS19\_CHLIR STANDARD; PRT; 88 AA.  
 AC O84529; Q9PJL8;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30S ribosomal protein S19.  
 GN RPSS OR RS19 OR CT524 OR TC0811.  
 OS Chlamydia trachomatis, and  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813, 83560;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C. trachomatis; STRAIN=D/UW-3/Cx;  
 RX MEDLINE=9900809; PubMed=9784136;  
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
 RA Davis R.W.;  
 RT "Genome sequence of an obligate intracellular pathogen of humans:  
 RT Chlamydia trachomatis";  
 RL Science 282:754-759(1998).  
 RL  
 RN  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C. muridarum; STRAIN=MoPn / Nigg;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RT pneumoniae AR39";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 RL  
 CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC  
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
 CC  
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CC EMBL: AE001323; AAC68125.1; -;  
 CC EMBL: AE002347; AAF73603.1; -;  
 CC HSSP: TC0811; IQKF.  
 CC InterPro: IPR002222; Ribosomal\_S19.  
 CC Pfam: PF00203; Ribosomal\_S19; 1.  
 CC PRINTS: PR00975; RIBOSOMALS19.  
 CC PRODOM: PD01012; Ribosomal\_S19; 1.  
 CC TIGRFAMs: TIGR01050; rpsS\_bact; 1.  
 CC PROSITE: PS00323; RIBOSOMAL\_S19; 1.  
 CC Ribosomal protein; tRNA-binding; Complete proteome.  
 CC KW Ribosomal protein; tRNA-binding; Complete proteome.  
 CC SEQUENCE 88 AA; 10233 MW; ABB042B14E4C22F6 CRC64;

Query Match 10.0%; Score 42.5; DB 1; Length 88;  
 Best Local Similarity 26.2%; Pred. No. 3.9e+02;  
 Matches 16; Conservative 11; Mismatches 27; Indels 7; Gaps 2;

QY 12 SPMSISENSLVAEFGSKSRVIENTEALVAVVEGLAWKKGCLRLGTHGSPPTASSO 71  
 DB 29 TPITWRSRSMITPENGHTFEV-HNGKKFLTVFVSETWVGHLG-----EFSPTRMFK 81

QY 72 S 72  
 DB 82 S 82

RESULT 11  
 AT12\_HSV4

ID AT12\_HSV4 STANDARD; PRT; 45 AA.  
 AC Q00041;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Alpha trans-inducing factor 82 kDa protein (Fragment).  
 GN 14 OR B7.  
 OS Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus  
 OS type 1 subtype 2).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=10333;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91202570; PubMed-1850013;  
 RA Whittaker G.R., Riggio M.P., Halliburton I.W., Killington R.A.,  
 RA Allen G.P., Meredith D.M.;  
 RT Antigenic and protein sequence homology between VP13/14, a herpes  
 RT simplex virus type 1 tegument protein, and gp10, a glycoprotein of  
 RT equine herpesvirus 1 and 4;  
 RL Virol. 65:2320-2326(1991).  
 CC -!- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT  
 CC ACTIVATION OF ALPHA GENES (BY SIMILARITY).

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CC EMBL: X17684; CAA35673.1; -;  
 CC PIR: S36709; S36709.  
 CC InterPro: IPR005051; Herpes\_UL46.  
 CC Pfam: PF03387; Herpes\_UL46; 1.  
 CC Transcription regulation; Trans-acting factor.  
 CC NON\_TER 45 45  
 CC SEQUENCE 45 AA; 4862 MW; AAE468C9C2B08BE4 CRC64;

Query Match 9.9%; Score 42; DB 1; Length 45;  
 Best Local Similarity 33.3%; Pred. No. 2e+02;  
 Matches 19; Conservative 4; Mismatches 16; Indels 18; Gaps 3;  
 QY 25 MDFSQKSS--RVIENTEALVAVVEGLAWKKGCLRLGTHGSPPTASSOATNNAI 79  
 DB 1 MEASGSARVSKNLIERRAV-----KCL-----LPTSDVMDAAYNAL 41

RESULT 12

YHGG\_ECOLI  
 ID YHGG\_ECOLI STANDARD; PRT; 78 AA.  
 AC P46845;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yhgG.  
 DE Hypothetical protein yhgG.  
 GN YHGG OR B3410 OR Z4765 OR ECS4252.  
 OS Escherichia coli, and  
 OS Escherichia coli, and  
 OS Escherichia coli, and  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562, 83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=K12 / MGL1655;  
 RX MEDLINE-97436617; PubMed-9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RA "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE-21074935; PubMed-11208551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.G.,  
 RA Welch R.A., Blattner F.R.;  
 RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:529-533(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE-21156231; PubMed-11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.;  
 RA "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12";  
 RL DNA Res. 8:11-22(2001).

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CC EMBL: U18997; AAA58208.1; -;  
 CC EMBL: AE000416; AAC76435.1; -;  
 CC EMBL: AE005563; AAG58511.1; -;  
 CC EMBL: AP002565; BAB37675.1; -;  
 CC ECGene: BGI2933; yhgG.  
 CC Hypothetical protein; Complete proteome.  
 CC SEQUENCE 78 AA; 8660 MW; 88976DE22CA9024B CRC64;

```

Query Match          9.9%; Score 42; DB 1; Length 78;
Best Local Similarity 27.3%; Pred. No. 3.8e+02;
Matches 15; Conservative 11; Mismatches 21; Indels 8; Gaps 2;

QY 8 SOSISPMRSISLAVDFSGOKSRVIENPTAELSAVVE---EGLAWRKGCCLR 59
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 23 SQTLPQPMINAMQLQESGKAVRIQEPDGLSGCKSCPEG-----KACLR 72

RESULT 13
TMOB_PSEME
ID TMOB_PSEME STANDARD; PRT; 83 AA.
AC Q00457;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Toluene-4-monooxygenase system protein B (BC 1.14.13.-).
GN TMOB.
OS Pseudomonas mendocina.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=300;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RC STRAIN=KRI;
RX MEDLINE=91358306; PubMed=1885512;
RA Yen K.-M., Karl M.R., Blatt L.M., Simon M.J., Winter R.B.,
RA Fausset P.R., Lu H.S., Harcourt A.A., Chen K.K.;
RT Cloning and characterization of a Pseudomonas mendocina KRI gene
RT cluster encoding toluene-4-monooxygenase.
RL J. Bacteriol. 173:5315-5327(1991).
CC -!- FUNCTION: HYDROXYLATES TOLUENE TO FORM P-CRESOL.
CC -!- COFACTOR: FAD; REQUIRES FE(+2) FOR ACTIVITY.
CC -!- PATHWAY: Toluene degradation; first step.
CC -!- SUBUNIT: THE MULTICOMPONENT ENZYME TOLUENE-4-MONOOXYGENASE
CC IS FORMED BY THE TMOA, TMOB, TMOG, TMOH, TMOI, TMOJ AND TMOF
CC POLYPEPTIDES.
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-----
EMBL; M65106; AAA26000.1;
KW Aromatic hydrocarbons catabolism; Oxidoreductase; Flavoprotein;
KW Monooxygenase; FAD; Iron.
PT INIT_MET 0
SQ SEQUENCE 83 AA; 9457 MW; 4729FE73F266F44 CRC64;

Query Match          9.9%; Score 42; DB 1; Length 83;
Best Local Similarity 26.5%; Pred. No. 4.1e+02;
Matches 13; Conservative 9; Mismatches 19; Indels 8; Gaps 2;

QY 6 CSSQISIP-----MRSISLAVDFSGOKSRVIENPTAELSAVVE 48
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 37 CVNRVAPREGVMVRKHKRSTELFPRDNTIAESGL--NPTEVIDVVFEE 83

RESULT 14
HFOB_METFO
ID HFOB_METFO STANDARD; PRT; 67 AA.
AC P48784;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Archaeal histone B.
GN HFOB.
OS Methanobacterium formicicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;

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Methanobacteriaceae; Methanobacterium.
NCBI_TaxID=2162;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JF-1;
RX MEDLINE=95138058; PubMed=7836329;
RA Darcy T.J., Sandman K.M., Reeve J.N.;
RT "Methanobacterium formicicum, a mesophilic methanogen, contains three
RT HFO histones."
RL J. Bacteriol. 177:858-860(1995).
CC -!- FUNCTION: BINDS AND COMPACT DNA (95 TO 150 BASE PAIRS) TO FORM
CC NUCLEOSOME-LIKE STRUCTURES THAT CONTAIN POSITIVE DNA SUPERCOILS.
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE HMF FAMILY OF ARCHAEAL HISTONES.
-----
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-----
EMBL; U12929; AAA67720.1;
DR HSSP; P48781; 1B67.
DR InterPro; IPR003958; CBFA_NFYB_domain.
DR InterPro; IPR004822; Histone_core.
DR Pfam; PF00808; CBFD_NFYB_HMF; 1.
DR DNA-binding; Multigene family.
KW SEQUENCE 67 AA; 7149 MW; 1132F83ACAD88445 CRC64;

Query Match          9.8%; Score 41.5; DB 1; Length 67;
Best Local Similarity 26.9%; Pred. No. 3.6e+02;
Matches 21; Conservative 14; Mismatches 20; Indels 23; Gaps 5;

QY 11 ISPMRSISLAVDFSGOKSRVIENPTAELSAVVEGLAWRKKG-----CLRGLTH- 63
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 IAFIGILKNA-----GAERVSDDAEALAKALE-----KGETIATEAVKLAKHA 50

QY 64 GSPTASSOSSATNMAIHR 81
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 51 GRKTV--RASDVELAVKR 66

RESULT 15
RS19_MYCGA
ID RS19_MYCGA STANDARD; PRT; 87 AA.
AC O52336;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19.
GN RPSS OR RPS19.
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5969Var.B;
RA Skamrov A., Feoktistova E., Goldman M., Beabealashvili R.;
RT Cloning and sequencing of Mycoplasma gallisepticum chromosome region
RT containing operons S10 and rin235."
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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EMBL:	AF0367708;	AAB953391.1;	-
HSP:	P80381;	LQKX	
InterPro:	IPR002222;	Ribosomal_S19.	
Pfam:	PF0203;	Ribosomal_S19.1.	
PRINTS:	PR00975;	RIBOSOMALS19.	
ProDom:	PD001012;	Ribosomal_S19; 1.	
TIGRFAMs:	TIGR01050;	rpss_bact; 1.	
PROSITE:	PS00323;	RIBOSOMAL_S19; 1.	
Ribosomal	protein;	rRNA-binding.	
SEQUENCE	87 AA;	9979 MW;	1C3FD0108656185EC CRC64;

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RESULT 16
C552_MARHY STANDARD;      PRT;      88 AA.
ID C552_MARHY ID
AC P82903;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c-552 (C552).
DE Marine bacterium hydrocarbonoclasticus (Pseudomonas nautica).
OS Bacterium, Proteobacteria, gamma subdivision; Alteromonadaceae;
OC Marinobacterales group; Marinobacter.
NCBI_TaxID=2743;
[1]
RN SEQUENCE.
RP STRAIN-617;
RC MEDLINE=95010061; PubMed=7925398;
RX Saitava L.M., Fauque G., Besson S., Moura I.;
RT "Physico-chemical and spectroscopic properties of the monohemic
RT cytochrome C552 from Pseudomonas nautica 617.";
RN Eur. J. Biochem. 224:1011-1017(1994).
RN [2]
RN SEQUENCE.
RC STRAIN-617;
RC Maras B., Schinina E., Di Leandro L., Pitari G., Malatesta F.;
RA Submitted (NOV-2001) to the SWISS-PROT data bank.
RX [3]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MASS SPECTROMETRY.
RN STRAIN-617;
RX MEDLINE=99299395; PubMed=10369779;
RC Brown K., Nurizzo D., Besson S., Shepard W., Moura J., Moura I.,
RA Tregoni M., Cambillau C.;
RM "MAD structure of Pseudomonas nautica dimeric cytochrome c552 mimicks
the c4 dihemic cytochrome domain association." ;
J. Mol. Biol. 289:1017-1028(1999).
CC -!- FUNCTION: ELECTRON DONOR FOR PERIPLASMIC NITRATE REDUCTASE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- PTM: BINDS ONE HEME GROUP PER MOLECULE.
CC -!- MASS SPECTROMETRY: MW=9466; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.
PDB: 1CNO; 22-JUL-99.
DR InterPro: IPR00345; Cyt_c_heme_bind.
DR InterPro: IPR003088; Cyt_C1.
DR InterPro: IPR002329; Cyt_C1C.
DR Pfam: PF00034; cytochrome_c_1.
DR PRINTS: PR00605; CYTCROME.CIC.
DR ProDom: PD004020; Cyt_C1C; 1.

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DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme; Periplasmic; 3D-structure.
FT BINDING 14 14 HEME (COVALENT).
FT BINDING 17 17 HEME (COVALENT).
FT METAL 18 18 IRON (HEME AXIAL LIGAND).
FT METAL 18 18 IRON (HEME AXIAL LIGAND).
FT METAL 36 36 IRON (HEME AXIAL LIGAND).
FT CONFLICT 36 36 K -> L (IN REF. 1).
FT CONFLICT 79 88 YASLPADGGQ -> GASXP (IN REF. 1).
FT CONFLICT 79 88 YASLPADGGQ -> GASXP (IN REF. 1).
SQ SEQUENCE 88 AA; 8847 MW; C8E8FEFEBG91AB2E0 CRC64;

Query Match 9.8%; Score 41.5; DB 1; Length 88;
Best Local Similarity 22.8%; Pred.No. 5e+02;
Matches 18; Conservative 13; Mismatches 29; Indels 19; Gaps 2;

QY 2 GRSCGSSQSPMRISLNVAMDFGQSRVIENPTALSVAVEGLAWRKKGCLRLG 61
Db 19 GONGISQVPIP-----NLAQKE-----QYLVAALKAYKAGQGGQADP 59
QY 62 THGSSTASSOSSATNNAIH 80
Db 60 MQGQATALSDADIANLAAY 78

RESULT 17
RS19_CHLPP
ID RS19_CHLPP STANDARD: PRT: 88 AA.
AC Q9ZTR1; Q9JRT8;
DC 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19.
GN RPSS OR RS19 OR CPN0643 OR CP0104.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
PC SEQUENCE FROM N.A.
RC STRAIN=RW029;
SC MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RT Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RL "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RN Nat. Genet. 21:385-389(1999).
RC SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RC "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RN Nucleic Acids Res. 28:1397-1406(2000).
RC SEQUENCE FROM N.A.
RC STRAIN=J138.
RX MEDLINE=20330349; PubMed=10871362;
RA Shiba T., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RC "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RN Nucleic Acids Res. 28:2311-2314(2000).
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
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RESULT 20	
GBG5_HUMAN	
ID GBG5_HUMAN	STANDARD;
AC P30670; Q61015;	PRT; 68 AA.
DT 01-APR-1993 / Rel 25	Created

DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-5 subunit.  
 GN GNG5 OR GNGT5.  
 OS Homo sapiens (Human),  
 OS Mus musculus (Mouse),  
 OS Rattus norvegicus (Rat), and  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606, 10090, 10116, 9913,  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human;  
 RX MEDLINE=99009227; PubMed=9790912;  
 RA Yu B., Aronson N.N. Jr.;  
 RL Structure of human G protein Ggamma5 gene GNG5.\*;  
 RL Biochem. Biophys. Res. Commun. 251:88-94(1998).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Blood;  
 RX MEDLINE=98318631; PubMed=9653160;  
 RA Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,  
 RA He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,  
 RA Wang Y.-X., Chen S.-J., Chen Z.;  
 RT Identification of genes expressed in human CD34(+) hematopoietic  
 RT stem/progenitor cells by expressed sequence tags and efficient full-  
 RT length cDNA cloning.\*;  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Brain;  
 RX Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine, and Rat; TISSUE=Liver;  
 RX MEDLINE=92195304; PubMed=1549114;  
 RA Fisher K.J., Aronson N.N. Jr.;  
 RT Characterization of the cDNA and genomic sequence of a G protein  
 RT gamma subunit (gamma 5).\*;  
 RL Mol. Cell. Biol. 12:1585-1591(1992).  
 RN (5)  
 RP SEQUENCE.  
 RC SPECIES=Bovine; TISSUE=Spleen;  
 RX MEDLINE=93356792; PubMed=8352779;  
 RA Morishita R., Masuda K., Niwa M., Kato K., Asano T.;  
 RT Identification of three forms of the gamma subunit of G proteins  
 RT isolated from bovine spleen.\*;  
 RL Biochem. Biophys. Res. Commun. 194:1221-1227(1993).  
 RN (6)  
 RP SEQUENCE OF 8-53 FROM N.A.  
 RC SPECIES=Mouse; STRAIN=CF-1 / Harlan;  
 RX MEDLINE=97011591; PubMed=8858601;  
 RA Williams C.J., Schultz R.M., Kopf G.S.;  
 RT G protein gene expression during mouse oocyte growth and maturation,  
 RT and preimplantation embryo development.\*;  
 RL Mol. Reprod. Dev. 44:315-323(1996).  
 CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE  
 CC INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE  
 CC SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE  
 CC GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-  
 CC EFFECTOR INTERACTION.  
 CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.  
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST SEVEN DIFFERENT GAMMA SUBUNITS  
 CC WITH POSSIBLE TISSUE-SPECIFIC DISTRIBUTION.  
 CC -1- SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.  
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 CC  
 CC EMBL; L22475; AAA03621.1;  
 CC Genew; HGNC:959; BAX.

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 CC  
 CC EMBL; AF085709; AAC72203.1;  
 CC EMBL; AF085709; AAC72203.1; JOINED.  
 CC EMBL; AC039355; AAC39869.1;  
 CC EMBL; BC003563; AAA03563.1;  
 CC EMBL; M57779; AAA30535.1;  
 CC EMBL; M57780; AAA41188.1;  
 CC EMBL; U38498; AAB01729.1;  
 CC PIR; JN0701; JN0701.  
 CC PIR; B42243; B42243.  
 CC Genew; HGNC:4408; GNG5.  
 CC MIM; 600874;  
 CC MIM; MGI:109164; Gng5.  
 CC InterPro; IPR001770; G-gamma.  
 CC Pfam; PF00631; G-gamma; 1.  
 CC PRINTS; PR00321; GPROTEIN.  
 CC ProDom; PD003783; G-gamma; 1.  
 CC SMART; SM00224; GGL; 1.  
 CC PROSITE; PS0058; G-PROTEIN\_GAMMA; 1.  
 CC Transducer; Prenylation; Lipoprotein; Lipoprotein; Multigene family.  
 CC KW TRANSFER; 65 65 GERANYL-GERANYL (BY SIMILARITY).  
 CC FT LIPID 65 65  
 CC FT PROPEP 66 68 REMOVED IN MATURE FORM (BY SIMILARITY).  
 CC SQ SEQUENCE 68 AA; 7318 MW; 9AF7A16558863602 CRC64;  
 CC  
 CC Query Match 9.6%; Score 40.5; DB 1; Length 68;  
 CC Best Local Similarity 36.4%; Pred No. 4.8e+02;  
 CC Matches 12; Conservative 5; Mismatches 15; Indels 1; Gaps 1;  
 CC  
 CC Qy 44 VAYEEGLAWRKKGCLRLGTHGCSPTASSQSSTN 76  
 CC Db 26 VKVSOAAADLKOFCLQNAQH-DPLLTVGVSSSTN 57  
 CC  
 CC RESULT 21  
 CC ID BAXC\_HUMAN STANDARD; PRT; 41 AA.  
 CC AC Q07815;  
 CC DT 01-FEB-1995 (Rel. 31, Created)  
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE BAX protein, cytoplasmic isoform gamma.  
 CC GN BAX.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC RN (1)  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=B-cell.  
 CC RX MEDLINE=93364978; PubMed=8358790;  
 RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;  
 RT Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 RT accelerates programmed cell death.\*;  
 RL Cell 74:609-619(1993).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC  
 CC EMBL; L22475; AAA03621.1;  
 CC Genew; HGNC:959; BAX.

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DR MM: 600040;
KW Apoptosis; Alternative splicing.
SQ SEQUENCE 41 AA; 4678 MW; D94639AAB8927859 CRC64;

Query Match
Best Local Similarity 9.5%; Score 40; DB 1; Length 41;
Matches 13; Conservative 5; Mismatches 12; Indels 12; Gaps 2;

QY 25 MDFSQKSRVTEPTALSVAVEEG-----LAWKKGKGLRL 60
      |||||
DB 1 MDGSG-----EQPRGVSSRIEQGEGWGRHPSNPWTCLRM 36

RESULT 22
HS2M-LYCSES
ID HS2M-LYCSES STANDARD; PRT; 56 AA.
AC P81161.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Heat shock 22 kDa protein, mitochondrial (fragments).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. SWEET;
RX MEDLINE=98345975; PubMed=9680997;
RA Banzet N., Richard C., Deveaux Y., Kazmaier M., Gagnon J.,
RA Triantaphyllides C.;
RT "Accumulation of small heat shock proteins, including mitochondrial
RT HSP22, induced by oxidative stress and adaptive response in tomato
RT cells";
RL Plant J. 13:519-527(1998).
CC -!- FUNCTION: MAY PLAY A PROTECTIVE ROLE AGAINST OXIDATIVE STRESS.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- INDUCTION: BY HEAT SHOCK, AND UNDER OTHER CONDITIONS OF STRESS,
CC SUCH AS INCREASED SALT CONCENTRATION AND STARVATION.
CC -!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
CC FAMILY.
DR InterPro: IPR02066; HSP20.
DR PROSITE: PS01031; HSP20; PARTIAL.
KW Heat shock; Mitochondrion.
FT NON_CONS 14 15
FT UNSURE 15 15
FT NON_CONS 35 36
FT UNSURE 36 36
FT NON_TER 56 56
SQ SEQUENCE 56 AA; 6446 MW; 2AB9F927C7720076 CRC64;

Query Match
Best Local Similarity 9.5%; Score 40; DB 1; Length 56;
Matches 9; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 38 PTEALSVAVEEGLAWKKGKGLRL 60
      |||||
DB 21 PVENRVVALENTLIMKNGVLKV 43

RESULT 23
RPON_THEAC
ID RPON_THEAC STANDARD; PRT; 72 AA.
AC Q9HLO9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE DNA-directed RNA polymerase subunit N (EC 2.7.7.6).
GN RPON OR TA0431.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.

```

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OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruedp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA News H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum";
RL Nature 407:308-313(2000).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -!- SIMILARITY: BELONGS TO THE ARCHAEABACTERIA RPON / EUKARYOTIC RPB10.
CC RNA POLYMERASE SUBUNIT FAMILY.
CC -----
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CC -----
DR EMBL: AL445064; CAC11573.1;
DR HSP: Q26147.1; EF4.
DR InterPro: IPR000268; RNA_pol_N.
DR Pfam: PF01194; RNA_pol_N; 1.
DR PROSITE: PS01112; RNA_POL_N_8KD; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
KW Metal-binding; Complete proteome.
FT METAL 7 7 ZINC (BY SIMILARITY).
FT METAL 10 10 ZINC (BY SIMILARITY).
FT METAL 53 53 ZINC (BY SIMILARITY).
FT METAL 54 54 ZINC (BY SIMILARITY).
SQ SEQUENCE 72 AA; 8368 MW; 792AFDA20E5447E2 CRC64;

Query Match
Best Local Similarity 9.5%; Score 40; DB 1; Length 72;
Matches 12; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 11 ISPMRSISENSLVAMDFSGQKSRVIENTEALSVAVEE 48
      |||||
DB 2 IIPVRCFSGRVIASDYGRYIKRVNEIKAEGRDPSPPE 39

RESULT 24
RPON_THEVO
ID RPON_THEVO STANDARD; PRT; 72 AA.
AC Q979K0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE DNA-directed RNA polymerase subunit N (EC 2.7.7.6).
GN RPON OR TV1161 OR TVG1188103.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GS51 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as

```

CC substrates.  
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +  
CC (RNA)(N).  
CC -I- SIMILARITY: BELONGS TO THE ARCHAEABACTERIA RPON / EUKARYOTIC RPBL0  
CC RNA POLYMERASE SUBUNIT FAMILY.

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CC -----  
CC EMBL: AP000995; BAB60303.1; -  
CC InterPro: IPR000268; RNA\_POL\_N.  
CC Pfam: PF01194; RNA\_POL\_N.1.  
CC PROSITE: PS01112; RNA\_POL\_N.8KD.1.  
CC Transferrase: DNA-directed RNA polymerase; Transcription; Zinc;  
CC Metal-binding; Complete proteome.  
CC FT METAL 7 7 ZINC (BY SIMILARITY).  
CC FT METAL 10 10 ZINC (BY SIMILARITY).  
CC FT METAL 53 53 ZINC (BY SIMILARITY).  
CC FT METAL 54 54 ZINC (BY SIMILARITY).  
CC SEQUENCE 72 AA; 8483 MW; 06AEC0AA7AC73CA6 CRC64;

Query Match 9.5%; Score 40; DB 1; Length 72;  
Best Local Similarity 28.9%; Pred. No. 5.9e+02;  
Matches 11; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 11 ISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEE 48  
| | | | : | | : | | : | |  
DB 2 IIPVRCGGRVIASDGYRLRINEIRSEGREPTAE 39

RESULT 25  
V187\_BPT7  
ID V187\_BPT7 STANDARD; PRT; 83 AA.  
AC P03788;  
DT 21-JUL-1986 (Rel. 01, Created).  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-MAR-1989 (Rel. 10, Last annotation update)  
DE Gene 18.7 protein.  
GN 18.7.  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83241725; PubMed=6864790;  
RA Dunn J.J., Studier F.W.;  
RT "Complete nucleotide sequence of bacteriophage T7 DNA and the  
RL J. Mol. Biol. 166:477-535(1983).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: V01146; CA24439.1; -  
CC PIR: A04413; W8BPG7.  
DR PIR: S42337; S42337.  
SQ SEQUENCE 83 AA; 9326 MW; B3DE055DE79A53C5 CRC64;

Query Match 9.3%; Score 39.5; DB 1; Length 83;  
Best Local Similarity 34.1%; Pred. No. 7.9e+02;  
Matches 15; Conservative 8; Mismatches 8; Indels 13; Gaps 3;

QY 4 SGCSSQISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEE 44  
| | | | : | | : | | : | |  
DB 47 SGCASESKLP-----EPPMVSVD-----SLMVEPNLTTEMLNY 80

Search completed: March 28, 2003, 09:06:08  
Job time : 24.5197 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 09:02:45 ; Search time 33.7323 Seconds  
(without alignments)  
239.394 Million cell updates/sec

File: us-09-936-697-6  
Perfect score: 423

Sequence: 1 QGRSCSSQSIIPMRISSEN.....SPTASSQSSATNMAHRSP 84

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 22614

Minimum DB seq length: 40  
Maximum DB seq length: 90

Post-processing: Minimum Match 0%  
Maximum Match 100%  
-Listing first 1000 summaries

Database: April 73  
1: Pir1  
2: Pir2  
3: Pir3  
4: Pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	54	12.8	80	2 T27603	hypothetical prote
2	51.5	12.2	76	2 E64324	DNA-directed RNA p
3	48	11.3	89	2 AG3246	conserved hypothet
4	47.5	11.2	90	2 F95310	hypothetical prote
5	46.5	11.0	62	2 E64510	hypothetical prote
6	46	10.9	77	2 S24471	gag polyprotein -
7	46	10.9	87	2 D82861	hypothetical prote
8	45.5	10.8	65	2 A82657	hypothetical prote
9	45.5	10.8	73	2 T25763	hypothetical prote
10	45.5	10.8	81	2 JC5345	hypothetical prote
11	45	10.6	60	2 A42960	cdcl protein - Clo
12	45	10.6	76	2 T53107	ferredoxin 2[4Fe-4
13	45	10.6	75	2 T53107	CD24 precursor - r
14	45	10.6	77	2 H69420	hydrogenase expres
15	45	10.6	79	2 D81246	hypothetical prote
16	45	10.6	82	2 D69087	metallothionein-li
17	45	10.6	86	2 C41139	hydrogenase expres
18	44.5	10.5	64	2 AB2271	protein kinase 3 (
19	44.5	10.5	79	2 S75293	periplasmic mercur
20	44	10.4	51	2 D85907	hypothetical prote
21	44	10.4	78	2 B90959	hypothetical prote
22	44	10.4	78	2 A75411	probable phage tai
23	43.5	10.3	83	2 G90914	hypothetical prote
24	43.5	10.3	87	2 S60284	excisionase (impor
25	43.5	10.3	89	2 AH2653	B12D protein - bar
26	43	10.2	82	1 G64370	hypothetical prote
27	42.5	10.0	52	2 D82682	conserved hypothet
28	42.5	10.0	64	2 AC2544	hypothetical prote
29	42.5	10.0	68	2 T00189	hypothetical prote

30	42.5	10.0	74	2 S72807	hypothetical prote
31	42.5	10.0	88	2 B71507	probable S19 ribos
32	42	9.9	43	2 S35580	cysteine proteinas
33	42	9.9	45	2 S36709	B7 protein - equin
34	42	9.9	53	2 C82776	hypothetical prote
35	42	9.9	64	2 C96933	hypothetical prote
36	42	9.9	73	2 F69062	molybdenum transp
37	42	9.9	78	2 D91160	hypothetical prote
38	42	9.9	78	2 C86006	hypothetical prote
39	42	9.9	78	2 E65136	hypothetical prote
40	42	9.9	79	2 A86517	hypothetical prote
41	42	9.9	79	2 B72106	hypothetical prote
42	42	9.9	81	2 D81565	hypothetical prote
43	42	9.9	86	2 AD1584	hypothetical prote
44	42	9.9	86	2 AE1230	hypothetical prote
45	42	9.9	89	2 A84086	hypothetical prote
46	41.5	9.8	72	2 A97136	zn-finger containi
47	41.5	9.8	77	2 B98247	hypothetical prote
48	41.5	9.8	80	2 S00858	T-cell receptor al
49	41.5	9.8	88	2 E72055	S19 ribosomal prot
50	41.5	9.8	88	2 H86570	S19 ribosomal prot
51	41	9.7	52	2 A34657	cathepsin E (EC 3.
52	41	9.7	60	2 I68870	interleukin 2 - we
53	41	9.7	62	2 I34512	interleukin 2 - mo
54	41	9.7	63	2 T03652	probable carbonate
55	41	9.7	66	2 F90146	DNA-directed RNA p
56	41	9.7	68	2 D53203	hypothetical prote
57	41	9.7	75	2 S24478	gag polyprotein -
58	41	9.7	86	2 E81144	hypothetical prote
59	40.5	9.6	68	2 B42243	GTP-binding regula
60	40.5	9.6	70	2 E70985	hypothetical prote
61	40.5	9.6	73	2 AG0172	proteoglycan core
62	40.5	9.6	77	2 AG3462	hypothetical prote
63	40	9.5	41	2 C47538	bcl-2-associated p
64	40	9.5	51	2 D81039	hypothetical prote
65	40	9.5	63	2 AC2553	hypothetical prote
66	40	9.5	64	2 S22044	gag polyprotein -
67	40	9.5	66	2 A43602	T-cell-stimulating
68	40	9.5	67	2 G97092	endoglucanase (tru
69	40	9.5	70	2 T02541	hypothetical prote
70	40	9.5	72	2 S24477	gag polyprotein -
71	40	9.5	73	2 S24472	gag polyprotein -
72	40	9.5	74	2 S24473	gag polyprotein -
73	40	9.5	75	2 S24475	late expression fa
74	40	9.5	75	2 S24474	voltage-dependent
75	40	9.5	76	2 T30403	putative small nuc
76	40	9.5	77	2 S31660	hypothetical prote
77	40	9.5	78	2 H90114	hypothetical prote
78	40	9.5	83	2 A82386	conserved hypothet
79	40	9.5	88	2 S77431	hypothetical prote
80	40	9.5	90	1 D69782	4-oxalocrotonate t
81	39.5	9.3	56	2 AE2413	probable transcrip
82	39.5	9.3	61	2 F86696	repressor protein
83	39.5	9.3	67	2 AF1487	hypothetical prote
84	39.5	9.3	67	2 AH1375	hypothetical prote
85	39.5	9.3	72	2 G97751	hypothetical prote
86	39.5	9.3	75	2 C81951	hypothetical prote
87	39.5	9.3	75	2 A70610	hypothetical prote
88	39.5	9.3	77	2 B95003	hypothetical prote
89	39.5	9.3	77	2 AD1945	hypothetical prote
90	39.5	9.3	81	2 F90454	hypothetical prote
91	39.5	9.3	83	1 W88PG7	gene 18.7 protein
92	39	9.2	45	1 C64901	ribosomal protein
93	39	9.2	45	1 D50889	30S ribosomal subu
94	39	9.2	46	2 E85798	30S ribosomal subu
95	39	9.2	46	2 PC4162	toxin-co-regulated
96	39	9.2	62	2 T06654	hypothetical prote
97	39	9.2	64	2 A48411	Myf5 homolog - chi
98	39	9.2	69	2 T44123	hypothetical prote
99	39	9.2	72	2 AD3532	hypothetical prote
100	39	9.2	77	2 B83269	hypothetical prote
101	39	9.2	81	1 C70910	hypothetical prote
102	39	9.2	81	2 A97803	hypothetical prote





249	35.5	8.4	65	2	A95330	hypothetical prote	322	34.5	8.2	64	2	H98033	hypothetical prote
250	35.5	8.4	69	2	A56378	GTP-binding regula	323	34.5	8.2	66	2	E41991	S2 protein - equin
251	35.5	8.4	69	2	D97809	hypothetical prote	324	34.5	8.2	67	2	T36000	hypothetical prote
252	35.5	8.4	71	2	T09587	metallothionein-li	325	34.5	8.2	68	2	AD1306	probable mercuric
253	35.5	8.4	75	2	S07730	H+-transporting tw	326	34.5	8.2	68	2	E82008	hypothetical prote
254	35.5	8.4	75	2	T04547	hypothetical prote	327	34.5	8.2	71	2	E98040	degenerative trans
255	35.5	8.4	78	2	E84686	hypothetical prote	328	34.5	8.2	72	2	S58489	hypothetical prote
256	35.5	8.4	79	2	F97432	hypothetical prote	329	34.5	8.2	72	2	I67891	yhdl protein - Esc
257	35.5	8.4	82	2	F90468	hypothetical prote	330	34.5	8.2	72	2	AE1875	hypothetical prote
258	35.5	8.4	82	2	A0617	copper binding pro	331	34.5	8.2	73	2	D64683	ribosomal protein
259	35.5	8.4	83	2	B46679	exonuclease [ampr	332	34.5	8.2	73	2	JE0035	hypothetical 9K pr
260	35.5	8.4	84	2	T06111	hypothetical prote	333	34.5	8.2	75	2	B33335	integrin PS2 m8 al
261	35.5	8.4	86	2	H96679	hypothetical prote	334	34.5	8.2	76	2	B82441	hypothetical prote
262	35.5	8.4	87	2	S78075	hypothetical prote	335	34.5	8.2	77	2	T16222	hypothetical prote
263	35.5	8.4	87	2	D56273	probable transpos	336	34.5	8.2	78	2	A10451	hypothetical prote
264	35.5	8.4	88	2	C90178	ISU ribosomal prot	337	34.5	8.2	79	2	B95867	conserved hypothet
265	35.5	8.4	88	2	T29934	hypothetical prote	338	34.5	8.2	80	2	AF3364	hypothetical prote
266	35.5	8.4	89	2	A4384	major merozoite su	339	34.5	8.2	81	2	T01671	vpu protein - huma
267	35.5	8.4	89	2	T17956	hypothetical prote	340	34.5	8.2	81	2	E59093	hypothetical prote
268	35.5	8.4	89	2	H69871	hypothetical prote	341	34.5	8.2	83	2	B95974	probable transcrip
269	35.5	8.4	89	2	D82528	hypothetical prote	342	34.5	8.2	84	2	E75545	conserved hypothet
270	35	8.3	40	2	A29184	hypothetical prote	343	34.5	8.2	85	2	T47903	ribosomal protein
271	35	8.3	50	2	F72765	vitellogenin - tur	344	34.5	8.2	85	2	B24886	P(-)lrrp(-) fibrin
272	35	8.3	53	2	S56726	probable ribosomal	345	34.5	8.2	85	2	F55171	conserved hypothet
273	35	8.3	54	2	S72975	calcium-dependent	346	34.5	8.2	85	2	F98037	conserved hypothet
274	35	8.3	55	2	AD2382	glutamate decarbox	347	34.5	8.2	86	2	T03007	ribosomal protein
275	35	8.3	61	2	A81781	hypothetical prote	348	34.5	8.2	86	2	S35979	hypothetical prote
276	35	8.3	62	2	I47018	probable membrane	349	34.5	8.2	86	2	H91296	hypothetical prote
277	35	8.3	63	2	F59147	antigen WCL [simil	350	34.5	8.2	87	2	G71107	hypothetical prote
278	35	8.3	63	2	B5879	conotoxin P5.1 pre	351	34.5	8.2	87	2	B86138	hypothetical prote
279	35	8.3	68	2	G59093	cannabinoid recept	352	34.5	8.2	87	2	AD2239	hypothetical prote
280	35	8.3	68	2	AF2089	hypothetical prote	353	34.5	8.2	87	2	A95026	hypothetical prote
281	35	8.3	69	2	T18075	hypothetical prote	354	34.5	8.2	89	2	B97897	ribosomal protein
282	35	8.3	70	1	ELVXCH	eglin C - medicina	355	34.5	8.2	89	2	D82717	30S ribosomal prot
283	35	8.3	70	2	ELXCH	hypothetical prote	356	34.5	8.2	89	2	T50144	30S ribosomal prot
284	35	8.3	72	2	A88023	interleukin 2 - mo	357	34.5	8.2	89	2	A96505	intermembrane prot
285	35	8.3	72	2	T03195	hypothetical prote	358	34.5	8.2	90	2	D38179	probable glycine-r
286	35	8.3	72	2	G71355	probable ribosomal	359	34.5	8.2	90	2	T49083	hypothetical prote
287	35	8.3	73	2	A29172	cathepsin B-like c	360	34.5	8.2	90	2	I65746	hypothetical prote
288	35	8.3	75	2	S19695	matting pheromone E	361	34	8.0	42	2	A95166	trioponyosin - huma
289	35	8.3	75	2	S17341	hypothetical prote	362	34	8.0	44	2	E84151	hypothetical prote
290	35	8.3	75	2	T24847	hypothetical prote	363	34	8.0	44	2	E84151	hypothetical prote
291	35	8.3	75	2	T06954	hypothetical prote	364	34	8.0	46	2	E90537	gene 1.1 protein -
292	35	8.3	77	2	AC3626	hypothetical prote	365	34	8.0	50	2	E90557	probable ribosomal
293	35	8.3	81	2	D97063	glutaredoxin [limpo	366	34	8.0	50	2	C72528	gp62 protein - Myc
294	35	8.3	82	2	T18102	uncharacterized pr	367	34	8.0	51	2	E72807	4-oxalocrotonate t
295	35	8.3	82	2	F82644	hypothetical prote	368	34	8.0	62	2	S31217	cathepsin B-like c
296	35	8.3	83	2	D97063	hypothetical prote	369	34	8.0	62	2	AD3240	hypothetical prote
297	35	8.3	83	2	JW0086	trichothecene 3-O-	370	34	8.0	64	2	S32026	Sp12 protein homol
298	35	8.3	84	2	T13498	hypothetical prote	371	34	8.0	64	2	E95284	hypothetical prote
299	35	8.3	84	2	G97294	NADH2 dehydrogenas	372	34	8.0	65	1	NTSR3C	neurotoxin 3 - bar
300	35	8.3	84	2	G97294	pvuII restriction	373	34	8.0	65	2	E82547	hypothetical prote
301	35	8.3	85	2	T30462	probable RNA-bind	374	34	8.0	65	2	AF3177	conserved hypothet
302	35	8.3	85	2	AT2765	hypothetical prote	375	34	8.0	66	1	NTSR2C	neurotoxin 2 - bar
303	35	8.3	85	2	AG3108	hypothetical prote	376	34	8.0	66	2	G82491	hypothetical prote
304	35	8.3	88	2	T13183	molybdopterin (mpt	377	34	8.0	66	2	T12847	hypothetical 7K pr
305	35	8.3	88	2	A48435	repressor protein	378	34	8.0	69	2	A61623	juvenile-hormone a
306	35	8.3	89	2	A48435	cysteine proteinas	379	34	8.0	69	2	T03361	gene e6 protein -
307	35	8.3	90	2	F90762	hypothetical prote	380	34	8.0	69	2	A61623	hypothetical prote
308	35	8.3	90	2	G85625	probable copy cont	381	34	8.0	69	2	T03361	hypothetical 7K pr
309	35	8.3	90	2	G85625	hypothetical prote	382	34	8.0	69	2	AB1333	gene e6 protein -
310	34.5	8.2	43	2	B57484	cell division cont	383	34	8.0	69	2	AB1333	hypothetical prote
311	34.5	8.2	43	2	A97416	hypothetical prote	384	34	8.0	71	2	T31215	hypothetical prote
312	34.5	8.2	45	2	T35464	hypothetical prote	385	34	8.0	71	2	AF2303	hypothetical prote
313	34.5	8.2	50	2	S50105	ATP synthase alpha	386	34	8.0	72	2	S49415	major carboxysome
314	34.5	8.2	55	2	A69152	DNA-dependent RNA	387	34	8.0	72	2	S54448	hypothetical prote
315	34.5	8.2	57	2	C41476	ribonucleoside-dip	388	34	8.0	72	2	B70517	hypothetical prote
316	34.5	8.2	58	2	S30499	protein-tyrosine k	389	34	8.0	72	2	AH3473	lactoylglutathione
317	34.5	8.2	58	2	D81150	hypothetical prote	390	34	8.0	73	2	D81394	aldehyde dehydroge
318	34.5	8.2	60	2	AD1832	hypothetical prote	391	34	8.0	74	1	N2KF1U	long neurotoxin 1
319	34.5	8.2	61	2	A35567	photosystem I 14k	392	34	8.0	74	2	F96670	hypothetical prote
320	34.5	8.2	61	2	T21264	hypothetical prote	393	34	8.0	75	2	D61399	hypothetical early
321	34.5	8.2	64	2	D46522	T-cell receptor et	394	34	8.0	75	2	AG1917	hypothetical prote

395	34	8.0	76	2	I59567	histone H2A - rat	468	33.5	7.9	84	2	S58483	hypothetical prote
396	34	8.0	77	2	C42519	A19L 8.3K protein	469	33.5	7.9	84	2	D87520	hypothetical prote
397	34	8.0	77	2	E97137	hypothetical prote	470	33.5	7.9	84	2	F84388	hypothetical prote
398	34	8.0	78	2	S03233	hypothetical prote	471	33.5	7.9	84	2	T51757	hypothetical prote
399	34	8.0	78	2	A03333	hypothetical prote	472	33.5	7.9	84	2	C97194	hypothetical prote
400	34	8.0	79	2	S03448	T-cell receptor al	473	33.5	7.9	84	2	AD1593	B. subtilis PBSX p
401	34	8.0	80	2	C95994	hypothetical prote	474	33.5	7.9	85	2	T16739	hypothetical prote
402	34	8.0	81	2	T17606	hypothetical prote	475	33.5	7.9	86	2	F87604	hypothetical prote
403	34	8.0	81	2	T38451	probable glycoprot	476	33.5	7.9	88	2	T25449	hypothetical prote
404	34	8.0	82	2	G81477	BoirA/irpA family p	477	33.5	7.9	88	2	AH0088	probable flagellar
405	34	8.0	82	2	D82020	hypothetical prote	478	33.5	7.9	89	1	W4B957	hypothetical prote
406	34	8.0	83	2	S78489	Ig kappa chain v r	479	33.5	7.9	89	2	T03951	hypothetical prote
407	34	8.0	84	1	W4WL	E4 kappa chain v r	480	33	7.8	41	2	A59149	sigma-conotoxin GV
408	34	8.0	84	2	S34099	Ig kappa chain v r	481	33	7.8	42	2	AD2520	hypothetical prote
409	34	8.0	84	2	S74779	W protein - Maedi/	482	33	7.8	43	2	S35378	cysteine proteinas
410	34	8.0	86	1	D46335	Ig kappa chain v r	483	33	7.8	47	2	AB0673	30S ribosomal prot
411	34	8.0	86	2	S16834	Ig kappa chain v r	484	33	7.8	47	2	AB0673	hypothetical prote
412	34	8.0	86	2	S16836	Ig kappa chain v r	485	33	7.8	53	2	H84193	hypothetical prote
413	34	8.0	86	2	S16827	Ig kappa chain v r	486	33	7.8	54	2	B56557	PIEMP2/ME5A (clone
414	34	8.0	86	2	S16839	Ig kappa chain v r	487	33	7.8	54	2	S45255	YJX protein homol
415	34	8.0	86	2	S16828	Ig kappa chain v r	488	33	7.8	55	2	P70183	protein-tyrosine k
416	34	8.0	86	2	S16835	Ig kappa chain v r	489	33	7.8	56	2	I70665	MHC HLA-A24 cell s
417	34	8.0	86	2	S16824	Ig kappa chain v r	490	33	7.8	56	2	H82847	hypothetical prote
418	34	8.0	86	2	S16829	Ig kappa chain v r	491	33	7.8	58	2	C95036	hypothetical prote
419	34	8.0	86	2	T00505	hypothetical prote	492	33	7.8	58	2	C97907	hypothetical prote
420	34	8.0	87	2	S34098	Ig kappa chain v r	493	33	7.8	59	2	AG2271	hypothetical prote
421	34	8.0	87	2	A38725	transferrin - shee	494	33	7.8	60	2	S18017	CAB/ELIP/HLIP supe
422	34	8.0	87	2	H70079	hypothetical prote	495	33	7.8	61	2	I59650	flocculant active
423	34	8.0	87	2	T03193	hypothetical prote	496	33	7.8	61	2	S60796	class II histocomp
424	34	8.0	87	2	O6B977	gene 6.7 protein -	497	33	7.8	62	2	D83531	M protein precuro
425	34	8.0	88	1	O6B977	hypothetical prote	498	33	7.8	62	2	T23216	carbon storage reg
426	34	8.0	88	2	O90567	hypothetical prote	499	33	7.8	64	2	B48411	herculin homolog -
427	34	8.0	88	2	A85492	unknown protein en	500	33	7.8	65	2	H55007	hypothetical prote
428	34	8.0	88	2	A97936	conserved hypotnet	501	33	7.8	65	2	D84156	hypothetical prote
429	34	8.0	90	1	WNBPM6	gene m protein - p	502	33	7.8	65	2	AH1024	hypothetical prote
430	34	8.0	90	2	G71568	ribosomal protein	503	33	7.8	66	2	A99455	hypothetical prote
431	34	8.0	90	2	E81260	nifu protein homol	504	33	7.8	66	2	B97981	hypothetical prote
432	34	8.0	90	2	G42457	hypothetical prote	505	33	7.8	67	2	I54475	HLA-DNA-related sm
433	34	8.0	90	2	F97577	hypothetical prote	506	33	7.8	68	2	G59969	hypothetical prote
434	34	8.0	90	2	A82798	hypothetical prote	507	33	7.8	68	2	I34256	hypothetical prote
435	33.5	7.9	45	2	D93982	ribosomal protein	508	33	7.8	70	2	S54439	hemusrv operon pro
436	33.5	7.9	50	2	S11615	hypothetical prote	509	33	7.8	71	2	G84810	probable proteinas
437	33.5	7.9	52	2	T19574	hypothetical prote	510	33	7.8	72	2	T03353	gene e14 protein -
438	33.5	7.9	54	2	B90538	hypothetical prote	511	33	7.8	72	2	A69252	archaeal histone A
439	33.5	7.9	59	2	B93795	hypothetical prote	512	33	7.8	73	2	A27497	hypothetical prote
440	33.5	7.9	64	2	D97915	hypothetical prote	513	33	7.8	74	2	G90798	Dpp receptor TKV,
441	33.5	7.9	65	2	AB3381	heavy metal bindin	514	33	7.8	74	2	I45714	hypothetical prote
442	33.5	7.9	66	2	D98068	degenerate transpo	515	33	7.8	74	2	B75199	alpha-amylose inhi
443	33.5	7.9	67	2	T16372	hypothetical prote	516	33	7.8	75	2	A31298	T-cell receptor be
444	33.5	7.9	67	2	F81618	hypothetical prote	517	33	7.8	75	2	S10358	protein-tyrosine k
445	33.5	7.9	68	2	T11837	H+-transporting tw	518	33	7.8	76	2	PC4256	histone H3.1 - alf
446	33.5	7.9	68	2	S72596	hypothetical prote	519	33	7.8	76	2	A38309	carbon storage reg
447	33.5	7.9	68	2	AE3561	hypothetical prote	520	33	7.8	76	2	I52570	carbon storage reg
448	33.5	7.9	69	2	B91001	hypothetical prote	521	33	7.8	76	2	D82844	glycophorin - huma
449	33.5	7.9	73	1	NFKNG6	omega-conotoxin GV	522	33	7.8	76	2	S75641	hypothetical prote
450	33.5	7.9	74	2	H82816	hypothetical prote	523	33	7.8	77	2	G82169	phage shock protei
451	33.5	7.9	75	2	A12832	kappa-casein - wat	524	33	7.8	77	2	S48011	hypothetical PHO80
452	33.5	7.9	75	2	T06508	trbk protein - Eot	525	33	7.8	77	2	S42162	glycophorin E prec
453	33.5	7.9	75	2	I62139	gene Midl protein	526	33	7.8	78	1	A34931	DNA-directed RNA p
454	33.5	7.9	76	2	AL1907	hypothetical prote	527	33	7.8	78	2	F64429	hypothetical prote
455	33.5	7.9	77	2	D91137	hypothetical prote	528	33	7.8	79	2	C75347	conserved hypotnet
456	33.5	7.9	77	2	S07311	hypothetical prote	529	33	7.8	80	1	C69782	hypothetical prote
457	33.5	7.9	79	2	H75498	hypothetical prote	530	33	7.8	80	2	A89880	hypothetical prote
458	33.5	7.9	79	2	T46591	hypothetical prote	531	33	7.8	80	2	D50965	hypothetical prote
459	33.5	7.9	80	2	C96523	FLI17.12 (impor	532	33	7.8	80	2	D85813	hypothetical prote
460	33.5	7.9	80	2	S59544	stress-induced pro	533	33	7.8	80	2	F64959	hypothetical prote
461	33.5	7.9	81	2	D95065	conserved domain p	534	33	7.8	80	2	AF2420	conserved hypotnet
462	33.5	7.9	81	2	E97932	hypothetical prote	535	33	7.8	81	2	C69186	hypothetical prote
463	33.5	7.9	82	2	S78241	photosystem I iron	536	33	7.8	81	2	H97567	conserved hypotnet
464	33.5	7.9	82	2	F84057	hypothetical prote	537	33	7.8	82	2	S28280	hypothetical prote
465	33.5	7.9	83	2	S62705	ribosomal protein	538	33	7.8	82	2	H86302	probable 50S ribos
466	33.5	7.9	83	2	B90338	hypothetical prote	539	33	7.8	83	2	C41378	hypothetical prote
467	33.5	7.9	83	2	AC3327	hypothetical prote	540	33	7.8	83	2		

541	33	7.8	83	2	T26545	hypothetical prote
542	33	7.8	84	2	protein YMR122w-a	hypothetical prote
543	33	7.8	85	2	arginine decarboxy	hypothetical prote
544	33	7.8	86	2	hypothetical prote	hypothetical prote
545	33	7.8	87	1	NapD protein - Esc	ribosomal protein
546	33	7.8	87	2	Ig kappa chain V r	hypothetical prote
547	33	7.8	87	2	S40221	hypothetical prote
548	33	7.8	87	2	B85860	nonhistone chromos
549	33	7.8	87	2	S41863	phosphocarrrier pro
550	33	7.8	87	2	T28330	phosphocarrrier pro
551	33	7.8	87	2	T48942	phosphocarrrier pro
552	33	7.8	87	2	H91015	phosphocarrrier pro
553	33	7.8	88	2	AQ0910	phosphocarrrier pro
554	33	7.8	88	2	AQ3180	phosphocarrrier pro
555	33	7.8	88	2	AQ2243	2'-aminobiphenyl-2
556	33	7.8	89	2	SQ7931	probable membrane
557	33	7.8	89	2	B86741	phosphocarrrier pro
558	33	7.8	90	2	C83960	phosphocarrrier pro
559	33	7.8	90	2	E82456	hypothetical prote
560	32.5	7.7	40	2	F87410	hypothetical prote
561	32.5	7.7	47	2	A56778	hypothetical prote
562	32.5	7.7	52	2	B81352	recombination prot
563	32.5	7.7	52	2	I37971	50S ribosomal prot
564	32.5	7.7	53	2	T36215	zinc finger protei
565	32.5	7.7	56	2	S31198	spdB protein - Str
566	32.5	7.7	57	2	I54529	metallothionein -
567	32.5	7.7	61	2	C97840	major histocompat
568	32.5	7.7	61	2	AQ3158	hypothetical prote
569	32.5	7.7	62	1	A45315	hypothetical prote
570	32.5	7.7	62	2	S29177	Hsp transporing tw
571	32.5	7.7	63	2	T12921	high-molecular-we
572	32.5	7.7	64	2	T21291	hypothetical prote
573	32.5	7.7	65	2	A49530	3C-like serine pro
574	32.5	7.7	65	2	S32904	hypothetical prote
575	32.5	7.7	66	2	A31395	hypothetical prote
576	32.5	7.7	67	2	A37235	hypothetical prote
577	32.5	7.7	68	2	I49136	dopamine transport
578	32.5	7.7	69	2	A72354	hypothetical prote
579	32.5	7.7	71	2	S21665	ribosomal protein
580	32.5	7.7	73	2	A83393	hypothetical prote
581	32.5	7.7	75	2	A43183	hypothetical prote
582	32.5	7.7	77	2	G90429	hypothetical prote
583	32.5	7.7	78	2	S48038	metallothionein-li
584	32.5	7.7	78	2	S11923	gas-vesicle protei
585	32.5	7.7	78	2	T44966	gas-vesicle protei
586	32.5	7.7	79	2	S55313	prolaxin S (nitrop
587	32.5	7.7	79	2	T10243	antifungal protein
588	32.5	7.7	79	2	T02461	hypothetical prote
589	32.5	7.7	79	2	S55456	GAM1 protein - Pla
590	32.5	7.7	80	1	G71267	conserved hypothet
591	32.5	7.7	80	2	A91099	pancreatic ribonuc
592	32.5	7.7	81	2	S41921	antigen B - tapewo
593	32.5	7.7	82	2	C64823	ss-DNA binding pro
594	32.5	7.7	82	2	H91346	probable DNA-bind
595	32.5	7.7	82	2	S07256	hypothetical prote
596	32.5	7.7	82	2	A02666	hypothetical prote
597	32.5	7.7	83	1	CP0534	cytochrome c554 -
598	32.5	7.7	83	2	B90342	hypothetical prote
599	32.5	7.7	83	2	T17752	hypothetical prote
600	32.5	7.7	83	2	C69724	thioredoxin-like p
601	32.5	7.7	83	2	T19171	hypothetical prote
602	32.5	7.7	83	2	A13439	exodeoxyribonuclea
603	32.5	7.7	84	2	C97995	degenerate transpo
604	32.5	7.7	85	2	S17463	glutathione transp
605	32.5	7.7	85	2	S07323	gas-vesicle protei
606	32.5	7.7	86	2	S26788	Ig heavy chain V r
607	32.5	7.7	86	2	S78142	ribosomal protein
608	32.5	7.7	86	2	A82661	plasmid stabilizat
609	32.5	7.7	86	2	H97542	hypothetical prote
610	32.5	7.7	86	2	A12761	hypothetical prote
611	32.5	7.7	87	2	A86992	hypothetical prote
612	32.5	7.7	87	2	S75480	hypothetical prote
613	32.5	7.7	87	2	G70780	hypothetical prote
614	32.5	7.7	87	2	G69281	hypothetical prote
615	32.5	7.7	87	2	T00775	hypothetical prote
616	32.5	7.7	87	2	T08641	hypothetical prote
617	32.5	7.7	88	2	D97092	hypothetical prote
618	32.5	7.7	88	2	E71977	ribosomal protein
619	32.5	7.7	89	2	D64529	hypothetical prote
620	32.5	7.7	89	2	D83372	hypothetical prote
621	32.5	7.7	89	2	F70953	nonhistone chromos
622	32.5	7.7	90	1	NSCHH7	phosphocarrrier pro
623	32.5	7.7	90	2	I76722	phosphocarrrier pro
624	32.5	7.7	90	2	E91139	phosphocarrrier pro
625	32.5	7.7	90	2	F84289	phosphocarrrier pro
626	32.5	7.7	90	2	T46580	hypothetical prote
627	32.5	7.7	90	2	AE0991	2'-aminobiphenyl-2
628	32.5	7.7	90	2	H85984	probable membrane
629	32.5	7.7	90	2	D97689	phosphocarrrier pro
630	32.5	7.7	90	2	AI2914	phosphocarrrier pro
631	32.5	7.7	90	2	H64039	hypothetical prote
632	32.5	7.7	90	2	S35577	hypothetical prote
633	32.5	7.7	90	2	H82619	hypothetical prote
634	32.5	7.7	90	2	C30609	hypothetical prote
635	32.5	7.7	90	2	A82402	Ig kappa chain V-1
636	32.5	7.7	90	2	A65510	hypothetical prote
637	32.5	7.7	90	2	E93852	hypothetical prote
638	32.5	7.7	90	2	I48681	hypothetical prote
639	32.5	7.7	90	2	S00580	185 kDa glycophosp
640	32.5	7.7	90	2	H31442	1-(5-phosphoribosy
641	32.5	7.7	90	2	I31444	ovomucoid, third d
642	32.5	7.7	90	2	B36943	chemoreceptor prot
643	32.5	7.7	90	2	AH1885	hypothetical prote
644	32.5	7.7	90	2	FEPE	ferredoxin 2[4Fe-4
645	32.5	7.7	90	2	AG2267	hypothetical prote
646	32.5	7.7	90	2	G72355	hypothetical prote
647	32.5	7.7	90	2	C72613	hypothetical prote
648	32.5	7.7	90	2	S35727	protein-tyrosine k
649	32.5	7.7	90	2	G87390	hypothetical prote
650	32.5	7.7	90	2	C72857	hypothetical prote
651	32.5	7.7	90	2	NIAT1F	short neurotoxin 1
652	32.5	7.7	90	2	A27580	short neurotoxin 1
653	32.5	7.7	90	2	S44215	genome polyprotein
654	32.5	7.7	90	2	H59103	hypothetical prote
655	32.5	7.7	90	2	B82752	high-molecular-we
656	32.5	7.7	90	2	H59944	hypothetical prote
657	32.5	7.7	90	2	B84589	hypothetical prote
658	32.5	7.7	90	2	AG1770	sigmas-controlled
659	32.5	7.7	90	2	S63968	hypothetical prote
660	32.5	7.7	90	2	T36447	4-oxalocrotonate i
661	32.5	7.7	90	2	S33366	ribosomal protein
662	32.5	7.7	90	2	A64929	hypothetical prote
663	32.5	7.7	90	2	D90930	ydIE protein - Esc
664	32.5	7.7	90	2	G90979	hypothetical prote
665	32.5	7.7	90	2	G96517	protein T2E6, 24 [i
666	32.5	7.7	90	2	B46245	marinostatin - Alt
667	32.5	7.7	90	2	H85778	androgen-induced g
668	32.5	7.7	90	2	S75543	hypothetical prote
669	32.5	7.7	90	2	A82808	hypothetical prote
670	32.5	7.7	90	2	D58225	hypothetical prote
671	32.5	7.7	90	2	H98044	hypothetical prote
672	32.5	7.7	90	2	E54965	hypothetical prote
673	32.5	7.7	90	2	T06349	glucan endo-1,3-be
674	32.5	7.7	90	2	C95178	hypothetical prote
675	32.5	7.7	90	2	C95178	hypothetical prote
676	32.5	7.7	90	2	H95280	hypothetical prote
677	32.5	7.7	90	2	H52M33	conserved hypothet
678	32.5	7.7	90	2	S31652	enterotoxin - vers
679	32.5	7.7	90	2	A87561	hypothetical prote
680	32.5	7.7	90	2	E97733	hypothetical prote
681	32.5	7.7	90	2	S60853	M protein precuro
682	32.5	7.7	90	2	G82724	hypothetical prote
683	32.5	7.7	90	2	S47648	nitric oxide syntha

687	32	7.6	68	2	H95264	hypothetical prote	760	32	7.6	86	2	S40226	glycoprotein B - h
688	32	7.6	68	2	Adi678	probable mercuic	761	32	7.6	86	2	S76775	hypothetical prote
689	32	7.6	69	1	QOE67	ybeB protein - Esc	762	32	7.6	86	2	T01496	hypothetical prote
690	32	7.6	69	2	G80713	hypothetical prote	763	32	7.6	86	2	E97027	probable transcrip
691	32	7.6	69	2	G85563	hypothetical prote	764	32	7.6	86	2	AF3172	DNA binding protei
692	32	7.6	69	2	B81902	hypothetical prote	765	32	7.6	87	2	S08401	neurotoxin homolo
693	32	7.6	69	2	J01703	hypothetical 7.3k	766	32	7.6	87	2	JN0669	neurotoxin-block1
694	32	7.6	69	2	C96021	hypothetical prote	767	32	7.6	87	2	JN0672	neurotoxin 4 precu
695	32	7.6	69	2	Adi147	hypothetical prote	768	32	7.6	87	2	S40232	glycoprotein B - h
696	32	7.6	69	2	Adi1506	hypothetical prote	769	32	7.6	87	2	S40220	glycoprotein B - h
697	32	7.6	70	1	TIPO1A	chymotrypsin inhib	770	32	7.6	87	2	S40222	glycoprotein B - h
698	32	7.6	70	2	S08845	M protein precursor	771	32	7.6	87	2	S40234	small nuclear ribo
699	32	7.6	70	2	G42524	hypothetical prote	772	32	7.6	87	2	B90161	hypothetical prote
700	32	7.6	70	2	H82954	GTP-binding regula	773	32	7.6	87	2	A82064	M-related prote
701	32	7.6	70	2	A42155	hypothetical prote	774	32	7.6	87	2	C75458	gene l8 protein -
702	32	7.6	71	2	H91105	hypothetical prote	775	32	7.6	87	2	T03315	hypothetical prote
703	32	7.6	71	2	C85951	hypothetical prote	776	32	7.6	88	2	H70932	B subtilis ytnI p
704	32	7.6	71	2	C95925	hypothetical 8.1 k	777	32	7.6	88	2	T34439	hydroxymethylbilan
705	32	7.6	71	2	C65079	hypothetical prote	778	32	7.6	88	2	AH1367	C8-2 protein - hep
706	32	7.6	71	2	D81389	hypothetical prote	779	32	7.6	88	2	AE2108	hypothetical prote
707	32	7.6	72	2	A86664	hypothetical prote	780	32	7.6	89	2	S23698	hydroxymethylbilan
708	32	7.6	72	2	A95351	Protein imported	781	32	7.6	89	2	S10002	hypothetical prote
709	32	7.6	72	2	I36840	C18L protein var	782	32	7.6	89	2	D84286	hypothetical prote
710	32	7.6	73	2	T28476	hypothetical prote	783	32	7.6	89	2	D84360	hypothetical prote
711	32	7.6	73	2	T03199	hypothetical prote	784	32	7.6	89	2	H36943	chemoreceptor prot
712	32	7.6	73	2	T07244	hypothetical prote	785	32	7.6	89	2	E69943	hypothetical prote
713	32	7.6	74	2	S61501	flagellar biosynth	786	32	7.6	89	2	G71378	hypothetical prote
714	32	7.6	75	2	B69391	DNA-directed RNA p	787	32	7.6	89	2	E65143	hypothetical 10.3k
715	32	7.6	75	2	S73297	hypothetical prote	788	32	7.6	90	2	A60526	complement C3 - ax
716	32	7.6	75	2	D97813	hypothetical prote	789	32	7.6	90	2	AH0464	probable membrane
717	32	7.6	76	2	S60827	M protein precursor	790	32	7.6	90	2	E97482	hypothetical 8.2k
718	32	7.6	76	2	A69391	DNA-directed RNA p	791	32	7.6	90	2	F97574	hypothetical prote
719	32	7.6	76	2	A72318	hypothetical prote	792	32	7.6	90	2	AF2795	hypothetical prote
720	32	7.6	76	2	D44007	apoptoxin IV - tra	793	31.5	7.4	45	2	T35208	hypothetical prote
721	32	7.6	76	2	AE2700	conserved hypotet	794	31.5	7.4	46	2	I54375	gene NF2 protein -
722	32	7.6	77	1	B32824	rhodotorucine A pr	795	31.5	7.4	48	2	JC6008	hypothetical 5.3k
723	32	7.6	77	2	T18049	hypothetical prote	796	31.5	7.4	48	2	AH2633	hypothetical prote
724	32	7.6	77	2	A71204	probable DNA-direc	797	31.5	7.4	49	2	B97874	degenerate transpo
725	32	7.6	77	2	AE2966	hypothetical prote	798	31.5	7.4	50	2	I52702	estrogen receptor
726	32	7.6	77	2	AE2097	hypothetical prote	799	31.5	7.4	51	2	A11731	hypothetical gene
727	32	7.6	78	2	B18883	hypothetical prote	800	31.5	7.4	51	2	E97394	hypothetical prote
728	32	7.6	78	2	T03641	glutathione S-tran	801	31.5	7.4	52	2	C91112	hypothetical prote
729	32	7.6	79	2	A49475	cerebroside sulfat	802	31.5	7.4	52	2	AC2566	hypothetical prote
730	32	7.6	79	2	J02128	metallothionein	803	31.5	7.4	52	2	F95269	hypothetical prote
731	32	7.6	79	2	B83400	hypothetical prote	804	31.5	7.4	52	2	G84912	hypothetical prote
732	32	7.6	79	2	AG0340	hypothetical prote	805	31.5	7.4	56	2	WMH51	ydbF protein - Esc
733	32	7.6	80	2	D71553	hypothetical prote	806	31.5	7.4	57	1	WMH24	3a protein - avian
734	32	7.6	80	2	J074875	hypothetical prote	807	31.5	7.4	57	2	C97937	transposase, uncha
735	32	7.6	80	2	A48996	hypothetical prote	808	31.5	7.4	58	2	B97333	ferredoxin [import
736	32	7.6	80	2	F98324	B cell surface ant	809	31.5	7.4	59	2	T06016	hypothetical prote
737	32	7.6	80	2	AH2958	hypothetical prote	810	31.5	7.4	60	2	A28859	pepsin A (EC 3.4.2
738	32	7.6	80	2	AE2207	hypothetical prote	811	31.5	7.4	60	2	AC1904	hypothetical prote
739	32	7.6	80	2	F97116	cell growth regula	812	31.5	7.4	62	2	C49570	plasma membrane ca
740	32	7.6	81	2	F75409	ribosomal protein	813	31.5	7.4	62	2	E97764	hypothetical prote
741	32	7.6	81	2	D75321	hypothetical prote	814	31.5	7.4	64	2	S17526	aconitate hydratase
742	32	7.6	82	2	D81056	ribosomal protein	815	31.5	7.4	64	2	AF3568	hypothetical prote
743	32	7.6	82	2	D81056	hypothetical prote	816	31.5	7.4	65	2	D86788	hypothetical prote
744	32	7.6	82	2	C81016	hypothetical prote	817	31.5	7.4	65	2	H81238	hypothetical prote
745	32	7.6	82	2	F89987	hypothetical prote	818	31.5	7.4	66	2	G72804	gp41.1 protein - M
746	32	7.6	83	2	E90859	hypothetical prote	819	31.5	7.4	67	2	T50506	hypothetical prote
747	32	7.6	83	2	H81188	hypothetical prote	820	31.5	7.4	67	2	AH0254	probable phage pro
748	32	7.6	83	2	S29325	hypothetical prote	821	31.5	7.4	68	2	S09382	fms protein - mous
749	32	7.6	83	2	B85760	hypothetical prote	822	31.5	7.4	68	2	SN0382	adenylate cyclase
750	32	7.6	83	2	H85523	hypothetical prote	823	31.5	7.4	69	2	PN0453	hypothetical prote
751	32	7.6	83	2	AE0554	conserved hypotet	824	31.5	7.4	69	2	D95250	antibiotic mercap
752	32	7.6	83	2	D64875	yciN protein - Esc	825	31.5	7.4	70	2	F83706	hypothetical prote
753	32	7.6	84	1	S01442	hypothetical Alzhe	826	31.5	7.4	70	2	AE1974	transcription regu
754	32	7.6	84	1	A45631	ribosomal protein	827	31.5	7.4	70	2	H95067	x4JM protein - Rhi
755	32	7.6	84	2	T03163	hypothetical prote	828	31.5	7.4	70	2	T28640	T-cell receptor et
756	32	7.6	85	2	C70523	hypothetical prote	829	31.5	7.4	71	2	B46522	hypothetical prote
757	32	7.6	85	2	T40431	hypothetical prote	830	31.5	7.4	71	2	F37840	ORF1 protein - Orf
758	32	7.6	85	2	E95976	hypothetical prote	831	31.5	7.4	71	2	AG2853	Hypothetical prote
759	32	7.6	86	2	C28195	Ig kappa chain v r	832	31.5	7.4	71	2	AG1893	hypothetical prote

833	31.5	7.4	72	2	T37089	probable IS elemen	906	31	7.3	55	2	A25988	mannose/glucose-sp
834	31.5	7.4	72	2	S13000	phosphopyruvate hy	907	31	7.3	55	2	S34330	sox protein - less
835	31.5	7.4	72	2	T47509	hypothetical prote	908	31	7.3	56	2	B72804	gp36 protein - Myc
836	31.5	7.4	72	2	AB3436	hypothetical prote	909	31	7.3	56	2	JW0095	p5 protein - human
837	31.5	7.4	72	2	AF2574	hypothetical prote	910	31	7.3	56	2	F82830	hypothetical prote
838	31.5	7.4	73	2	S78719	protein YER091c-a	911	31	7.3	56	2	E82787	hypothetical prote
839	31.5	7.4	74	2	G83293	hypothetical prote	912	31	7.3	57	2	E61479	cytochrome c - Try
840	31.5	7.4	74	2	A16648	hypothetical prote	913	31	7.3	57	2	P69120	hypothetical prote
841	31.5	7.4	74	2	AH1590	hypothetical prote	914	31	7.3	57	2	P69183	hypothetical prote
842	31.5	7.4	74	2	AH2642	hypothetical prote	915	31	7.3	58	2	C81787	hypothetical prote
843	31.5	7.4	75	2	S23602	hypothetical prote	916	31	7.3	59	2	A27606	ig heavy chain V-a
844	31.5	7.4	75	2	E82761	conserved hypotet	917	31	7.3	59	2	G91095	hypothetical prote
845	31.5	7.4	75	2	T10753	conserved hypotet	918	31	7.3	59	2	C85941	hypothetical prote
846	31.5	7.4	76	2	T19717	hypothetical prote	919	31	7.3	60	2	T03816	hypothetical prote
847	31.5	7.4	77	2	AH1279	hypothetical prote	920	31	7.3	60	2	A41212	tick anticoagulant
848	31.5	7.4	77	2	AH1642	hypothetical prote	921	31	7.3	61	2	D84210	hypothetical prote
849	31.5	7.4	78	2	T30726	hypothetical prote	922	31	7.3	61	2	C75321	preprotein translo
850	31.5	7.4	78	2	AH1969	hypothetical prote	923	31	7.3	61	2	AF1344	B. subtilis ywmg p
851	31.5	7.4	79	1	A70312	conserved hypotet	924	31	7.3	61	2	A11714	B. subtilis ywmg p
852	31.5	7.4	80	2	T10823	antifungal protein	925	31	7.3	61	2	AE3182	hypothetical prote
853	31.5	7.4	80	2	E64307	ferredoxin - Metha	926	31	7.3	62	1	CCB017	ubiquinol-cytochro
854	31.5	7.4	80	2	T38250	hypothetical prote	927	31	7.3	62	2	C70057	4-oxalocrotonate t
855	31.5	7.4	80	2	A29556	hypothetical prote	928	31	7.3	62	2	S38378	probable serine/th
856	31.5	7.4	81	1	CE9880	conserved hypotet	929	31	7.3	62	2	C83944	hypothetical prote
857	31.5	7.4	81	2	S39511	photosystem I iron	930	31	7.3	62	2	C82647	hypothetical prote
858	31.5	7.4	81	2	T44031	hypothetical prote	931	31	7.3	63	1	Q8ECLM	yaia protein - Esc
859	31.5	7.4	82	2	T07076	metallothionein ty	932	31	7.3	63	2	AD0550	conserved hypotet
860	31.5	7.4	82	2	T07114	metallothionein-11	933	31	7.3	63	2	C85534	hypothetical prote
861	31.5	7.4	82	2	E83191	conserved hypotet	934	31	7.3	63	2	G90683	hypothetical prote
862	31.5	7.4	82	2	F71890	hypothetical prote	935	31	7.3	63	2	JC4002	carbomycin resista
863	31.5	7.4	83	2	AB2519	hypothetical prote	936	31	7.3	63	2	D86673	hypothetical prote
864	31.5	7.4	84	2	S03239	hypothetical prote	937	31	7.3	63	2	AE9231	hypothetical prote
865	31.5	7.4	84	2	AG2301	hypothetical prote	938	31	7.3	63	2	S58623	hypothetical prote
866	31.5	7.4	85	2	AC2523	hypothetical prote	939	31	7.3	63	2	T33630	hypothetical prote
867	31.5	7.4	86	2	S72340	hypothetical prote	940	31	7.3	63	2	S29654	juvenile-hormone e
868	31.5	7.4	86	2	P64527	hypothetical prote	941	31	7.3	64	2	D84219	hypothetical prote
869	31.5	7.4	86	2	E71978	hypothetical prote	942	31	7.3	64	2	F97207	probable transcrip
870	31.5	7.4	87	2	A84679	hypothetical prote	943	31	7.3	65	2	JC2380	subtilisin inhibit
871	31.5	7.4	87	2	T03716	reverse transcript	944	31	7.3	66	2	H71940	copper-associated
872	31.5	7.4	87	2	C87533	hypothetical prote	945	31	7.3	66	2	S47027	DNA-directed RNA p
873	31.5	7.4	88	2	B97057	ribosomal protein	946	31	7.3	67	1	PWMS8	H+-transporting tw
874	31.5	7.4	88	2	A97425	hypothetical prote	947	31	7.3	67	2	C86830	hypothetical prote
875	31.5	7.4	88	2	AB1901	hypothetical prote	948	31	7.3	67	2	C81174	hypothetical prote
876	31.5	7.4	89	2	S13517	retinoic acid rece	949	31	7.3	67	2	T35269	small hypotet
877	31.5	7.4	89	2	G69730	holin component xh	950	31	7.3	67	2	S76880	milk band E protei
878	31.5	7.4	90	2	S03700	nonhistone chroms	951	31	7.3	68	2	AE1511	17K common-antigen
879	31.5	7.4	90	2	A89183	hypothetical prote	952	31	7.3	68	2	AE3441	protease-inhibit
880	31	7.3	40	2	B81705	segment 12 protein	953	31	7.3	69	2	S66650	ribosomal protein
881	31	7.3	43	2	H27142	hypothetical prote	954	31	7.3	69	2	J01257	hypothetical 7.6K
882	31	7.3	44	2	S05348	nitrogenase (EC 1.	955	31	7.3	69	2	JC4731	mob protein 69 - E
883	31	7.3	44	2	A82865	hypothetical prote	956	31	7.3	69	2	G98318	hypothetical prote
884	31	7.3	45	2	A24669	calmodulin-related	957	31	7.3	69	2	AB2483	hypothetical prote
885	31	7.3	46	2	B29184	vitellogenin - duc	958	31	7.3	70	2	A30518	ig heavy chain V-A
886	31	7.3	46	2	E90676	hypothetical prote	959	31	7.3	70	2	B72286	ferredoxin - Therm
887	31	7.3	46	2	H85526	hypothetical prote	960	31	7.3	70	2	AB1103	mercury transport
888	31	7.3	47	2	S62336	cystatin C, paroti	961	31	7.3	70	2	E82148	conserved hypotet
889	31	7.3	47	2	E84357	50S ribosomal prot	962	31	7.3	70	2	T12849	hypothetical prote
890	31	7.3	48	2	B69173	ribosomal protein	963	31	7.3	70	2	A12632	conserved hypotet
891	31	7.3	49	2	B82007	hypothetical prote	964	31	7.3	70	2	AG2846	cold shock protein
892	31	7.3	49	2	A82422	hypothetical prote	965	31	7.3	71	2	I49244	MI protein - mouse
893	31	7.3	50	2	J01600	repC' protein - cl	966	31	7.3	71	2	F84312	hypothetical prote
894	31	7.3	50	2	A60745	major outer membra	967	31	7.3	71	2	J00147	hypothetical 7.7K
895	31	7.3	50	2	H96530	hypothetical prote	968	31	7.3	71	2	AC0229	probable membrane
896	31	7.3	51	2	S11815	opacity protein (c	969	31	7.3	71	2	AC0229	hypothetical prote
897	31	7.3	51	2	AF2492	hypothetical prote	970	31	7.3	72	1	H97623	trypsin inhibitor
898	31	7.3	52	2	T43384	hypothetical prote	971	31	7.3	72	1	TIMB	ferredoxin 2[4Fe-4
899	31	7.3	53	2	S44404	NADH2 dehydrogenas	972	31	7.3	72	2	S49186	retinoic acid rece
900	31	7.3	53	2	F28286	hypothetical prote	973	31	7.3	72	2	S49021	cellulase (EC 3.2.
901	31	7.3	53	2	AC3113	hypothetical prote	974	31	7.3	72	2	F10937	NrdH-ferredoxin impo
902	31	7.3	54	2	I46202	galanin - dog (ira	975	31	7.3	72	2	F95136	hypothetical prote
903	31	7.3	54	2	S24179	histone H1.a, hepa	976	31	7.3	72	2	D70167	trypsin inhibitor
904	31	7.3	54	2	H82718	hypothetical prote	977	31	7.3	73	2	JC1066	hypothetical prote
905	31	7.3	55	2	P70186	protein-tyrosine k	978	31	7.3	73	2	A84271	hypothetical prote

979 31 7.3 73 2 E84286  
 980 31 7.3 73 2 C64021  
 981 31 7.3 73 2 S12242 rap  
 982 31 7.3 73 2 D21155  
 983 31 7.3 73 2 E84048  
 984 31 7.3 73 2 S13515  
 985 31 7.3 74 2 S127539  
 986 31 7.3 74 2 F71080  
 987 31 7.3 74 2 C69882  
 988 31 7.3 74 2 E97870  
 989 31 7.3 75 2 A38646  
 990 31 7.3 75 2 T08193  
 991 31 7.3 75 2 T01621  
 992 31 7.3 76 2 C82122  
 993 31 7.3 76 2 T40983  
 994 31 7.3 76 2 C44007  
 995 31 7.3 76 2 A95337  
 996 31 7.3 77 2 D69432  
 997 31 7.3 77 2 T02773  
 998 31 7.3 78 2 E64104  
 999 31 7.3 78 2 A24352  
 1000 31 7.3 78 2 A75084

# ALIGNMENTS

RESULT 1  
 127603  
 hypothetical protein ZC477.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T27603  
 submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid ZC477.  
 A:Reference number: Z20392  
 A:Accession: T27603  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-80 <DUZ>  
 A:Cross-references: EMBL:U40802; PIDN:AAA81504.1; CESP:ZC477.4  
 C:Genetics:  
 A:Gene: CESP:ZC477.4

Query Match 12.8%; Score 54; DB 2; Length 80;  
 Best Local Similarity 28.4%; Pred. No. 39;  
 Matches 23; Conservative 9; Mismatches 35; Indels 14; Gaps 2;  
 QY 6 CSOSISPMRISSESLVAMDFSGKSRVIENTEALSVAVVEGLAWRKKGCLRLGTHGS 65  
 DB 4 CSPLKILPGASSSSSSSTA-----SSQIRPPLSLASLSEELRVEECGSPRVGAKES 56  
 QY 66 -----PTASSOSSATNNAI 79  
 DB 57 SEYCTEQPAOSSYSREDKLCI 77

RESULT 2  
 E64324  
 DNA-directed RNA polymerase (EC 2.7.7.6) subunit N - Methanococcus jannaschii  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 23-Apr-1999  
 C:Accession: E64324  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: E64324  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
 A:Residues: 1-76 <BUL>  
 A:Cross-references: GB:U67475; GB:L77117; NID:g1590930; PID:g1590941; TIGR:MJ0196; PI  
 C:Genetics:  
 A:Map position: FOR190573-190803  
 A:Start codon: GTG  
 C:Superfamily: DNA-directed RNA polymerase II chain RPB10  
 C:Keywords: nucleotidyltransferase; transcription

Query Match 12.2%; Score 51.5; DB 2; Length 76;  
 Best Local Similarity 30.0%; Pred. No. 71;  
 Matches 15; Conservative 10; Mismatches 18; Indels 7; Gaps 2;

QY 13 PMRISSESLVAMDFSGKSRVIENTEALSVAVVEGLAWRKKGCLRL 60  
 DB 7 PIRCFSGNVIAVEVEEYKERILKGENPKDVL-----DDLGIKKYCCRRM 51

RESULT 3  
 AG3246  
 conserved hypothetical protein Atu6153 [imported] - Agrobacterium tumefaciens (strain  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C:Accession: AG3246  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam  
 ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID:11743193  
 A:Accession: AG3246  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-89 <KUR>  
 A:Cross-references: GB:AE008690; PIDN:AAL46389.1; PID:g17744182; GSPDB:GN00189  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atu6153  
 A:Genome: Plasmid

Query Match 11.3%; Score 48; DB 2; Length 89;  
 Best Local Similarity 41.2%; Pred. No. 2,2e+02;  
 Matches 14; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

QY 28 SGQKSRVIENTEALSVAVVEGLAWRKKGCLRLG 61  
 DB 29 SQRKSRV-----PCSLAVISSMLHROKGAVRIG 56

RESULT 4  
 F95310  
 hypothetical protein Sma0736 [imported] - Sinorhizobium meliloti (strain 1021) magap1  
 C:Species: Sinorhizobium meliloti  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C:Accession: F95310  
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B  
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K  
 .  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli  
 A:Reference number: A95262; MUID:21396509; PMID:11481432  
 A:Accession: F95310  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-90 <KUR>  
 A:Cross-references: GB:AE006469; PIDN:AAK65048.1; PID:g14523480; GSPDB:GN00165  
 A:Experimental source: strain 1021, megaplasmid pSymA  
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl  
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau

hebaut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: Sma0736  
 A:Genome: plasmid

Query Match 11.2%; Score 47.5; DB 2; Length 90;  
 Best Local Similarity 22.1%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 15; Mismatches 19; Indels 19; Gaps 3;  
 QY 11 ISPMRISLNSLVAMDFSGOKSRVIENTEALSVAVVEGLW-----RRKGCGLRL-GT 62  
 DB 11 VAPPKDLDDSTMSAADFA-----QLFGVYTOGGMSWETFYERQADGIFRLSGT 59  
 QY 63 HGSPTASS 70  
 DB 60 RKTNTPS 67

RESULT 5  
 E64510  
 hypothetical protein MJEBCL05 - Methanococcus jannaschii plasmid PURB800  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 22-Oct-1999  
 C:Accession: E64510  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
 rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Glodek, A.;  
 Science 273, 1058-1073, 1996  
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
 A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*  
 A:Reference number: A64300; MUID:96337999; PMID:8688087  
 A:Accession: E64510  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-62 <BUL>  
 A:Cross-references: GB:L77118; MID:g1500644; TIGR:MJEBCL05; PIDN:AAC37071.1; PID:g1500645  
 C:Genetics:  
 A:Map position: ECLFOR3265-3453  
 A:Genome: plasmid  
 A:Start codon: GTG  
 A:Note: This stable 58-kilobase pair plasmid is also designated ECL (large extrachromosomal)

Query Match 11.0%; Score 46.5; DB 2; Length 62;  
 Best Local Similarity 28.6%; Pred. No. 2.1e+02;  
 Matches 12; Conservative 8; Mismatches 21; Indels 1; Gaps 1;  
 QY 15 RSIENSLSVAMDFSGOKSRVIENTEALSVAVVEGLAWKK 55  
 DB 18 KVAERFLKDLSSQGNWKEIRAEARAKKQLEEGIAWK 59

RESULT 6  
 S24471  
 gag polyprotein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S24471; S24483  
 R:Salminen, M.  
 submitted to the EMBL Data Library, October 1991  
 A:Reference number: S24471  
 A:Accession: S24471  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-77 <SAL>  
 A:Cross-references: EMBL:Z11145; MID:g60073; PIDN:CAA77496.1; PID:g60074  
 C:Superfamily: AIDS-related virus gag polyprotein  
 C:Keywords: polyprotein

Query Match 10.9%; Score 46; DB 2; Length 77;  
 Best Local Similarity 23.4%; Pred. No. 3.1e+02;

Matches 15; Conservative 7; Mismatches 14; Indels 28; Gaps 2;  
 QY 29 GOKSRV-----ENPEALSVAVEEG-----LAWRKGCGLRL 60  
 DB 1 GHKARYLAQAMSKATNAATIMQGNFRNQRKTKVCFNCGKQGHIAARNCRARRKKGKWC 60  
 QY 61 GTHG 64  
 DB 61 GREG 64

RESULT 7  
 D82861  
 hypothetical protein XFa0004 [imported] - *Xylella fastidiosa* (strain 9a5c)  
 C:Species: *Xylella fastidiosa*  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: D82861  
 R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide S  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: D82861  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-87 <SIM>  
 A:Cross-references: GB:AE003851; MID:g9112238; PIDN:AAF85573.1; GSPDB:GN00130; XFSC  
 A:Experimental source: strain 9a5c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga,  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Car  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.;  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.;  
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.B.; Marques, M.V.; Marti  
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki,  
 F.G.; Nunes, L.R.; Oliveira, A.J.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sa  
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Si  
 M.Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: Xfa0004  
 A:Genome: plasmid  
 A:Note: plasmid pXF5.1

Query Match 10.9%; Score 46; DB 2; Length 87;  
 Best Local Similarity 28.1%; Pred. No. 3.6e+02;  
 Matches 16; Conservative 10; Mismatches 23; Indels 8; Gaps 3;  
 QY 14 MRSISENSLVAMDFSGOKSRVIENTEALSVAVVEGLAWRKGCGLRLGTHGSP 66  
 DB 1 MNTISESELA--DFVKNQAVKKLHIQNDAEKYEIFAT--LTWKEGDWHLVTTTRCKP 53

RESULT 8  
 A82657  
 hypothetical protein XFL634 [imported] - *Xylella fastidiosa* (strain 9a5c)  
 C:Species: *Xylella fastidiosa*  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: A82657  
 R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide S  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: A82657  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-65 <SIM>  
 A:Cross-references: GB:AE003990; MID:g9106683; PIDN:AAF84443.1; GSPDB:G  
 A:Experimental source: strain 9a5c



R;SIMPSON, A.J.G.; Reinach, F.C.; Ariu, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigle Chado, M.A.; Madeira, A.M.B.N.; Madeira, R.M.F.; Martins, M.V.; Marques, M.V.; Martins, A.; R;G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328

C:Contents: annotation

C:Genetics:

A:Gene: XF1634

Query Match 10.8%; Score 45.5; DB 2; Length 65;  
Best Local Similarity 33.3%; Pred. No. 2.9e+02;  
Matches 11; Conservative 6; Mismatches 11; Indels 5; Gaps 1;

QY 44 VAVEGLAWRK-----GCLRLTGHSPTASSQ 71  
Db 16 ICIENTALARKKNIYLPNCCTSLHSAPTATAK 48

RESULT 9

T25763  
hypothetical protein F46F11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
A:Description: The sequence of C. elegans cosmid F46F11.  
A:Reference number: Z20083  
A:Accession: T25763  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-73 <PAU>  
A:Cross-references: EMBL:U88173; PIDN:AA842366.1; GSPDB:GN00019; CESP:F46F11.4  
A:Experimental source: strain Bristol N2; clone F46F11  
C:Genetics:  
A:Gene: CESP:F46F11.4  
A:Map position: 1  
A:Introns: 38/2

Query Match 10.8%; Score 45.5; DB 2; Length 73;  
Best Local Similarity 29.4%; Pred. No. 3.3e+02;  
Matches 10; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 26 DFSGQKSRVIENTEALS-----VAVEGLAWRK 54  
Db 8 DRLGKVRKRNPSDTIGDLKLIAAQTGRWEK 41

RESULT 10

JC5345  
cd1 protein - Clostridium difficile  
C:Species: Clostridium difficile  
C:Date: 27-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 15-Oct-1999  
C:Accession: JC5345  
R;Braun, V.; Hundsberger, T.; Leukel, P.; Sauerborn, M.; von Eichel-Streiber, C. Gene 181, 29-38, 1996  
A:Title: Definition of the single integration site of the pathogenicity locus in Clostr A:Reference number: JC5340; MUID:97128764; PMID:8973304  
A:Accession: JC5345  
A:Molecule type: DNA  
A:Residues: 1-81 <BRA>  
A:Cross-references: EMBL:X92982; NID:gl770128; PIDN:CAA63566.1; PID:e212011; PID:gl77013 A:Experimental source: strain VP110463  
C:Genetics:  
A:Gene: cdu1

R;SIMPSON, A.J.G.; Reinach, F.C.; Ariu, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigle Chado, M.A.; Madeira, A.M.B.N.; Madeira, R.M.F.; Martins, M.V.; Marques, M.V.; Martins, A.; R;G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328

C:Contents: annotation

C:Genetics:

A:Gene: XF1634

Query Match 10.8%; Score 45.5; DB 2; Length 81;  
Best Local Similarity 25.3%; Pred. No. 3.8e+02;  
Matches 14; Conservative 8; Mismatches 22; Indels 11; Gaps 1;

QY 9 QSISPMRSISNSLVAMDFSGQKSRVIENTEALSVAVEGLAWRKGCGLRLGTH 63  
Db 5 QKIPGVGKATEKSLIMIGYTIKSLKADANPAOMY-----ERECLMRGOH 48

RESULT 11

A42960  
ferredoxin 2[4Fe-4S] - Methanosarcina thermophila  
C:Species: Methanosarcina thermophila  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 13-Nov-1998  
C:Accession: A42960  
R;Clements, A.P.; Ferry, J.G. J. Bacteriol. 174, 5244-5250, 1992  
A:Title: Cloning, nucleotide sequence, and transcriptional analyses of the gene encod A:Reference number: A42960; MUID:92355496; PMID:1379583  
A:Contents: TM-1  
A:Accession: A42960  
A:Molecule type: DNA  
A:Residues: 1-60 <CLE>  
A:Note: sequence extracted from NCBI backbone (NCBIN:110322, NCBIP:110324)  
C:Genetics:  
A:Gene: fdx4

C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology  
C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein  
F;3-59/Domain: ferredoxin 2[4Fe-4S] homology <FER>  
F;10,13,16,51/binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F;20,41,44,47/binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 10.6%; Score 45; DB 2; Length 60;  
Best Local Similarity 42.9%; Pred. No. 3e+02;  
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 24 AMDFSGQKSRVIENTEALSVAVEGLA 51  
Db 7 ADECSGCGSCVDECPSEAITLDEKGA 34

RESULT 12

I53107  
CD24 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I53107; S25146  
R;Shirasawa, T.; Akashi, T.; Sakamoto, K.; Takahashi, H.; Maruyama, N.; Hirokawa, K. Dev. Dyn. 198, 1-13, 1993  
A:Title: Gene expression of CD24 core peptide molecule in developing brain and develo A:Reference number: I53107; MUID:94122434; PMID:8292828  
A:Accession: I53107  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-76 <RES>  
A:Cross-references: EMBL:Z11663; NID:g55901; PIDN:CAA77731.1; PID:g55902  
C:Keywords: phosphatidylinositol linkage

Query Match 10.6%; Score 45; DB 2; Length 76;  
Best Local Similarity 24.4%; Pred. No. 4e+02;  
Matches 19; Conservative 10; Mismatches 15; Indels 34; Gaps 4;

QY 6 CSSQSISPMRSISNSLVAMDFSGQKSRVIENTEALSVAVEGLAWRKGCGLRLGTHG 64  
Db 26 CNOTSVAP-----FSGNOSISAPNPTNATT-----RSGC-----55

QY 65 SPTASSQSATNMAIHR 82  
Db 56 ---SSLSQTAGLLALSLS 70

RESULT 13

A:Residues: 1-79 <REI>  
A:Cross-references: EMBL:U61973; NID:g1655850; PID:g1655851  
A:Experimental source: apple flesh cortical tissue  
C:Genetics:  
A:Gene: AMT1  
C:Superfamily: metallothionein  
C:Keywords: metal binding

Query Match 10.6%; Score 45; DB 2; Length 79;  
Best Local Similarity 30.6%; Pred. No. 4.2e+02;  
Matches 15; Conservative 7; Mismatches 21; Indels 6; Gaps 2;

QY 4 SCGSSOSIPMRISSENS--LVAMDFSGSKRVIENTPEALSVAVEEG 49  
|||:::|||:::|||:::|||:::|||:::|||  
Db 19 SCGCGMAPDLSTMEGSTTETLMGVAPQKSHM--EASENGVAAENG 64

RESULT 16  
D69087  
hydrogenase expression/formalation protein hycP - Methanobacterium thermoautotrophicum  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 24-Sep-1999  
C:Accession: D69087  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge,  
J.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jwa  
k1, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
B. Bacterial 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H  
A:Reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: D69087  
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-82 <MTH>  
A:Cross-references: GB:AEO00924; GB:AEO00666; NID:g2622777; PIDN:AAB86122.1; PID:g2  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1649  
C:Superfamily: hydrogenase expression/formaton protein hypC

Query Match 10.6%; Score 45; DB 2; Length 82;  
Best Local Similarity 28.9%; Pred. No. 4.4e+02;  
Matches 11; Conservative 9; Mismatches 14; Indels 4; Gaps 1;

QY 18 SENSLVAMDFSGQSKSRV----IENPTSEALSVAVEGLA 51  
|||:::|||:::|||:::|||:::|||:::|||  
Db 14 SEDNTATDFGVRQQVKLDLVDDVEEGRYVLVHSGYA 51

RESULT 17  
C41139  
protein kinase 3 (EC 2.7.1.-) - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jul-2000  
C:Accession: C41139  
R:Liu, X.; Feng, X.H.; Watson, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 6951-6955, 1991  
A:Title: Differential accumulation of transcripts encoding protein kinase homologs  
A:Reference number: A41139; MUID:91334384; PMID:1714582  
C:Accession: C41139  
A:Molecule type: mRNA  
A:Residues: 1-86 <LIN>  
A:Cross-references: GB:M69032; NID:g169139; PIDN:AAA50774.1; PID:g169140  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase  
C:Keywords: phosphotransferase  
F:1-86/Domain: protein kinase homology (fragment) <KIN>

Query Match 10.6%; Score 45; DB 2; Length 86;  
Best Local Similarity 25.4%; Pred. No. 4.6e+02;  
Matches 18; Conservative 7; Mismatches 20; Indels 26; Gaps 4;

QY 6 CSSOSISPMRSISNSLVAMD-----FSGQSKSR-----VTENPTSALSVAVEGLAW 52  
|||:::|||:::|||:::|||:::|||:::|||  
Db 23 CYKADVSPTFEFTNHKLHVDTLVVVVISITDKSRESYTAFFAEAPTAFS----- 73

QY 53 RKGGLRLGTH 63  
DB 74 --RSC--VGTH 80

## RESULT 18

AB2271

periplasmic mercuric ion binding protein [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AB2271  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AB2271  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-64 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA875420.1; PID:g17132855; GSPDB:GN001179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: asl3721

Query Match 10.5%; Score 44.5; DB 2; Length 64;  
Best Local Similarity 16.1%; Pred. No. 3.7e+02;  
Matches 8; Conservative 20; Mismatches 17; Indels 3; Gaps 1;

QY 4 SGCSQSISPMRSISNSLVAMDFGSGKSRVNIENPTALSVAVEGLA 51  
DB 13 SACANNITNAKTVDDVAIQAD---PQTKLVNVTQASSETSIIKDALA 57

## RESULT 19

S75293

hypothetical protein srr2333 - Synecocystis sp. (strain PCC 6803)  
C:Species: Synecocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
R:Kaneko, T.; Sato, K.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S75293  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-79 <KAN>  
A:Cross-references: EMBL:D90904; GB:AB001339; NID:g16152225; PIDN:BAAL7207.1; PID:d101794  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 10.5%; Score 44.5; DB 2; Length 79;  
Best Local Similarity 22.1%; Pred. No. 4.8e+02;  
Matches 15; Conservative 14; Mismatches 34; Indels 5; Gaps 1;

QY 16 SISNSLVAMDFGSGKSRVNIENPTALSVAVEGLAWRKGCRLRLTGHSPTASSQSAT 75  
DB 7 SVGOLAPVEKILLGNHOGVLNRLAMGIIPDKPIQLLRKAGL-----GGPLHLRIGSTT 61

QY 76 NNAIHRSS 83  
DB 62 EVAMRSE 69

## RESULT 20

DB5807

hypothetical protein 22988 [imported] - Escherichia coli (strain O157:H7, substrain EDL5)  
C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: DB5807  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: AB5480; MUID:21074935; PMID:11206551  
A:Accession: DB5807  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-51 <STO>  
A:Cross-references: GB:AE005174; NID:g12516000; PIDN:AA056920.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL533  
C:Genetics:  
A:Gene: 22988

Query Match 10.4%; Score 44; DB 2; Length 51;  
Best Local Similarity 32.0%; Pred. No. 3.2e+02;  
Matches 8; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 37 NPTALSVAVEEGLAWRKKGCLRLG 61  
DB 20 SPAEIFMWTGCVVSWRRAALRS 44

## RESULT 21

B90959

probable phage tail protein [imported] - Escherichia coli (strain O157:H7, substrain  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: B90959  
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: B90959  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-78 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA836065.1; PID:g13362110; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 050952  
C:Genetics:  
A:Gene: EC2642

Query Match 10.4%; Score 44; DB 2; Length 78;  
Best Local Similarity 32.0%; Pred. No. 5.3e+02;  
Matches 8; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 37 NPTALSVAVEEGLAWRKKGCLRLG 61  
DB 47 SPAEIFMWTGCVVSWRRAALRS 71

## RESULT 22

A75411

hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C:Accession: A75411  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567265  
A:Accession: A75411  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-78 <WHI>  
A:Cross-references: GB:AE001978; GB:AE000513; NID:g6459059; PIDN:AAF10892.1; PID:g645  
A:Experimental source: strain R1  
C:Genetics:



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 09:08:20 ; Search time 27.1181 Seconds  
(without alignments)  
181.900 Million cell updates/sec

Sequence: US-09-936-697-6  
1 OGRSGSSQSSISPMRSISEN.....SPTASSQSSATNMAHRSQP 84

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 29382

Minimum DB seq length: 40

Maximum DB seq length: 90

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 1000 summaries

Public Applications: AA  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*  
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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep.\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.5	12.9	60	9	US-09-925-299-1024
2	54.5	12.9	60	10	US-09-925-299-1024
3	51.5	12.2	83	10	US-09-908-711-103
4	51.5	12.1	84	10	US-09-864-761-47521
5	50.5	11.9	80	9	US-10-125-258-6
6	48.5	11.5	82	10	US-09-864-761-42490
7	47	11.1	89	9	US-09-764-872-393
8	46.5	11.0	78	10	US-09-764-887-218
9	46	10.9	68	9	US-10-079-854-131
10	46	10.9	68	10	US-09-764-878-131
11	46	10.9	68	10	US-09-764-860-468
12	46	10.9	69	9	US-10-092-154-700
13	46	10.8	69	10	US-09-764-847-700
14	45.5	10.8	56	9	US-09-925-299-1460
15	45.5	10.8	56	10	US-09-925-299-1460
16	45.5	10.8	58	9	US-09-925-299-1372
17	45.5	10.8	58	9	US-09-925-299-1437
18	45.5	10.8	58	9	US-09-925-299-1493
19	45.5	10.8	58	9	US-09-925-299-1528

20	45.5	10.8	58	10	US-09-925-301-1647	Sequence 1647, Ap
21	45.5	10.8	58	10	US-09-925-299-1372	Sequence 1372, Ap
22	45.5	10.8	58	10	US-09-925-299-1437	Sequence 1437, Ap
23	45.5	10.8	58	10	US-09-925-299-1493	Sequence 1493, Ap
24	45.5	10.8	58	10	US-09-925-299-1528	Sequence 1528, Ap
25	45.5	10.8	60	10	US-09-764-877-1350	Sequence 1350, Ap
26	45.5	10.8	72	9	US-09-738-626-6764	Sequence 6764, Ap
27	45.5	10.8	72	10	US-09-864-761-38891	Sequence 38891, A
28	45	10.6	76	10	US-09-963-896-5	Sequence 5, Appl
29	44.5	10.5	61	9	US-09-809-391-615	Sequence 615, App
30	44.5	10.5	65	9	US-09-925-299-1416	Sequence 1416, Ap
31	44.5	10.5	65	10	US-09-925-299-1416	Sequence 1416, Ap
32	44	10.4	63	9	US-09-983-802-611	Sequence 611, App
33	44	10.4	68	10	US-09-925-300-1560	Sequence 1560, App
34	44	10.4	79	10	US-09-884-441-460	Sequence 460, App
35	43.5	10.3	52	10	US-09-864-761-44542	Sequence 44542, A
36	43.5	10.3	55	10	US-08-879-957-111	Sequence 111, App
37	43.5	10.3	55	10	US-09-867-550-588	Sequence 588, App
38	43.5	10.3	72	10	US-09-764-877-1500	Sequence 1500, App
39	43	10.2	66	10	US-09-764-877-1799	Sequence 1799, App
40	43	10.2	79	9	US-10-002-344A-213	Sequence 213, App
41	42.5	10.0	61	10	US-09-879-957-208	Sequence 208, App
42	42.5	10.0	79	10	US-09-864-761-48228	Sequence 48228, A
43	42.5	10.0	87	10	US-09-864-761-33792	Sequence 33792, A
44	42	9.9	44	10	US-09-864-761-40508	Sequence 40508, A
45	42	9.9	62	10	US-09-864-761-47330	Sequence 47330, A
46	42	9.9	63	10	US-09-864-761-34262	Sequence 34262, A
47	42	9.9	71	9	US-09-985-480-365	Sequence 365, App
48	42	9.9	71	10	US-09-764-860-397	Sequence 397, App
49	42	9.9	78	10	US-10-014-774-9	Sequence 9, Appl
50	42	9.9	78	10	US-09-755-501-10	Sequence 10, Appl
51	42	9.9	83	10	US-09-764-869-1093	Sequence 1093, Ap
52	42	9.9	83	10	US-09-864-761-41234	Sequence 41234, A
53	41.5	9.8	45	10	US-09-864-761-43127	Sequence 43127, A
54	41.5	9.8	78	9	US-09-909-5678-41	Sequence 41, Appl
55	41	9.7	43	10	US-09-864-761-42091	Sequence 42091, A
56	41	9.7	53	10	US-09-925-301-1639	Sequence 1639, App
57	41	9.7	63	10	US-09-877-258-2	Sequence 2, Appl
58	41	9.7	67	9	US-09-796-592-2075	Sequence 2075, Ap
59	41	9.7	67	9	US-09-796-592-2315	Sequence 2315, Ap
60	41	9.7	70	12	US-09-895-913A-280	Sequence 280, App
61	41	9.7	90	10	US-10-001-879-198	Sequence 198, App
62	40.5	9.6	69	10	US-09-982-809-5	Sequence 5, Appl
63	40.5	9.6	71	9	US-10-001-876-151	Sequence 151, App
64	40	9.5	47	9	US-09-983-802-656	Sequence 656, App
65	40	9.5	49	10	US-09-864-761-41352	Sequence 41352, A
66	40	9.5	56	10	US-09-919-124-48	Sequence 48, Appl
67	40	9.5	65	10	US-09-864-761-48202	Sequence 48202, A
68	40	9.5	68	9	US-09-984-245-132	Sequence 132, App
69	40	9.5	69	9	US-10-043-487-398	Sequence 398, App
70	40	9.5	71	9	US-09-764-872-351	Sequence 351, App
71	40	9.5	72	9	US-09-983-802-655	Sequence 655, App
72	40	9.5	72	10	US-09-954-512-1	Sequence 1, Appl
73	40	9.5	73	10	US-09-864-761-44101	Sequence 44101, A
74	40	9.5	74	9	US-09-986-480-352	Sequence 352, App
75	40	9.5	74	10	US-09-864-761-36451	Sequence 36451, A
76	40	9.5	85	9	US-10-002-344A-147	Sequence 147, App
77	40	9.5	85	10	US-09-864-761-34433	Sequence 34433, A
78	40	9.5	85	10	US-10-001-873-34	Sequence 34, Appl
79	40	9.5	90	10	US-09-864-761-40114	Sequence 40114, A
80	40	9.5	90	10	US-09-864-761-40114	Sequence 40114, A
81	39.5	9.3	53	9	US-09-796-592-1814	Sequence 1814, Ap
82	39.5	9.3	53	9	US-09-796-592-2071	Sequence 2071, Ap
83	39.5	9.3	68	10	US-09-864-761-44168	Sequence 44168, A
84	39.5	9.3	68	10	US-09-864-761-47104	Sequence 47104, A
85	39.5	9.3	75	10	US-09-867-550-336	Sequence 336, App
86	39.5	9.3	84	10	US-09-867-550-596	Sequence 596, App
87	39.5	9.3	84	10	US-09-925-300-1166	Sequence 1166, App
88	39.5	9.3	87	10	US-09-864-761-43703	Sequence 43703, A
89	39.5	9.3	87	10	US-09-864-761-44930	Sequence 44930, A
90	39.5	9.3	89	10	US-09-815-242-4918	Sequence 4918, Ap
91	39	9.2	47	10	US-09-864-761-34601	Sequence 34601, A
92	39	9.2	47	10	US-09-864-761-43815	Sequence 43815, A

93	39	9.2	52	10	US-09-864-761-38091	Sequence 38091, A	166	37	8.7	55	10	US-09-864-761-38777	Sequence 38777, A
94	39	9.2	55	10	US-09-925-301-1589	Sequence 1589, A	167	37	8.7	56	10	US-09-879-957-134	Sequence 134, App
95	39	9.2	58	10	US-09-867-550-980	Sequence 980, App	168	37	8.7	56	10	US-09-945-173-9	Sequence 9, Appl
96	39	9.2	60	10	US-09-864-761-45291	Sequence 45291, A	169	37	8.7	57	10	US-09-071-838-294	Sequence 294, App
97	39	9.2	60	10	US-09-864-761-49088	Sequence 49088, A	170	37	8.7	59	9	US-09-796-692-1321	Sequence 1321, App
98	39	9.2	62	10	US-09-864-761-41167	Sequence 41167, A	171	37	8.7	59	9	US-09-796-692-1328	Sequence 1328, App
99	39	9.2	65	12	US-10-078-929-24	Sequence 24, Appl	172	37	8.7	59	9	US-09-796-692-1800	Sequence 1800, App
100	39	9.2	72	9	US-10-103-829-24	Sequence 709, App	173	37	8.7	59	9	US-09-796-692-2062	Sequence 2062, App
101	39	9.2	72	9	US-09-848-664-22	Sequence 22, Appl	174	37	8.7	59	9	US-10-092-154-845	Sequence 845, App
102	39	9.2	75	10	US-10-091-572-333	Sequence 333, App	175	37	8.7	59	10	US-09-864-761-40483	Sequence 40483, A
103	39	9.2	76	10	US-09-915-582-71	Sequence 71, Appl	176	37	8.7	59	10	US-09-764-847-845	Sequence 845, App
104	39	9.2	76	10	US-09-915-582-89	Sequence 89, Appl	177	37	8.7	60	10	US-09-864-761-45374	Sequence 45374, A
105	39	9.2	83	10	US-09-864-761-35244	Sequence 35244, A	178	37	8.7	61	9	US-09-925-299-1513	Sequence 1513, App
106	39	9.2	90	10	US-09-939-980-524	Sequence 524, App	179	37	8.7	61	9	US-09-864-761-38452	Sequence 38452, A
107	39	9.1	49	9	US-09-864-761-44912	Sequence 44912, A	180	37	8.7	61	10	US-09-925-299-1513	Sequence 1513, App
108	38.5	9.1	50	9	US-10-083-357-843	Sequence 843, App	181	37	8.7	62	9	US-09-796-692-1724	Sequence 1724, App
109	38.5	9.1	53	10	US-09-742-659-8	Sequence 8, Appl	182	37	8.7	62	9	US-10-000-256A-217	Sequence 217, App
110	38.5	9.1	66	10	US-09-864-761-36073	Sequence 36073, A	183	37	8.7	62	9	US-09-867-550-1998	Sequence 1998, App
111	38.5	9.1	107	67	US-09-764-869-1072	Sequence 1072, App	184	37	8.7	65	9	US-09-764-872-424	Sequence 424, App
112	38.5	9.1	74	9	US-10-001-887-135	Sequence 135, App	185	37	8.7	69	10	US-09-908-711-104	Sequence 104, App
113	38.5	9.1	74	9	US-10-878-603-7	Sequence 7, Appl	186	37	8.7	70	9	US-09-796-692-2254	Sequence 2254, App
114	38.5	9.1	74	9	US-10-092-154-806	Sequence 806, App	187	37	8.7	70	10	US-09-220-920-98	Sequence 98, Appl
115	38.5	9.1	74	10	US-09-864-761-806	Sequence 806, App	188	37	8.7	71	9	US-09-764-868-1092	Sequence 1092, App
116	38.5	9.1	75	10	US-09-864-761-44991	Sequence 44991, A	189	37	8.7	71	9	US-10-016-157A-192	Sequence 192, App
117	38.5	9.1	76	9	US-10-066-127-6	Sequence 6, Appl	190	37	8.7	78	9	US-10-083-357-936	Sequence 936, App
118	38.5	9.1	82	10	US-09-867-550-114	Sequence 114, App	191	37	8.7	79	10	US-09-864-761-47232	Sequence 47232, A
119	38.5	9.1	84	10	US-09-864-761-44395	Sequence 44395, A	192	37	8.7	79	10	US-09-864-761-40801	Sequence 40801, A
120	38.5	9.1	84	10	US-09-864-761-42438	Sequence 42438, A	193	37	8.7	86	9	US-09-974-879-170	Sequence 170, App
121	38.5	9.1	85	9	US-09-522-334-28	Sequence 28, Appl	194	37	8.7	86	10	US-09-764-877-1480	Sequence 1480, App
122	38	9.0	44	10	US-09-864-761-41106	Sequence 41106, A	195	37	8.7	87	10	US-09-925-301-1433	Sequence 1433, App
123	38	9.0	44	10	US-09-925-300-946	Sequence 946, App	196	37	8.7	87	10	US-09-815-248-13	Sequence 13, Appl
124	38	9.0	59	10	US-09-864-761-46850	Sequence 46850, A	197	37	8.7	88	9	US-10-116-255-34	Sequence 34, Appl
125	38	9.0	62	10	US-09-864-761-35144	Sequence 35144, A	198	36.5	8.6	43	10	US-09-864-761-40819	Sequence 40819, A
126	38	9.0	301	62	US-09-939-980-301	Sequence 301, App	199	36.5	8.6	50	10	US-09-864-761-34528	Sequence 34528, A
127	38	9.0	72	9	US-09-796-692-1776	Sequence 1776, App	200	36.5	8.6	50	10	US-09-864-761-41230	Sequence 41230, A
128	38	9.0	73	9	US-09-864-761-48180	Sequence 48180, A	201	36.5	8.6	52	10	US-09-864-761-39855	Sequence 39855, A
129	38	9.0	73	10	US-09-864-761-36328	Sequence 36328, A	202	36.5	8.6	52	10	US-09-864-761-41763	Sequence 41763, A
130	38	9.0	77	10	US-09-864-761-36328	Sequence 36328, A	203	36.5	8.6	55	9	US-10-000-256A-139	Sequence 139, App
131	38	9.0	77	10	US-09-820-893-51	Sequence 51, Appl	204	36.5	8.6	59	9	US-09-974-879-162	Sequence 162, App
132	38	9.0	80	9	US-10-001-835-153	Sequence 153, App	205	36.5	8.6	62	10	US-09-855-341-15	Sequence 15, Appl
133	38	9.0	80	9	US-09-864-761-46562	Sequence 46562, A	206	36.5	8.6	63	10	US-09-864-761-40078	Sequence 40078, A
134	38	9.0	82	9	US-09-983-802-592	Sequence 592, App	207	36.5	8.6	64	9	US-09-796-692-1823	Sequence 1823, App
135	38	9.0	85	9	US-09-808-387-34	Sequence 34, Appl	208	36.5	8.6	64	9	US-09-796-692-2078	Sequence 2078, App
136	38	9.0	85	9	US-10-002-344A-186	Sequence 186, App	209	36.5	8.6	64	10	US-09-764-869-864	Sequence 864, App
137	38	9.0	90	9	US-09-976-059-12	Sequence 12, Appl	210	36.5	8.6	64	10	US-09-764-869-864	Sequence 864, App
138	38	9.0	90	9	US-09-833-802-171	Sequence 171, Appl	211	36.5	8.6	65	9	US-10-091-572-330	Sequence 330, App
139	37.5	8.9	40	10	US-09-864-761-48390	Sequence 48390, A	212	36.5	8.6	67	10	US-09-864-761-40159	Sequence 40159, A
140	37.5	8.9	41	10	US-09-864-761-40731	Sequence 40731, A	213	36.5	8.6	70	10	US-09-864-761-44403	Sequence 44403, A
141	37.5	8.9	51	10	US-09-864-761-43411	Sequence 43411, A	214	36.5	8.6	71	9	US-09-981-876-170	Sequence 170, App
142	37.5	8.9	61	10	US-09-864-761-35421	Sequence 35421, A	215	36.5	8.6	72	9	US-09-148-545-170	Sequence 153, App
143	37.5	8.9	61	10	US-09-867-550-2086	Sequence 2086, App	216	36.5	8.6	72	9	US-09-866-050A-153	Sequence 304, App
144	37.5	8.9	63	10	US-09-864-761-41905	Sequence 41905, A	217	36.5	8.6	72	9	US-09-866-050A-304	Sequence 10, Appl
145	37.5	8.9	64	10	US-09-925-300-1765	Sequence 1765, App	218	36.5	8.6	72	10	US-09-783-320-10	Sequence 41584, A
146	37.5	8.9	65	9	US-10-092-154-735	Sequence 735, App	219	36.5	8.6	72	10	US-09-864-761-41584	Sequence 33, Appl
147	37.5	8.9	65	10	US-09-764-847-735	Sequence 735, App	220	36.5	8.6	73	8	US-08-424-550B-33	Sequence 1446, App
148	37.5	8.9	66	10	US-09-864-761-38695	Sequence 38695, A	221	36.5	8.6	73	8	US-09-796-692-1446	Sequence 1542, App
149	37.5	8.9	67	8	US-08-424-550B-383	Sequence 383, App	222	36.5	8.6	74	9	US-09-796-692-1542	Sequence 1896, App
150	37.5	8.9	71	9	US-09-925-299-1225	Sequence 1225, App	223	36.5	8.6	74	9	US-09-796-692-1896	Sequence 2024, App
151	37.5	8.9	71	9	US-09-925-299-1225	Sequence 1225, App	224	36.5	8.6	74	9	US-09-796-692-2024	Sequence 33436, A
152	37.5	8.9	74	9	US-10-042-141-57	Sequence 57, Appl	225	36.5	8.6	74	9	US-09-864-761-33436	Sequence 38805, A
153	37.5	8.9	74	9	US-09-796-692-1469	Sequence 1469, App	226	36.5	8.6	77	10	US-09-864-761-38805	Sequence 38805, A
154	37.5	8.9	74	9	US-09-796-692-1911	Sequence 1911, App	227	36.5	8.6	77	10	US-09-864-761-38805	Sequence 38805, A
155	37.5	8.9	74	9	US-09-796-692-1951	Sequence 1951, App	228	36.5	8.6	78	10	US-09-864-761-38805	Sequence 38805, A
156	37.5	8.9	74	9	US-09-726-643-57	Sequence 57, Appl	229	36.5	8.6	79	10	US-09-864-761-38805	Sequence 38805, A
157	37.5	8.9	74	10	US-09-908-711-77	Sequence 77, Appl	230	36.5	8.6	81	9	US-10-001-857-156	Sequence 156, App
158	37.5	8.9	75	10	US-09-764-877-1681	Sequence 1681, App	231	36.5	8.6	81	9	US-09-864-761-45835	Sequence 45835, A
159	37.5	8.9	86	10	US-09-981-108-30	Sequence 30, Appl	232	36.5	8.6	81	10	US-09-864-761-45835	Sequence 489, App
160	37.5	8.9	87	10	US-09-867-550-1468	Sequence 1468, App	233	36.5	8.6	81	10	US-09-764-877-1409	Sequence 50, Appl
161	37.5	8.9	89	9	US-10-102-806-829	Sequence 829, App	234	36.5	8.6	82	9	US-10-012-542-489	Sequence 2161, App
162	37.5	8.9	89	10	US-09-925-297-543	Sequence 543, App	235	36.5	8.6	83	9	US-09-908-931B-50	Sequence 18, Appl
163	37	8.7	42	10	US-09-864-761-43616	Sequence 43616, A	236	36.5	8.6	83	9	US-09-796-692-2161	Sequence 855, App
164	37	8.7	44	10	US-09-864-761-46624	Sequence 46624, A	237	36.5	8.6	84	9	US-10-013-379-18	
165	37	8.7	49	10	US-09-864-761-44834	Sequence 44834, A	238	36.5	8.6	85	10	US-09-764-869-855	

239	36.5	8.6	86	10	US-09-925-300-1139	Sequence 1139, App	312	35.5	8.4	67	9	US-09-796-692-871	Sequence 871, App
240	36.5	8.6	90	9	US-10-101-454A-92	Sequence 92, Appl	313	35.5	8.4	67	9	US-09-796-692-1492	Sequence 1492, App
241	36.5	8.6	90	9	US-09-764-872-374	Sequence 374, App	314	35.5	8.4	67	10	US-09-873-880-20	Sequence 20, Appl
242	36	8.5	42	10	US-09-864-761-39032	Sequence 39032, A	315	35.5	8.4	68	10	US-09-764-869-941	Sequence 941, Appl
243	36	8.5	43	10	US-09-916-494A-20	Sequence 20, Appl	316	35.5	8.4	69	10	US-09-864-761-44260	Sequence 44260, A
244	36	8.5	44	10	US-09-864-761-40752	Sequence 40752, A	317	35.5	8.4	70	10	US-09-864-761-38015	Sequence 38015, A
245	36	8.5	46	10	US-09-864-761-33369	Sequence 33369, A	318	35.5	8.4	70	12	US-10-027-348-9	Sequence 9, Appl
246	36	8.5	48	10	US-10-012-542-487	Sequence 487, App	319	35.5	8.4	74	10	US-09-864-761-48935	Sequence 48935, A
247	36	8.5	50	10	US-09-864-761-37356	Sequence 37356, A	320	35.5	8.4	76	9	US-10-003-344A-199	Sequence 199, App
248	36	8.5	51	10	US-09-800-729-176	Sequence 176, App	321	35.5	8.4	76	10	US-09-864-761-37234	Sequence 37234, A
249	36	8.5	52	10	US-09-867-550-1088	Sequence 1088, App	322	35.5	8.4	77	10	US-09-864-761-37341	Sequence 37341, A
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251	36	8.5	56	10	US-09-864-761-40879	Sequence 40879, A	324	35.5	8.4	80	10	US-09-867-550-1924	Sequence 1924, App
252	36	8.5	56	10	US-09-919-124-46	Sequence 46, Appl	325	35.5	8.4	81	9	US-09-974-879-519	Sequence 519, App
253	36	8.5	57	10	US-09-864-761-35315	Sequence 35315, A	326	35.5	8.4	81	10	US-09-734-569-96	Sequence 96, App
254	36	8.5	57	10	US-09-864-761-40621	Sequence 40621, A	327	35.5	8.4	82	10	US-09-867-550-550	Sequence 550, App
255	36	8.5	59	10	US-09-864-761-47122	Sequence 47122, A	328	35.5	8.4	83	10	US-09-864-761-34004	Sequence 34004, A
256	36	8.5	59	9	US-10-012-542-415	Sequence 415, App	329	35.5	8.4	85	10	US-09-731-872-476	Sequence 476, App
257	36	8.5	60	9	US-09-984-271-176	Sequence 176, App	330	35.5	8.4	86	10	US-09-800-729-97	Sequence 97, Appl
258	36	8.5	62	9	US-09-996-140-137	Sequence 137, App	331	35.5	8.4	87	9	US-09-759-1308-368	Sequence 368, App
259	36	8.5	62	9	US-09-764-877-1136	Sequence 1136, App	332	35.5	8.4	87	9	US-09-983-802-544	Sequence 544, App
260	36	8.5	63	9	US-10-083-357-900	Sequence 900, App	333	35.5	8.4	89	9	US-10-102-806-769	Sequence 769, App
261	36	8.5	63	10	US-09-864-761-46037	Sequence 46037, A	334	35	8.3	43	9	US-10-116-252-26	Sequence 26, Appl
262	36	8.5	65	10	US-09-864-761-37813	Sequence 37813, A	335	35	8.3	44	10	US-09-843-845-16	Sequence 16, Appl
263	36	8.5	67	10	US-09-800-729-177	Sequence 177, App	336	35	8.3	44	10	US-09-864-761-41915	Sequence 41915, A
264	36	8.5	69	10	US-09-864-761-47955	Sequence 47955, A	337	35	8.3	44	10	US-09-864-761-48304	Sequence 48304, A
265	36	8.5	70	9	US-10-001-835-1599	Sequence 159, App	338	35	8.3	45	9	US-09-925-299-1016	Sequence 1016, App
266	36	8.5	70	10	US-09-864-761-40767	Sequence 40767, A	339	35	8.3	45	10	US-09-925-299-1016	Sequence 1016, App
267	36	8.5	71	10	US-09-864-761-42914	Sequence 42914, A	340	35	8.3	45	12	US-10-001-879-181	Sequence 181, App
268	36	8.5	71	10	US-09-864-761-46025	Sequence 46025, A	341	35	8.3	46	10	US-09-864-761-47782	Sequence 47782, A
269	36	8.5	73	10	US-09-867-550-2034	Sequence 2034, App	342	35	8.3	47	10	US-09-864-761-42636	Sequence 42636, A
270	36	8.5	74	9	US-09-738-626-4797	Sequence 4797, App	343	35	8.3	48	10	US-09-745-008-28	Sequence 28, Appl
271	36	8.5	75	10	US-09-864-761-35553	Sequence 35553, A	344	35	8.3	50	10	US-09-764-877-1587	Sequence 1587, App
272	36	8.5	77	10	US-09-864-761-40989	Sequence 40989, A	345	35	8.3	51	10	US-09-864-761-32923	Sequence 32923, A
273	36	8.5	77	9	US-10-112-793-26	Sequence 26, Appl	346	35	8.3	52	9	US-09-984-245-326	Sequence 326, App
274	36	8.5	77	10	US-09-864-761-47447	Sequence 47447, A	347	35	8.3	52	9	US-09-984-245-326	Sequence 326, App
275	36	8.5	78	9	US-10-001-857-173	Sequence 173, App	348	35	8.3	52	10	US-09-864-761-40071	Sequence 40071, A
276	36	8.5	79	10	US-10-178-213-293	Sequence 293, App	349	35	8.3	52	10	US-09-864-761-35168	Sequence 35168, A
277	36	8.5	79	10	US-09-864-761-40746	Sequence 40746, A	350	35	8.3	55	9	US-10-038-010-38	Sequence 38, Appl
278	36	8.5	81	10	US-08-424-5508-187	Sequence 187, App	351	35	8.3	57	9	US-09-895-793-565	Sequence 565, App
279	36	8.5	83	10	US-09-864-761-41593	Sequence 41593, A	352	35	8.3	57	9	US-09-895-793-565	Sequence 565, App
280	36	8.5	83	10	US-09-800-729-178	Sequence 178, App	353	35	8.3	57	9	US-09-895-793-565	Sequence 565, App
281	36	8.5	83	10	US-09-764-877-1712	Sequence 1712, App	354	35	8.3	57	10	US-09-759-143-565	Sequence 565, App
282	36	8.5	88	10	US-09-864-761-48010	Sequence 48010, A	355	35	8.3	57	10	US-09-780-669-565	Sequence 565, App
283	36	8.5	89	10	US-09-864-761-46485	Sequence 46485, A	356	35	8.3	57	10	US-09-822-827-565	Sequence 565, App
284	36	8.5	90	9	US-09-925-299-1529	Sequence 1529, App	357	35	8.3	58	10	US-09-879-957-131	Sequence 131, App
285	36	8.5	90	9	US-10-083-357-1282	Sequence 1282, App	358	35	8.3	58	10	US-09-925-302-651	Sequence 651, App
286	36	8.5	90	9	US-09-925-299-1529	Sequence 1529, App	359	35	8.3	58	10	US-09-864-761-42605	Sequence 42605, A
287	35.5	8.4	47	9	US-10-178-213-294	Sequence 294, App	360	35	8.3	59	9	US-10-091-572-406	Sequence 406, App
288	35.5	8.4	47	10	US-09-764-860-371	Sequence 371, App	361	35	8.3	59	10	US-09-864-761-39483	Sequence 39483, A
289	35.5	8.4	50	9	US-10-091-572-349	Sequence 349, App	362	35	8.3	59	10	US-09-864-761-39622	Sequence 39622, A
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291	35.5	8.4	51	10	US-09-864-761-42029	Sequence 42029, A	364	35	8.3	59	10	US-09-800-729-171	Sequence 171, App
292	35.5	8.4	52	9	US-10-117-604-8	Sequence 8, Appl	365	35	8.3	60	10	US-09-745-008-29	Sequence 29, Appl
293	35.5	8.4	53	9	US-09-796-692-1014	Sequence 1014, App	366	35	8.3	62	9	US-09-984-245-327	Sequence 327, App
294	35.5	8.4	53	9	US-09-796-692-1108	Sequence 1108, App	367	35	8.3	62	9	US-09-984-245-327	Sequence 327, App
295	35.5	8.4	53	9	US-09-796-692-1108	Sequence 1108, App	368	35	8.3	63	9	US-09-984-245-327	Sequence 327, App
296	35.5	8.4	53	9	US-09-796-692-1121	Sequence 1121, App	369	35	8.3	63	9	US-09-984-245-327	Sequence 327, App
297	35.5	8.4	53	9	US-09-796-692-1574	Sequence 1574, App	370	35	8.3	64	10	US-09-864-761-34561	Sequence 34561, A
298	35.5	8.4	55	10	US-10-092-154-968	Sequence 968, App	371	35	8.3	64	10	US-09-864-761-48795	Sequence 48795, A
299	35.5	8.4	55	10	US-09-764-847-968	Sequence 968, App	372	35	8.3	65	10	US-09-864-761-40420	Sequence 40420, A
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301	35.5	8.4	56	9	US-09-742-096-24	Sequence 24, Appl	374	35	8.3	66	9	US-10-001-876-127	Sequence 127, App
302	35.5	8.4	56	9	US-09-796-692-794	Sequence 794, App	375	35	8.3	70	10	US-10-092-154-722	Sequence 154-722
303	35.5	8.4	56	9	US-09-796-692-1159	Sequence 1159, App	376	35	8.3	70	10	US-09-864-761-37542	Sequence 37542, A
304	35.5	8.4	56	9	US-09-796-692-1431	Sequence 1431, App	377	35	8.3	70	10	US-09-864-761-47961	Sequence 47961, A
305	35.5	8.4	56	9	US-09-796-692-1603	Sequence 1603, App	378	35	8.3	70	10	US-09-764-847-722	Sequence 722, App
306	35.5	8.4	56	9	US-09-796-692-2134	Sequence 2134, App	379	35	8.3	74	10	US-09-764-869-1207	Sequence 1207, App
307	35.5	8.4	58	9	US-09-796-692-2209	Sequence 2209, App	380	35	8.3	75	9	US-09-764-877-1504	Sequence 1504, App
308	35.5	8.4	59	9	US-10-012-542-336	Sequence 336, App	381	35	8.3	75	10	US-09-910-009A-262	Sequence 262, App
309	35.5	8.4	60	10	US-09-764-869-1236	Sequence 1236, App	382	35	8.3	75	10	US-09-864-761-34641	Sequence 34641, A
310	35.5	8.4	63	10	US-09-925-300-1332	Sequence 1332, App	383	35	8.3	75	10	US-09-864-761-40845	Sequence 40845, A
311	35.5	8.4	63	10	US-09-864-761-36194	Sequence 36194, A	384	35	8.3	76	9	US-10-092-154-881	Sequence 881, App

385	35	8.3	76	10	US-09-764-869-843	Sequence 843, App	458	34	8.0	46	10	US-09-864-761-42687	Sequence 42687, A
386	35	8.3	76	10	US-09-764-847-881	Sequence 881, App	459	34	8.0	46	10	US-09-864-761-45352	Sequence 45352, A
387	35	8.3	76	10	US-09-867-550-1402	Sequence 1402, App	460	34	8.0	53	10	US-09-864-761-40784	Sequence 40784, A
388	35	8.3	79	9	US-09-774-639-288	Sequence 288, App	461	34	8.0	53	10	US-09-864-761-40784	Sequence 1983, App
389	35	8.3	79	9	US-09-869-730-281	Sequence 281, App	462	34	8.0	54	9	US-09-796-692-1440	Sequence 1440, App
390	35	8.3	79	10	US-09-864-761-38211	Sequence 38211, A	463	34	8.0	54	9	US-09-796-692-2411	Sequence 2411, App
391	35	8.3	80	9	US-09-869-391-716	Sequence 716, App	464	34	8.0	54	10	US-09-867-550-1364	Sequence 1364, App
392	35	8.3	83	10	US-09-764-877-1070	Sequence 1070, App	465	34	8.0	55	10	US-09-908-711-80	Sequence 80, Appl
393	35	8.3	84	9	US-09-866-050A-388	Sequence 388, App	466	34	8.0	55	10	US-09-864-761-45639	Sequence 45639, A
394	35	8.3	85	10	US-09-925-297-762	Sequence 762, App	467	34	8.0	56	10	US-09-864-761-40894	Sequence 40894, A
395	35	8.3	86	10	US-09-864-761-35345	Sequence 35345, A	468	34	8.0	56	10	US-09-864-761-40894	Sequence 562, App
396	35	8.3	86	10	US-09-864-761-35345	Sequence 4, Appl	469	34	8.0	59	9	US-09-895-793-562	Sequence 562, App
397	35	8.3	88	10	US-09-815-248-4	Sequence 72, Appl	470	34	8.0	59	9	US-09-895-793-562	Sequence 562, App
398	35	8.3	88	10	US-09-733-254-72	Sequence 72, Appl	471	34	8.0	59	10	US-09-759-143-562	Sequence 562, App
399	35	8.3	88	10	US-09-904-615-72	Sequence 72, Appl	472	34	8.0	59	10	US-09-864-761-39239	Sequence 39239, A
400	35	8.3	88	10	US-09-864-761-46314	Sequence 46314, A	473	34	8.0	59	10	US-09-780-669-562	Sequence 562, App
401	34.5	8.2	40	10	US-09-864-761-41728	Sequence 41728, A	474	34	8.0	59	10	US-09-823-827-562	Sequence 562, App
402	34.5	8.2	42	10	US-09-864-761-35257	Sequence 35257, A	475	34	8.0	59	10	US-09-867-550-1164	Sequence 1164, App
403	34.5	8.2	46	9	US-09-989-919-115	Sequence 115, App	476	34	8.0	60	10	US-09-864-761-44332	Sequence 44332, A
404	34.5	8.2	47	9	US-10-000-256A-138	Sequence 138, App	477	34	8.0	61	9	US-10-091-483-166	Sequence 166, App
405	34.5	8.2	48	10	US-09-925-297-830	Sequence 830, App	478	34	8.0	61	10	US-09-864-761-34897	Sequence 34897, A
406	34.5	8.2	49	10	US-09-832-355A-19	Sequence 19, Appl	479	34	8.0	61	10	US-09-864-761-34897	Sequence 166, App
407	34.5	8.2	49	10	US-09-864-761-43231	Sequence 43231, A	480	34	8.0	62	10	US-09-864-761-40187	Sequence 40187, A
408	34.5	8.2	50	10	US-09-764-877-1447	Sequence 1447, App	481	34	8.0	66	10	US-09-864-761-48880	Sequence 48880, A
409	34.5	8.2	50	10	US-09-864-761-41057	Sequence 41057, A	482	34	8.0	66	10	US-09-864-761-48880	Sequence 790, App
410	34.5	8.2	53	10	US-09-864-761-44405	Sequence 44405, A	483	34	8.0	68	10	US-09-864-761-48084	Sequence 48084, A
411	34.5	8.2	57	10	US-09-925-300-1138	Sequence 1138, App	484	34	8.0	68	10	US-09-764-847-790	Sequence 790, App
412	34.5	8.2	57	10	US-09-864-761-37163	Sequence 37163, A	485	34	8.0	69	10	US-09-864-761-38134	Sequence 38134, A
413	34.5	8.2	57	10	US-09-867-550-1480	Sequence 1480, App	486	34	8.0	70	10	US-09-864-761-38134	Sequence 92, Appl
414	34.5	8.2	58	10	US-09-984-610-30	Sequence 30, Appl	487	34	8.0	72	10	US-09-929-924-17	Sequence 17, Appl
415	34.5	8.2	59	10	US-09-867-550-1618	Sequence 1618, App	488	34	8.0	74	9	US-09-910-009A-234	Sequence 234, App
416	34.5	8.2	60	9	US-09-774-639-237	Sequence 237, App	489	34	8.0	74	10	US-09-864-761-34188	Sequence 34188, A
417	34.5	8.2	60	10	US-09-969-730-305	Sequence 305, App	490	34	8.0	74	10	US-09-864-761-34188	Sequence 2, Appl
418	34.5	8.2	61	9	US-09-864-761-47405	Sequence 47405, A	491	34	8.0	75	10	US-09-819-058-2	Sequence 36339, A
419	34.5	8.2	62	9	US-10-004-381-24	Sequence 24, Appl	492	34	8.0	76	9	US-09-864-761-33639	Sequence 300, App
420	34.5	8.2	62	9	US-09-796-692-894	Sequence 894, App	493	34	8.0	77	9	US-10-023-066A-75	Sequence 75, Appl
421	34.5	8.2	64	10	US-09-764-860-429	Sequence 429, App	494	34	8.0	79	10	US-09-866-050A-652	Sequence 652, App
422	34.5	8.2	64	10	US-09-864-761-36120	Sequence 36120, A	495	34	8.0	79	10	US-09-864-761-46443	Sequence 46443, A
423	34.5	8.2	66	9	US-09-864-761-47581	Sequence 47581, A	496	34	8.0	81	10	US-09-867-550-1756	Sequence 1756, App
424	34.5	8.2	67	10	US-10-001-835-165	Sequence 165, App	497	34	8.0	84	10	US-09-764-864-1570	Sequence 1570, App
425	34.5	8.2	67	10	US-09-723-674-180	Sequence 180, App	498	34	8.0	84	10	US-10-076-785-46	Sequence 46, Appl
426	34.5	8.2	68	9	US-09-864-761-49092	Sequence 49092, A	499	34	8.0	86	9	US-09-925-297-855	Sequence 855, App
427	34.5	8.2	68	10	US-09-764-854-146	Sequence 146, App	500	34	8.0	86	9	US-10-083-357-1031	Sequence 1031, App
428	34.5	8.2	70	10	US-09-764-878-146	Sequence 146, App	501	34	8.0	86	9	US-10-092-154-532	Sequence 532, App
429	34.5	8.2	72	9	US-09-854-816-63	Sequence 93, Appl	502	34	8.0	86	10	US-09-864-761-44003	Sequence 44003, A
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431	34.5	8.2	72	10	US-09-764-864-1557	Sequence 1557, App	504	34	8.0	86	10	US-09-764-847-532	Sequence 532, App
432	34.5	8.2	74	9	US-09-764-847-634	Sequence 634, App	505	34	8.0	88	9	US-09-764-847-532	Sequence 1127, App
433	34.5	8.2	75	9	US-09-969-730-155	Sequence 155, App	506	34	8.0	88	9	US-09-764-868-1127	Sequence 841, App
434	34.5	8.2	75	9	US-09-764-873-125	Sequence 125, App	507	34	8.0	89	10	US-09-922-154-841	Sequence 841, App
435	34.5	8.2	77	10	US-09-764-872-378	Sequence 378, App	508	34	8.0	89	10	US-09-764-847-841	Sequence 22, Appl
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444	34.5	8.2	84	10	US-09-764-847-897	Sequence 897, App	517	33.5	7.9	47	10	US-09-864-761-47396	Sequence 47396, A
445	34.5	8.2	86	10	US-09-925-300-1270	Sequence 1270, App	518	33.5	7.9	48	10	US-09-864-761-47396	Sequence 41608, A
446	34.5	8.2	86	10	US-09-764-870-477	Sequence 477, App	519	33.5	7.9	48	10	US-09-864-761-41608	Sequence 81, Appl
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533	33.5	7.9	63	10	US-09-864-761-48173	Sequence 48173, A	606	33	7.8	67	10	US-09-867-350-1694	Sequence 1694, App
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603	33	7.8	67	9	US-10-002-344A-259	Sequence 259, App	676	32.5	7.7	61	9	US-09-981-876-138	Sequence 138, App

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678	32.5	7.7	61	10	US-09-921-397-33	Sequence 33, Appl	751	32	7.6	52	9	US-09-925-299-1413	Sequence 1413, App
679	32.5	7.7	62	10	US-09-756-998-10	Sequence 10, Appl	752	32	7.6	52	10	US-09-864-761-47200	Sequence 47200, A
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681	32.5	7.7	62	10	US-09-904-615-108	Sequence 108, App	754	32	7.6	52	10	US-09-925-301-1619	Sequence 1619, App
682	32.5	7.7	62	10	US-09-864-761-38019	Sequence 38019, App	755	32	7.6	52	10	US-09-925-299-1413	Sequence 1413, App
683	32.5	7.7	62	10	US-09-864-761-38019	Sequence 38019, App	756	32	7.6	53	9	US-09-935-916A-46	Sequence 46, Appl
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686	32.5	7.7	64	10	US-09-864-761-40179	Sequence 40179, A	759	32	7.6	53	10	US-09-764-847-573	Sequence 573, App
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702	32.5	7.7	82	9	US-09-989-920-168	Sequence 168, App	775	32	7.6	58	9	US-09-812-302-8	Sequence 8, Appl
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709	32.5	7.7	84	10	US-09-764-877-1985	Sequence 1985, App	782	32	7.6	60	9	US-09-866-050A-181	Sequence 181, App
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## ALIGNMENTS

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RESULT 1
US-09-925-299-1024
; Sequence 1024, Application US/09925299
; Publication No. US20020040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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Best Local Similarity 50.0%; Pred. No. 11;
Matches 14; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

QY 58 LRLGTHGSPAS-SQSSATNMATHRSOP 84
| | | | | | | | | | | | | | | | | |
Db 33 LELATXGDPASASQSGITGVSHRAQP 60
| | | | | | | | | | | | | | | | | |

RESULT 2
US-09-925-299-1024
; Sequence 1024, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1024
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (26)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-925-299-1024
Query Match 12.9%; Score 54.5; DB 10; Length 60;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 14; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

QY 58 LRLGTHGSPAS-SQSSATNMATHRSOP 84
| | | | | | | | | | | | | | | | | |
Db 33 LELATXGDPASASQSGITGVSHRAQP 60
| | | | | | | | | | | | | | | | | |

RESULT 3
US-09-908-711-103
; Sequence 103, Application US/09908711
; Patent No. US20020045230A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA128
; CURRENT APPLICATION NUMBER: US/09/908,711
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US01/01360
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,867
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01344

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; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01345
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,888
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01329
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,905
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01354
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,891
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01339
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,869
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01340
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,874
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01334
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,898
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01320
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,853
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01349
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,902
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01239
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,870
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01348
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,882
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01347
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,896
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01307
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,864
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01341
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,856
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01336
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,868
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01312
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-908-711-103

Query Match      12.2%; Score 51.5; DB 10; Length 83;
Best Local Similarity 27.5%; Pred. No. 41;
Matches 19; Conservative 8; Mismatches 33; Indels 9; Gaps 2;

Qy 15 RSISENSLVAMDF-SGOKSRVIENTPEALSVAVEGLAWKK-----GCLRLGTHGS 65
Db 9 RDVGECDLPQMEVGVSGXSRPRTTPASGPRHSRRKAPMRRRLPSQWNNPGTRPGSAAQ 68
Qy 66 PTASSOSSA 74
Db 69 PWGSSQASS 77

RESULT 4
US-09-864-761-47521
; Sequence 47521, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aseomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47521
; LENGTH: 84

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL158153.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 6.7
; OTHER INFORMATION: EST_HUMAN HIT: B573555.1, EVALUE 1.60e-02
; OTHER INFORMATION: SWISSPROT HIT: Q91641, EVALUE 3.00e-25
US-09-864-761-47521

Query Match 12.1%; Score 51; DB 10; Length 84;
Best Local Similarity 27.8%; Pred. No. 48;
Matches 15; Conservative 6; Mismatches 7; Indels 26; Gaps 2;

; 29 GOKSRVIEPN-----TEALSVAV-----EEGLAWRKKG 56
|||:::| | | | | | | | | | | | | | | | | | | | | |
; 11 GOKARLSRLRGVSGKHCLTFEYHMGVGGTGLLSVYLKKEEDSESLIWRRG 64
|||:::| | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-10-125-258-6
; Sequence 6, Application US/10125258
; Publication No. US20030028920A1
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Hermann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Prespall, James K.
; APPLICANT: Weaver, Janice L.
; APPLICANT: Weaver, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 78
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-125-258-6

Query Match 11.9%; Score 50.5; DB 9; Length 80;
Best Local Similarity 28.8%; Pred. No. 51;
Matches 17; Conservative 10; Mismatches 23; Indels 9; Gaps 1;

; 16 SISLSNVAMDFSGKSRVNIENPEALSVAVEGLAWRKKGCLRLGTHGSPASSQSSA 74
|||:::| | | | | | | | | | | | | | | | | | | | | |
; 2 SLSCLFLVALVGAESRIADDDVVLPMMVSR-----VRDRTHGSVTVNSDGT 51
|||:::| | | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-09-864-761-42490
; Sequence 42490, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmice-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL139289.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 3.9
; OTHER INFORMATION: EST_HUMAN HIT: BE272485.1, EVALUE 5.00e-30
US-09-864-761-42490

Query Match 11.5%; Score 48.5; DB 10; Length 82;
Best Local Similarity 33.3%; Pred. No. 93;
Matches 15; Conservative 7; Mismatches 18; Indels 5; Gaps 2;

; 37 NPTE-----ALSVAVEEGLA-WRKKGCLRLGTHGSPASSQSSATN 76
|||:::| | | | | | | | | | | | | | | | | | | | | |
; 9 NPTDTNALVAAVAAGKGLSNWRPSSGSGPGAGQGAGTLAGTS 53
|||:::| | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-09-764-872-393
; Sequence 393, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125

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Query Match 10.9%; Score 46; DB 9; Length 68;  
Best Local Similarity 47.4%; Pred. No. 1.4e+02.

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RESULT 12
US-10-092-154-700
: Sequence 700, Application US/10092154
: Publication No. US20030054375A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC009C1
: CURRENT APPLICATION NUMBER: US/10/092.154
: CURRENT FILING DATE: 2002-03-07

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; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-092-154-700

Query Match          10.9%; Score 46; DB 9; Length 69;
Best Local Similarity 37.9%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 56 GCLRLGTHGSPPTASSOSATNMAIHRSP 84
DB 31 GLKLLGSSPPPTILASOSAGITGMHCXOP 59

RESULT 13
US-09-764-847-700
; Sequence 700, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (57)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-847-700

Query Match          10.9%; Score 46; DB 10; Length 69;
Best Local Similarity 37.9%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

QY 56 GCLRLGTHGSPPTASSOSATNMAIHRSP 84
DB 31 GLKLLGSSPPPTILASOSAGITGMHCXOP 59

RESULT 14
US-09-925-299-1460
; Sequence 1460, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1460
; LENGTH: 56
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-925-299-1460

Query Match          10.8%; Score 45.5; DB 9; Length 56;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRLGTHGSPPTASSQ-----SSAT 75
DB 6 NPLVNLTVSPKRNSSLDTRKKPCRESKKFNTHSRPKSSHOLKRKSST 53

RESULT 15
US-09-925-299-1460
; Sequence 1460, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1460
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1460

Query Match          10.8%; Score 45.5; DB 10; Length 56;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRLGTHGSPPTASSQ-----SSAT 75
DB 6 NPLVNLTVSPKRNSSLDTRKKPCRESKKFNTHSRPKSSHOLKRKSST 53

RESULT 16
US-09-925-299-1372
; Sequence 1372, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1372
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1372

Query Match          10.8%; Score 45.5; DB 9; Length 58;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRLGTHGSPPTASSQ-----SSAT 75
DB 8 NPLVNLTVSPKRNSSLDTRKKPCRESKKFNTHSRPKSSHOLKRKSST 55

```



RESULT 19  
US-09-925-299-1528  
; Sequence 1528, Application US/09925299  
; Publication No. US20030040617A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.

```

RESULT 21
US-09-925-299-1372
; Sequence 1372, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1372

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; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1372

Query Match      10.8%; Score 45.5; DB 10; Length 58;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRIGTHGSPASSQ-----SSAT 75
Db 8 NPLVNLTVSPKRNSSLDTRKKPCRESKFKFNTHSRPKSSHOLKRKRSST 55

RESULT 22
US-09-925-299-1437
; Sequence 1437, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1437
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1437

Query Match      10.8%; Score 45.5; DB 10; Length 58;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRIGTHGSPASSQ-----SSAT 75
Db 8 NPLVNLTVSPKRNSSLDTRKKPCRESKFKFNTHSRPKSSHOLKRKRSST 55

RESULT 23
US-09-925-299-1493
; Sequence 1493, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1493
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1493

Query Match      10.8%; Score 45.5; DB 10; Length 58;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;

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Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRIGTHGSPASSQ-----SSAT 75
Db 8 NPLVNLTVSPKRNSSLDTRKKPCRESKFKFNTHSRPKSSHOLKRKRSST 55

RESULT 24
US-09-925-299-1528
; Sequence 1528, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1528
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1528

Query Match      10.8%; Score 45.5; DB 10; Length 58;
Best Local Similarity 35.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 6; Mismatches 16; Indels 9; Gaps 3;

QY 37 NPTEALSVAVE--EGLAWRKKG---LRIGTHGSPASSQ-----SSAT 75
Db 8 NPLVNLTVSPKRNSSLDTRKKPCRESKFKFNTHSRPKSSHOLKRKRSST 55

RESULT 25
US-09-764-877-1350
; Sequence 1350, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1350
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1350

Query Match      10.8%; Score 45.5; DB 10; Length 60;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 16; Conservative 6; Mismatches 25; Indels 1; Gaps 1;

QY 38 PTEALSVAVEEGLAWRKKGCLRLGTHGS-PTASSQSATNNATHRSOP 84
Db 6 PCQFFVFLVEMGFHHVQCAGLELLTSGDPTTSASQSAGITGMSHCAQP 53

Search completed: March 28, 2003, 09:19:20
JOB time : 31.1181 secs

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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 09:03:25 ; Search time 24.4724 Seconds  
(without alignments)  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 20297

Minimum DB seq length: 40

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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258	33	7.8	46	4	US-08-483-533-30	Sequence 30, Appl	331	32	7.6	45	1	US-08-175-069A-12	Sequence 12, Appl
259	33	7.8	46	4	US-09-283-471A-30	Sequence 30, Appl	332	32	7.6	45	4	US-08-461-539B-12	Sequence 12, Appl
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262	33	7.8	50	2	US-08-399-411-56	Sequence 56, Appl	335	32	7.6	47	4	US-08-776-059-19	Sequence 19, Appl
263	33	7.8	50	4	US-08-316-855A-56	Sequence 56, Appl	336	32	7.6	48	3	US-08-804-439A-101	Sequence 101, Appl
264	33	7.8	50	4	US-09-366-472-56	Sequence 56, Appl	337	32	7.6	51	1	US-08-188-228-34	Sequence 34, Appl
265	33	7.8	50	4	US-09-328-706-56	Sequence 56, Appl	338	32	7.6	51	1	US-08-332-643-34	Sequence 34, Appl
266	33	7.8	50	5	PCT-US93-05640-38	Sequence 38, Appl	339	32	7.6	51	1	US-08-905-223-489	Sequence 489, App
267	33	7.8	51	4	US-09-150-460B-21	Sequence 21, Appl	340	32	7.6	53	4	US-08-469-537A-10	Sequence 10, Appl
268	33	7.8	51	4	US-09-314-268-100	Sequence 100, App	341	32	7.6	54	2	US-08-469-537A-31	Sequence 31, Appl
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270	33	7.8	54	1	US-08-167-035-29	Sequence 29, Appl	343	32	7.6	57	4	US-08-434-295-7	Sequence 7, Appl
271	33	7.8	54	1	US-08-208-887A-29	Sequence 29, Appl	344	32	7.6	58	3	US-08-434-295-7	Sequence 7, Appl
272	33	7.8	54	2	US-08-459-537A-9	Sequence 9, Appl	345	32	7.6	58	3	US-08-434-295-8	Sequence 8, Appl
273	33	7.8	54	2	US-08-459-537A-33	Sequence 33, Appl	346	32	7.6	58	3	US-08-434-295-9	Sequence 9, Appl
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275	33	7.8	54	4	US-09-280-598-31	Sequence 31, Appl	348	32	7.6	58	4	US-09-431-500A-7	Sequence 7, Appl
276	33	7.8	55	2	US-08-456-647B-2	Sequence 2, Appl	349	32	7.6	58	4	US-09-431-500A-8	Sequence 8, Appl
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279	33	7.8	59	2	US-08-392-816-18	Sequence 18, Appl	352	32	7.6	58	4	US-09-431-498-7	Sequence 7, Appl
280	33	7.8	60	3	US-08-061-564A-9	Sequence 6, Appl	353	32	7.6	58	4	US-09-431-498-8	Sequence 8, Appl
281	33	7.8	66	3	US-08-508-645C-11	Sequence 11, Appl	354	32	7.6	58	4	US-09-431-499-7	Sequence 7, Appl
282	33	7.8	68	3	US-08-026-033-31	Sequence 31, Appl	355	32	7.6	58	4	US-09-431-499-8	Sequence 8, Appl
283	33	7.8	68	4	US-08-905-223-419	Sequence 419, App	356	32	7.6	58	4	US-09-431-499-9	Sequence 9, Appl
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285	33	7.8	70	4	US-08-908-643C-9	Sequence 9, Appl	358	32	7.6	60	4	US-09-188-930-320	Sequence 320, App
286	33	7.8	76	3	US-08-817-811-22	Sequence 22, Appl	359	32	7.6	60	4	US-09-149-476-671	Sequence 671, App
287	33	7.8	81	4	US-08-858-207A-450	Sequence 450, App	360	32	7.6	62	1	US-08-464-531-117	Sequence 117, App
288	33	7.8	85	2	US-08-162-081B-46	Sequence 46, Appl	361	32	7.6	62	1	US-08-461-598-117	Sequence 117, App
289	33	7.8	85	2	US-08-780-872-46	Sequence 46, Appl	362	32	7.6	62	2	US-08-322-137-117	Sequence 117, App
290	33	7.8	85	4	US-09-085-957-46	Sequence 46, Appl	363	32	7.6	62	2	US-08-209-521-17	Sequence 17, App
291	33	7.8	87	2	US-08-485-721-11	Sequence 11, Appl	364	32	7.6	64	4	US-09-188-930-122	Sequence 122, App
292	33	7.8	87	2	US-08-392-935-11	Sequence 11, Appl	365	32	7.6	64	4	US-08-961-810-127	Sequence 127, App
293	33	7.8	87	5	PCT-US93-08326-11	Sequence 11, Appl	366	32	7.6	64	4	US-08-352-002B-127	Sequence 127, App
294	33	7.8	87	5	US-08-424-022A-4	Sequence 4, Appl	367	32	7.6	64	5	PCT-US92-00282-17	Sequence 17, App
295	32.5	7.7	47	1	US-09-227-357-241	Sequence 241, App	368	32	7.6	68	3	US-08-312-272-30	Sequence 30, Appl
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297	32.5	7.7	50	4	US-09-220-528-108	Sequence 108, App	370	32	7.6	70	1	US-08-193-863-2	Sequence 2, Appl
298	32.5	7.7	50	4	US-08-026-145-6	Sequence 6, Appl	371	32	7.6	70	1	US-08-377-833-2	Sequence 2, Appl
299	32.5	7.7	52	1	US-07-985-692-4	Sequence 4, Appl	372	32	7.6	70	1	US-08-324-502-2	Sequence 2, Appl
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302	32.5	7.7	53	1	US-08-321-659B-10	Sequence 10, Appl	375	32	7.6	70	1	US-09-367-953B-106	Sequence 106, App
303	32.5	7.7	53	1	US-08-334-489-7	Sequence 7, Appl	376	32	7.6	70	6	517189-3	Patent No. 517189
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308	32.5	7.7	53	2	PCT-US93-11696-4	Sequence 4, Appl	381	32	7.6	77	2	US-08-480-478-33	Sequence 33, Appl
309	32.5	7.7	53	5	US-09-134-001C-5046	Sequence 5046, App	382	32	7.6	77	2	US-08-486-397-4	Sequence 4, Appl
310	32.5	7.7	61	4	US-09-268-364-10	Sequence 10, Appl	383	32	7.6	77	2	US-08-486-399-4	Sequence 4, Appl
311	32.5	7.7	62	4	US-08-633-879C-16	Sequence 16, Appl	384	32	7.6	77	2	US-08-486-399-4	Sequence 4, Appl
312	32.5	7.7	62	2	US-09-073-297-10	Sequence 10, Appl	385	32	7.6	77	2	US-08-486-399-4	Sequence 4, Appl
313	32.5	7.7	66	4	US-08-248-839C-114	Sequence 114, App	386	32	7.6	77	2	US-08-461-965-4	Sequence 4, Appl
314	32.5	7.7	71	4	US-09-254-332B-29	Sequence 29, App	387	32	7.6	77	2	US-08-326-110A-33	Sequence 33, Appl
315	32.5	7.7	73	2	US-08-905-223-272	Sequence 272, App	388	32	7.6	77	2	US-08-634-641-4	Sequence 4, Appl
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436	7.4	43	3	US-09-277-685-73	Sequence 73, Appli	509	31	7.3	60	5	PCT-US93-11154-4	Sequence 4, Appli
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452	31.5	7.4	61	US-08-871-355A-181	Sequence 181, App	525	31	7.3	64	4	US-08-961-810-125	Sequence 125, App
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465	31.5	7.4	90	US-08-168-228-16	Sequence 16, Appli	538	31	7.3	66	4	US-09-134-001C-5385	Sequence 5385, Ap

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545	31	7.3	70	4	US-09-367-953B-83	Sequence 83, Appl	618	30.5	7.2	54	2	US-09-431-500A-10	Sequence 10, Appl
546	31	7.3	70	6	5182364-4	Patent No. 5182364	619	30.5	7.2	54	4	US-09-165-422-15	Sequence 15, Appl
547	31	7.3	71	4	US-09-146-054-9	Sequence 9, Appl	620	30.5	7.2	54	4	US-09-431-488-10	Sequence 10, Appl
548	31	7.3	71	4	US-09-056-556-233	Sequence 233, Appl	621	30.5	7.2	54	4	US-09-431-489-10	Sequence 10, Appl
549	31	7.3	71	4	US-09-666-977A-9	Sequence 9, Appl	622	30.5	7.2	56	1	US-08-274-366-1	Sequence 1, Appl
550	31	7.3	71	4	US-08-078-556-228	Sequence 228, Appl	623	30.5	7.2	56	1	US-08-572-951-36	Sequence 36, Appl
551	31	7.3	72	1	US-08-280-443-11	Sequence 11, Appl	624	30.5	7.2	56	3	US-08-735-491-4	Sequence 4, Appl
552	31	7.3	72	1	US-08-457-459-11	Sequence 11, Appl	625	30.5	7.2	56	3	US-08-941-445A-33	Sequence 33, Appl
553	31	7.3	72	1	US-08-535-678-11	Sequence 11, Appl	626	30.5	7.2	56	3	US-08-941-445A-33	Sequence 33, Appl
554	31	7.3	72	3	US-09-023-082A-78	Sequence 78, Appl	627	30.5	7.2	56	5	PCT-US95-07828-1	Sequence 1, Appl
555	31	7.3	72	4	US-08-965-056-83	Sequence 83, Appl	628	30.5	7.2	57	4	US-09-605-785-561	Sequence 561, Appl
556	31	7.3	72	4	US-08-965-056-83	Sequence 83, Appl	629	30.5	7.2	59	2	US-08-470-720-14	Sequence 14, Appl
557	31	7.3	72	5	PCT-US95-02275-11	Sequence 566, Appl	630	30.5	7.2	60	4	US-08-857-076-26	Sequence 26, Appl
558	31	7.3	74	1	US-07-956-700B-32	Sequence 11, Appl	631	30.5	7.2	61	2	US-08-482-142-162	Sequence 162, Appl
559	31	7.3	74	1	US-08-476-537-32	Sequence 32, Appl	632	30.5	7.2	61	2	US-08-482-142-162	Sequence 162, Appl
560	31	7.3	74	1	US-08-485-607-32	Sequence 32, Appl	633	30.5	7.2	61	4	US-08-484-296-162	Sequence 162, Appl
561	31	7.3	74	2	US-08-475-879-32	Sequence 32, Appl	634	30.5	7.2	65	4	US-08-961-083-146	Sequence 146, Appl
562	31	7.3	74	4	US-09-433-043B-32	Sequence 32, Appl	635	30.5	7.2	66	4	US-09-079-812E-31	Sequence 31, Appl
563	31	7.3	75	4	US-09-134-001C-5321	Sequence 5321, Ap	636	30.5	7.2	67	5	US-08-207-481-45	Sequence 45, Appl
564	31	7.3	76	4	US-08-737-109-20	Sequence 20, Appl	637	30.5	7.2	67	5	PCT-US95-02889-52	Sequence 52, Appl
565	31	7.3	76	1	US-07-881-075-6	Sequence 6, Appl	638	30.5	7.2	69	1	US-08-137-800-40	Sequence 40, Appl
566	31	7.3	76	1	US-08-120-827-6	Sequence 6, Appl	639	30.5	7.2	69	1	US-08-477-383-40	Sequence 40, Appl
567	31	7.3	76	1	US-08-428-875-6	Sequence 6, Appl	640	30.5	7.2	69	1	US-08-480-750-40	Sequence 40, Appl
568	31	7.3	76	1	US-08-227-357-255	Sequence 255, Appl	641	30.5	7.2	69	4	US-09-007-905-31	Sequence 31, Appl
569	31	7.3	77	1	US-08-530-163-7	Sequence 7, Appl	642	30.5	7.2	69	4	US-09-233-074-31	Sequence 31, Appl
570	31	7.3	77	1	US-08-094-851-6	Sequence 6, Appl	643	30.5	7.2	70	4	US-08-857-076-29	Sequence 29, Appl
571	31	7.3	77	1	US-08-482-111-7	Sequence 7, Appl	644	30.5	7.2	70	4	US-09-620-093A-6	Sequence 6, Appl
572	31	7.3	77	2	US-08-436-420-29	Sequence 29, Appl	645	30.5	7.2	72	3	US-08-338-579A-105	Sequence 105, Appl
573	31	7.3	77	5	PCT-US94-08167-6	Sequence 14, Appl	646	30.5	7.2	72	3	US-08-338-579A-105	Sequence 105, Appl
574	31	7.3	77	5	US-08-640-847C-14	Sequence 6, Appl	647	30.5	7.2	73	4	US-09-254-352B-28	Sequence 28, Appl
575	31	7.3	78	1	US-08-094-851-8	Sequence 8, Appl	648	30.5	7.2	74	1	US-08-203-806B-13	Sequence 13, Appl
576	31	7.3	78	1	US-08-722-001-5	Sequence 5, Appl	649	30.5	7.2	74	1	US-09-017-754A-13	Sequence 13, Appl
577	31	7.3	78	4	US-08-905-223-452	Sequence 452, Appl	650	30.5	7.2	75	1	US-08-594-031-99	Sequence 99, Appl
578	31	7.3	78	5	PCT-US94-08167-8	Sequence 8, Appl	651	30.5	7.2	77	1	US-08-325-547-8	Sequence 8, Appl
579	31	7.3	80	4	US-09-091-219-6	Sequence 6, Appl	652	30.5	7.2	77	2	US-08-726-306A-32	Sequence 32, Appl
580	31	7.3	82	2	US-08-117-952-756	Sequence 756, Appl	653	30.5	7.2	77	3	US-08-475-668A-211	Sequence 211, Appl
581	31	7.3	84	1	US-07-842-089B-45	Sequence 45, Appl	654	30.5	7.2	77	3	US-08-485-551A-211	Sequence 211, Appl
582	31	7.3	84	3	US-08-264-485-45	Sequence 45, Appl	655	30.5	7.2	78	4	US-08-465-033A-24	Sequence 24, Appl
583	31	7.3	84	3	US-09-045-632-6	Sequence 6, Appl	656	30.5	7.2	79	1	US-08-465-033A-24	Sequence 24, Appl
584	31	7.3	84	4	US-09-404-671-6	Sequence 6, Appl	657	30.5	7.2	79	2	US-08-444-733-4	Sequence 4, Appl
585	31	7.3	85	2	US-08-592-646A-18	Sequence 18, Appl	658	30.5	7.2	79	2	US-08-464-134-4	Sequence 4, Appl
586	31	7.3	85	3	US-08-772-440-32	Sequence 32, Appl	659	30.5	7.2	79	2	US-08-464-134-4	Sequence 4, Appl
587	31	7.3	85	4	US-09-165-422-18	Sequence 18, Appl	660	30.5	7.2	79	2	US-08-464-134-4	Sequence 4, Appl
588	31	7.3	86	1	US-08-602-010A-34	Sequence 34, Appl	661	30.5	7.2	79	5	PCT-US95-06266-4	Sequence 4, Appl
589	31	7.3	86	1	US-08-680-726B-34	Sequence 34, Appl	662	30.5	7.2	81	1	US-08-259-672-8	Sequence 8, Appl
590	31	7.3	86	4	US-09-092-409-34	Sequence 34, Appl	663	30.5	7.2	81	1	US-08-459-351-8	Sequence 8, Appl
591	31	7.3	86	4	US-09-309-572-20	Sequence 20, Appl	664	30.5	7.2	81	1	US-08-460-533-8	Sequence 8, Appl
592	31	7.3	87	4	US-09-134-001C-3391	Sequence 3391, Ap	665	30.5	7.2	81	5	PCT-US94-06654-8	Sequence 8, Appl
593	31	7.3	88	3	US-09-043-632-7	Sequence 7, Appl	666	30.5	7.2	82	1	US-08-465-380-25	Sequence 25, Appl
594	31	7.3	88	4	US-09-415-785A-116	Sequence 116, Appl	667	30.5	7.2	82	2	US-08-465-380-25	Sequence 25, Appl
595	31	7.3	88	4	US-08-944-465-116	Sequence 116, Appl	668	30.5	7.2	82	2	US-08-465-380-49	Sequence 49, Appl
596	31	7.3	88	4	US-09-415-868-116	Sequence 116, Appl	669	30.5	7.2	82	2	US-08-480-478-54	Sequence 54, Appl
597	31	7.3	88	4	US-09-415-868-116	Sequence 116, Appl	670	30.5	7.2	82	2	US-08-486-397-25	Sequence 25, Appl
598	31	7.3	88	4	US-08-341-843B-28	Sequence 28, Appl	671	30.5	7.2	82	2	US-08-486-397-25	Sequence 25, Appl
599	31	7.3	90	2	US-08-427-497B-33	Sequence 33, Appl	672	30.5	7.2	82	2	US-08-486-399-25	Sequence 25, Appl
600	31	7.3	90	3	US-09-035-619-24	Sequence 24, Appl	673	30.5	7.2	82	2	US-08-486-399-25	Sequence 25, Appl
601	30.5	7.2	40	4	US-09-514-006-24	Sequence 24, Appl	674	30.5	7.2	82	2	US-08-461-965-25	Sequence 25, Appl
602	30.5	7.2	40	4	US-09-227-357-580	Sequence 580, Appl	675	30.5	7.2	82	2	US-08-461-965-25	Sequence 25, Appl
603	30.5	7.2	41	4	US-09-174-465D-8	Sequence 8, Appl	676	30.5	7.2	82	2	US-08-326-110A-54	Sequence 54, Appl
604	30.5	7.2	41	4	US-09-599-564A-8	Sequence 8, Appl	677	30.5	7.2	82	2	US-08-634-641-25	Sequence 25, Appl
605	30.5	7.2	41	4	US-09-201-227A-27	Sequence 27, Appl	678	30.5	7.2	82	2	US-08-634-641-25	Sequence 25, Appl
606	30.5	7.2	43	4	US-09-461-697-304	Sequence 304, Appl	679	30.5	7.2	82	3	US-09-249-471-25	Sequence 25, Appl
607	30.5	7.2	43	4	US-08-857-076-69	Sequence 69, Appl	680	30.5	7.2	82	3	US-09-249-471-25	Sequence 25, Appl
608	30.5	7.2	45	4	US-08-963-851-5	Sequence 5, Appl	681	30.5	7.2	82	3	US-09-249-472-25	Sequence 25, Appl
609	30.5	7.2	45	4	US-08-817-787-12	Sequence 12, Appl	682	30.5	7.2	82	3	US-09-249-472-25	Sequence 25, Appl
610	30.5	7.2	47	4	US-09-155-107-11	Sequence 11, Appl	683	30.5	7.2	82	3	US-09-249-451-25	Sequence 25, Appl
611	30.5	7.2	49	4			684	30.5	7.2	82	3	US-09-249-451-25	Sequence 25, Appl

685	30.5	7.2	82.	3	US-08-809-455-25	Sequence 25, Appl	758	30	7.1	61	3	US-09-249-472-61	Sequence 61, Appl
686	30.5	7.2	82	3	US-08-809-455-49	Sequence 49, Appl	759	30	7.1	61	3	US-09-249-451-61	Sequence 61, Appl
687	30.5	7.2	82	3	US-09-249-461-25	Sequence 25, Appl	760	30	7.1	61	3	US-08-809-455-61	Sequence 61, Appl
688	30.5	7.2	82	3	US-09-249-461-49	Sequence 49, Appl	761	30	7.1	61	3	US-09-249-461-61	Sequence 61, Appl
689	30.5	7.2	82	3	US-08-881-771A-3	Sequence 3, Appl	762	30	7.1	61	3	US-09-249-448-61	Sequence 61, Appl
690	30.5	7.2	82	3	US-09-249-448-25	Sequence 25, Appl	763	30	7.1	61	4	US-08-205-697A-32	Sequence 32, Appl
691	30.5	7.2	82	3	US-09-249-448-49	Sequence 49, Appl	764	30	7.1	61	4	US-08-456-748B-3	Sequence 3, Appl
692	30.5	7.2	83	4	US-08-981-988A-8	Sequence 8, Appl	765	30	7.1	61	4	US-08-702-525-32	Sequence 32, Appl
693	30.5	7.2	83	4	US-08-981-988A-8	Sequence 8, Appl	766	30	7.1	61	5	PCT-US95-02576-32	Sequence 32, Appl
694	30.5	7.2	83	4	US-08-981-988A-9	Sequence 9, Appl	767	30	7.1	62	1	US-08-215-084A-5	Sequence 5, Appl
695	30.5	7.2	83	4	US-08-981-988A-9	Sequence 9, Appl	768	30	7.1	62	1	US-08-463-212-5	Sequence 5, Appl
696	30.5	7.2	84	2	US-08-482-142-161	Sequence 161, Appl	769	30	7.1	62	1	US-08-463-211-5	Sequence 5, Appl
697	30.5	7.2	84	2	US-08-478-162-161	Sequence 161, Appl	770	30	7.1	62	1	US-09-537-357-11	Sequence 11, Appl
698	30.5	7.2	84	2	US-09-109-266-22	Sequence 22, Appl	771	30	7.1	63	4	US-08-887-534A-94	Sequence 94, Appl
699	30.5	7.2	84	4	US-08-484-296-161	Sequence 161, Appl	772	30	7.1	64	1	US-07-842-089B-2	Sequence 2, Appl
700	30.5	7.2	87	2	US-08-461-590B-21	Sequence 21, Appl	773	30	7.1	64	1	US-07-842-089B-56	Sequence 56, Appl
701	30.5	7.2	87	2	US-08-576-626A-43	Sequence 43, Appl	774	30	7.1	64	1	US-07-842-089B-57	Sequence 57, Appl
702	30.5	7.2	88	4	US-09-675-305-4	Sequence 4, Appl	775	30	7.1	64	1	US-07-842-089B-59	Sequence 59, Appl
703	30	7.1	40	4	US-09-082-379B-969	Sequence 969, Appl	776	30	7.1	64	1	US-08-264-485-2	Sequence 2, Appl
704	30	7.1	40	4	US-09-335-304B-969	Sequence 969, Appl	777	30	7.1	64	1	US-08-264-485-56	Sequence 56, Appl
705	30	7.1	41	2	US-07-921-447-10	Sequence 10, Appl	778	30	7.1	64	1	US-08-264-485-57	Sequence 57, Appl
706	30	7.1	41	4	US-09-398-395A-34	Sequence 34, Appl	779	30	7.1	64	1	US-08-264-485-59	Sequence 59, Appl
707	30	7.1	42	1	US-07-842-089B-3	Sequence 3, Appl	780	30	7.1	64	1	US-08-091-569-22	Sequence 22, Appl
708	30	7.1	42	1	US-08-264-485-3	Sequence 3, Appl	781	30	7.1	64	1	US-08-203-676-22	Sequence 22, Appl
709	30	7.1	42	4	US-08-988-856B-30	Sequence 30, Appl	782	30	7.1	64	2	US-08-209-521-19	Sequence 19, Appl
710	30	7.1	43	1	US-07-998-003A-10	Sequence 10, Appl	783	30	7.1	64	2	US-08-209-521-20	Sequence 20, Appl
711	30	7.1	43	1	US-08-453-274B-10	Sequence 10, Appl	784	30	7.1	64	2	US-08-822-238-22	Sequence 22, Appl
712	30	7.1	43	1	US-08-453-695A-10	Sequence 10, Appl	785	30	7.1	64	4	US-08-961-810-129	Sequence 129, Appl
713	30	7.1	43	1	US-08-268-161A-10	Sequence 10, Appl	786	30	7.1	64	4	US-08-961-810-130	Sequence 130, Appl
714	30	7.1	43	2	US-08-453-702A-10	Sequence 10, Appl	787	30	7.1	64	4	US-08-352-902B-129	Sequence 129, Appl
715	30	7.1	43	4	US-09-099-639-10	Sequence 10, Appl	788	30	7.1	64	4	US-08-352-902B-130	Sequence 130, Appl
716	30	7.1	43	5	PCT-US93-12588-10	Sequence 10, Appl	789	30	7.1	65	1	US-07-842-089B-55	Sequence 55, Appl
717	30	7.1	43	5	PCT-US93-08071-10	Sequence 10, Appl	790	30	7.1	65	1	US-07-842-089B-58	Sequence 58, Appl
718	30	7.1	44	1	US-08-110-786A-5	Sequence 5, Appl	791	30	7.1	65	1	US-08-264-485-55	Sequence 55, Appl
719	30	7.1	46	4	US-08-905-223-467	Sequence 467, Appl	792	30	7.1	65	1	US-08-264-485-58	Sequence 58, Appl
720	30	7.1	47	1	US-08-442-063A-51	Sequence 51, Appl	793	30	7.1	65	4	US-09-268-364-6	Sequence 6, Appl
721	30	7.1	47	3	US-09-100-414B-63	Sequence 63, Appl	794	30	7.1	65	4	US-09-227-357-289	Sequence 289, Appl
722	30	7.1	47	4	US-09-303-323-63	Sequence 63, Appl	795	30	7.1	65	4	US-09-134-001C-4870	Sequence 4870, Appl
723	30	7.1	51	1	US-08-905-223-491	Sequence 491, Appl	796	30	7.1	65	4	US-08-905-223-379	Sequence 379, Appl
724	30	7.1	51	4	US-08-208-108-11	Sequence 11, Appl	797	30	7.1	67	4	US-08-905-223-435	Sequence 435, Appl
725	30	7.1	51	4	US-09-077-951-33	Sequence 33, Appl	798	30	7.1	67	4	US-08-905-223-435	Sequence 435, Appl
726	30	7.1	52	1	US-08-117-083-16	Sequence 16, Appl	799	30	7.1	67	4	US-09-134-001C-5238	Sequence 5238, Appl
727	30	7.1	54	2	US-08-469-537A-29	Sequence 29, Appl	800	30	7.1	67	4	US-09-134-001C-5310	Sequence 5310, Appl
728	30	7.1	54	3	US-08-483-304-20	Sequence 20, Appl	801	30	7.1	70	1	US-08-330-163-27	Sequence 27, Appl
729	30	7.1	54	3	US-08-483-474-20	Sequence 20, Appl	802	30	7.1	70	1	US-08-482-111-27	Sequence 27, Appl
730	30	7.1	54	4	US-09-308-446C-13	Sequence 13, Appl	803	30	7.1	70	4	US-09-367-953B-68	Sequence 68, Appl
731	30	7.1	55	2	US-08-456-647B-42	Sequence 42, Appl	804	30	7.1	70	4	US-09-367-953B-70	Sequence 70, Appl
732	30	7.1	55	2	US-08-237-401A-42	Sequence 42, Appl	805	30	7.1	70	4	US-09-367-953B-78	Sequence 78, Appl
733	30	7.1	55	4	US-09-361-707-91	Sequence 91, Appl	806	30	7.1	71	4	US-09-367-953B-101	Sequence 101, Appl
734	30	7.1	55	4	US-09-361-707-92	Sequence 92, Appl	807	30	7.1	71	4	US-08-840-767-44	Sequence 44, Appl
735	30	7.1	55	4	US-09-361-707-99	Sequence 99, Appl	808	30	7.1	71	4	US-08-859-207A-540	Sequence 540, Appl
736	30	7.1	55	4	US-09-361-707-100	Sequence 100, Appl	809	30	7.1	71	4	US-09-930-181-6	Sequence 6, Appl
737	30	7.1	56	4	US-09-058-459-48	Sequence 48, Appl	810	30	7.1	72	1	US-08-468-674B-61	Sequence 61, Appl
738	30	7.1	56	4	US-09-058-459-49	Sequence 49, Appl	811	30	7.1	72	1	US-08-280-443-4	Sequence 4, Appl
739	30	7.1	56	4	US-09-127-926-48	Sequence 48, Appl	812	30	7.1	72	1	US-08-457-459-4	Sequence 4, Appl
740	30	7.1	56	4	US-09-127-926-49	Sequence 49, Appl	813	30	7.1	72	1	US-08-555-678-4	Sequence 61, Appl
741	30	7.1	56	4	US-09-127-926-86	Sequence 86, Appl	814	30	7.1	72	1	US-08-780-571-61	Sequence 61, Appl
742	30	7.1	56	4	US-09-127-926-87	Sequence 87, Appl	815	30	7.1	72	5	US-08-469-260A-233	Sequence 233, Appl
743	30	7.1	56	4	US-09-223-357-671	Sequence 671, Appl	816	30	7.1	73	1	PCT-US95-02275-4	Sequence 4, Appl
744	30	7.1	59	4	US-09-149-476-680	Sequence 680, Appl	817	30	7.1	73	5	PCT-US92-05532-3	Sequence 3, Appl
745	30	7.1	59	4	US-08-446-692-107	Sequence 107, Appl	818	30	7.1	74	4	US-09-134-001C-4092	Sequence 4092, Appl
746	30	7.1	60	2	US-08-488-351A-107	Sequence 107, Appl	819	30	7.1	75	1	US-08-642-255-130	Sequence 130, Appl
747	30	7.1	60	2	US-08-248-838C-155	Sequence 155, Appl	820	30	7.1	75	1	US-08-397-633A-47	Sequence 47, Appl
748	30	7.1	60	4	US-08-928-213B-181	Sequence 181, Appl	821	30	7.1	75	2	US-08-961-564A-7	Sequence 7, Appl
749	30	7.1	61	1	US-08-194-211A-3	Sequence 3, Appl	822	30	7.1	76	2	US-08-248-839C-67	Sequence 67, Appl
750	30	7.1	61	1	US-08-399-636-117	Sequence 117, Appl	823	30	7.1	76	4	US-09-448-806C-9	Sequence 9, Appl
751	30	7.1	61	2	US-08-463-380-61	Sequence 61, Appl	824	30	7.1	77	1	US-07-991-867B-44	Sequence 44, Appl
752	30	7.1	61	2	US-08-486-397-61	Sequence 61, Appl	825	30	7.1	77	2	US-07-991-867B-46	Sequence 46, Appl
753	30	7.1	61	2	US-08-486-399-61	Sequence 61, Appl	826	30	7.1	77	2	US-08-544-332-44	Sequence 44, Appl
754	30	7.1	61	2	US-08-461-965-61	Sequence 61, Appl	827	30	7.1	77	2	US-08-544-332-46	Sequence 46, Appl
755	30	7.1	61	2	US-08-634-641-61	Sequence 61, Appl	828	30	7.1	77	4	US-09-025-131-20	Sequence 20, Appl
756	30	7.1	61	2	US-08-490-676A-15	Sequence 15, Appl	829	30	7.1	77	4	US-09-370-861A-44	Sequence 44, Appl
757	30	7.1	61	3	US-09-249-471-61	Sequence 61, Appl	830	30	7.1	77	4	US-09-370-861A-46	Sequence 46, Appl



831	30	7.1	78	1	US-08-468-674B-73	Sequence 73, Appl	904	29.5	7.0	56	2	US-08-306-078-4	Sequence 4, Appl
832	30	7.1	78	1	US-08-780-571-73	Sequence 73, Appl	905	29.5	7.0	57	3	US-08-955-937A-5	Sequence 5, Appl
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836	30	7.1	79	4	US-09-336-447A-98	Sequence 98, Appl	909	29.5	7.0	60	4	US-09-076-804-4	Sequence 4, Appl
837	30	7.1	79	4	US-09-134-001C-3226	Sequence 3226, Ap	910	29.5	7.0	63	4	US-09-134-001C-4792	Sequence 2, Appl
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839	30	7.1	80	1	US-08-377-687-59	Sequence 59, Appl	912	29.5	7.0	65	6	5320958-16	Sequence 210, App
840	30	7.1	80	4	US-08-777-192-59	Sequence 59, Appl	913	29.5	7.0	67	3	US-08-475-668A-210	Sequence 162, App
841	30	7.1	80	4	US-08-971-982-59	Sequence 59, Appl	914	29.5	7.0	67	3	US-09-065-474-162	Sequence 210, App
842	30	7.1	80	4	US-09-461-657-464	Sequence 464, App	915	29.5	7.0	67	3	US-08-485-551A-210	Sequence 210, App
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848	30	7.1	83	4	US-08-974-549A-191	Sequence 191, App	921	29.5	7.0	69	1	US-08-358-160-157	Sequence 157, App
849	30	7.1	83	4	US-08-854-050-9	Sequence 9, Appl	922	29.5	7.0	70	2	US-08-117-952-780	Sequence 780, App
850	30	7.1	83	4	US-09-430-323-9	Sequence 9, Appl	923	29.5	7.0	70	2	US-08-117-952-781	Sequence 781, App
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852	30	7.1	84	2	US-08-353-476-80	Sequence 80, Appl	925	29.5	7.0	72	1	US-08-182-175A-87	Sequence 87, Appl
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857	30	7.1	85	3	US-08-851-843A-11	Sequence 11, Appl	930	29.5	7.0	80	1	US-08-464-164-4	Sequence 4, Appl
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875	29.5	7.0	40	3	US-09-035-619-25	Sequence 25, Appl	948	29.5	7.0	87	2	US-08-486-399-44	Sequence 44, Appl
876	29.5	7.0	40	4	US-09-514-006-22	Sequence 22, Appl	949	29.5	7.0	87	2	US-08-461-965-44	Sequence 44, Appl
877	29.5	7.0	40	4	US-09-514-006-25	Sequence 25, Appl	950	29.5	7.0	87	2	US-08-634-641-44	Sequence 44, Appl
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# ALIGNMENTS

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RESULT 1
US-09-100-804-30
; Sequence 30, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONZALEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: L0461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441

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; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; Query Match 11.8%; Score 50; DB 3; Length 68;
; Best Local Similarity 31.4%; Pred. No. 17;
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;
; RESULT 2
; US-09-331-930A-22
; Sequence 22, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; APPLICANT: COLLIER, GREGORY
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007 00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCI/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
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;
; Query Match 10.8%; Score 45.5; DB 4; Length 73;
; Best Local Similarity 29.4%; Pred. No. 77;
; Matches 10; Conservative 7; Mismatches 12; Indels 5; Gaps 1;
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; QY 26 DFSGQSKSVIENTEALS-----VAVEEGLAWRK 54
; DB 8 DLGKVKIKCNFSDTIGDLKKLIAAQTGTREK 41
;
; RESULT 3
; US-09-083-521-5
; Sequence 5, Application US/09083521
; Patent No. 6048970
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/083,521  
FILING DATE: Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERRONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0527 US  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 76 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1216498  
US-09-083-521-5

Query Match 10.6%; Score 45; DB 3; Length 76;  
Best Local Similarity 24.4%; Pred. No. 95;  
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RESULT 4  
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Sequence 615, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
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EARLIER FILING DATE: 1997-03-07  
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: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/043,674  
: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/043,669  
: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/043,312  
: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/043,313  
: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/043,672  
: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/043,315  
: EARLIER FILING DATE: 1997-04-11  
: EARLIER APPLICATION NUMBER: 60/048,974  
: EARLIER FILING DATE: 1997-06-06  
: EARLIER APPLICATION NUMBER: 60/056,886  
: EARLIER FILING DATE: 1997-08-22  
: EARLIER APPLICATION NUMBER: 60/056,877  
: EARLIER FILING DATE: 1997-08-22  
: EARLIER APPLICATION NUMBER: 60/056,889  
: EARLIER FILING DATE: 1997-08-22  
: EARLIER APPLICATION NUMBER: 60/056,893  
: EARLIER FILING DATE: 1997-08-22  
: EARLIER APPLICATION NUMBER: 60/056,630  
: EARLIER FILING DATE: 1997-08-22  
: EARLIER APPLICATION NUMBER: 60/056,878

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 10.5% Score 44.5; DB 4; Length 61;
Best Local Similarity 37.9%; Pred. No. 80;
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 51 AWRKKGCLRLGTHGSSPTASSOSSATNMAI 79
Db 33 AWRPSG-----GTGTSSSSQSSQTQSEFL 54

RESULT 5
US-08-776-059-18
; Sequence 18, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jurgen
; APPLICANT: BAUR, Axel
; APPLICANT: ZINKE, Holger
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776,059B
; CURRENT FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: PCT/EP96/02273
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 95109949.8
; EARLIER FILING DATE: 1995-06-26
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Saponaria officinalis
US-08-776-059-18

Query Match 10.4% Score 44; DB 4; Length 47;
Best Local Similarity 34.8%; Pred. No. 64;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 25 MDFSQKSRVIENTEALSAVAVE 47
Db 6 MDAVNKKARVKNKNEARFLIIAIQ 28

RESULT 6
US-09-227-357-611
; Sequence 611, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins

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[illegible]

```

RESULT 8
US-09-574-141A-20
; Sequence 20, Application US/09574141A
; Patent No. 6395490
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Meng, Baozhong
; TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
; FILE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
; FILE REFERENCE: 07678/035005
; CURRENT APPLICATION NUMBER: US/09/574,141A
; CURRENT FILING DATE: 2000-05-18
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: 60/047,147
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: 60/069,902
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 09/081,320
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 80
; ORGANISM: Rupestris stem pitting associated virus
US-09-574-141A-20

Query Match          10.4%; Score 44; DB 4; Length 80;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 31 KSRVLEN--PTEALSVAVEGLAWRK 54
Db 40 ESIIVNGCPSEALATVKEVLGGLK 65

RESULT 9
US-09-707-780-20
; Sequence 20, Application US/09707780
; Patent No. 6399308
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Meng, Baozhong
; TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
; FILE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
; FILE REFERENCE: 07678/035006
; CURRENT APPLICATION NUMBER: US/09/707,780
; CURRENT FILING DATE: 2000-11-07
; PRIOR FILING DATE: 1998-05-19
; PRIOR APPLICATION NUMBER: 60/047,147
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: 60/069,902
; PRIOR FILING DATE: 1997-12-17
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; TYPE: PRT
; LENGTH: 80
; ORGANISM: Rupestris stem pitting associated virus
US-09-707-780-20

Query Match          10.4%; Score 44; DB 4; Length 80;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 31 KSRVLEN--PTEALSVAVEGLAWRK 54
Db 40 ESIIVNGCPSEALATVKEVLGGLK 65

RESULT 10
US-08-630-915A-111
; Sequence 11, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOMLKS, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; FILE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; FILE REFERENCE: USING SAME
; CURRENT APPLICATION NUMBER: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-111

Query Match          10.3%; Score 43.5; DB 4; Length 55;
Best Local Similarity 41.4%; Pred. No. 94;
Matches 12; Conservative 8; Mismatches 4; Indels 5; Gaps 2;

QY 16 SISNSLVAMDFS-GQKSRVNIPTALS 43
Db 23 TVNKGSLVALGFGDQGEAR----PEELN 47

RESULT 11
US-09-267-177-12
; Sequence 12, Application US/09267177
; Patent No. 6287856
; GENERAL INFORMATION:
; APPLICANT: Poet, Steven E.
; APPLICANT: Ritchie, Branson W.
; APPLICANT: Niagro, Frank D.
; APPLICANT: Lukert, Phil D.
; TITLE OF INVENTION: Vaccines against Circovirus Infections
; FILE REFERENCE: 21099,0057
; CURRENT APPLICATION NUMBER: US/09/267,177
; CURRENT FILING DATE: 1999-03-12
; EARLIER FILING DATE: 60/077,890
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 74

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REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 208:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-915A-208

Query Match 10.0%; Score 42.5; DB 4; Length 61;  
Best Local Similarity 33.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY 9 QSIQSPMRISSENSLVAMDFSGKSRVIENP 38  
DB 6 QTLXPFSVTEELNEFE-KGETMEVIEKP 34

## RESULT 15

US-07-641-971B-5  
Sequence 5, Application US/07641971B  
Patent No. 5236706  
GENERAL INFORMATION:  
APPLICANT: Debre, Patrice  
APPLICANT: Mossalayi, Mohammed D  
TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE  
TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation  
STREET: 556 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/641-971B  
FILING DATE: 19910116  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 90016254  
FILING DATE: 24-JAN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fishman, Irving M  
REGISTRATION NUMBER: 30258  
REFERENCE/DOCKET NUMBER: 4-17921/+/DEB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-277-4832  
TELEFAX: 908-277-4306  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-07-641-971B-5

Query Match 9.9%; Score 42; DB 1; Length 40;  
Best Local Similarity 37.9%; Pred. No. 94;

Matches 11; Conservative 6; Mismatches 8; Indels 4; Gaps 1;  
QY 12 SPMSRISSENSLVAMDFSGKSRVIENPTE 40  
DB 1 APVRSLN----CTLRDSGOKSLVMSGPYE 25

## RESULT 16

US-07-781-248A-5  
Sequence 5, Application US/07781248A  
Patent No. 5246699  
GENERAL INFORMATION:  
APPLICANT: Debre, Patrice  
APPLICANT: Mossalayi, Mohammed D  
TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation  
STREET: 556 Morris Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/781,248A  
FILING DATE: 19911230  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 90103565  
FILING DATE: 09-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Ikeler, Barbara J.  
REGISTRATION NUMBER: 36,170  
REFERENCE/DOCKET NUMBER: 4-18065/A/DEB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-277-3368  
TELEFAX: 908-277-4306  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-07-781-248A-5

Query Match 9.9%; Score 42; DB 1; Length 40;  
Best Local Similarity 37.9%; Pred. No. 94;  
Matches 11; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 12 SPMSRISSENSLVAMDFSGKSRVIENPTE 40  
DB 1 APVRSLN----CTLRDSGOKSLVMSGPYE 25

## RESULT 17

US-08-776-059-16  
Sequence 16, Application US/08776059B  
Patent No. 6271368  
GENERAL INFORMATION:  
APPLICANT: LENTZEN, Hans  
APPLICANT: ECK, Jurgen  
APPLICANT: BAUR, Axel  
APPLICANT: ZINKE, Holger  
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)



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: FILE REFERENCE: 674503-2003
: CURRENT APPLICATION NUMBER: US/08/776,059B
: CURRENT FILING DATE: 1999-06-19
: EARLIER APPLICATION NUMBER: PCT/EP96/02273
: EARLIER FILING DATE: 1996-06-25
: EARLIER APPLICATION NUMBER: 95109949.8
: EARLIER FILING DATE: 1995-06-26
: NUMBER OF SEQ ID NOS: 56
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 47
: TYPE: PRT
: ORGANISM: Saponaria officinalis
US-08-776-059-16

Query Match          9.9%; Score 42; DB 4; Length 47;
Best Local Similarity 30.8%; Pred. No. 1.2e+02;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 22 LVAMDFGQKSRVIENTEALSVAVE 47
      | | : : | | | : | | : :
Db 3 LTFMEAVNKRAVKVKNREARFLIAIQ 28

RESULT 18
US-09-134-001C-2848
: Sequence 2848, Application US/09134001C
: Patent No. 6380370
: GENERAL INFORMATION:
: APPLICANT: LYNN CONCETTE-STAMM et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
: FILE REFERENCE: GTC-001
: CURRENT APPLICATION NUMBER: US/09/134,001C
: CURRENT FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/055,779
: PRIOR FILING DATE: 1997-08-14
: NUMBER OF SEQ ID NOS: 5674
: SEQ ID NO 2848
: LENGTH: 78
: TYPE: PRT
: ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2848

Query Match          9.9%; Score 42; DB 4; Length 78;
Best Local Similarity 27.3%; Pred. No. 2.5e+02;
Matches 18; Conservative 9; Mismatches 21; Indels 18; Gaps 3;

QY 31 KSRVIENP-----TEALSVAVEEGLAWKCKGLRGTHGSPPTASSQSSA-----TNNA 78
      | | : | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 KQVWKPKPGVGDKEPKYISVAISERTVGTGK-----STSGSDQPAQSSSSPSSSHSSQ 58
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 79 IHRSQP 84
      | : | |
Db 59 AHQPQP 64

RESULT 19
US-09-134-001C-2848
: Patent No. 5171684
: APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.
: TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
: MONOOXYGENASE OF PSEUDOMONAS MENDOCINA KR-1
: NUMBER OF SEQUENCES: 41
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/590,374
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 177,631
: FILING DATE: 05-APR-1988
: SEQ ID NO:3

```

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;
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-023-082A-76
;
; Query Match 9.8%; Score 41.5; DB 3; Length 87;
; Best Local Similarity 19.3%; Pred. No. 3.4e+02;
; Matches 16; Conservative 15; Mismatches 31; Indels 21; Gaps 3;
;
; QY 14 MRSISENSLVAMDFSGQ-----KSRVIENPTSEALSVAVEEGLAWRKKG---C 57
; DB 2 VKAINSNYILAMNKKGLYKSEFNNDCCKLERIEENGNTYA-----SFNWHNGROMY 56
;
; QY 58 LRLGTHGSPASSOSSATNMAIH 80
; DB 57 VALNGKGAAPRRGQKTRKNTSAH 79
;
;
; RESULT 21
; US-08-927-219-49
; Sequence 49, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Naohisha
; APPLICANT: Kaisaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; TITLE OF INVENTION: AND HNF-4ALPHA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927.219
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,679
; FILING DATE: 30-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,056
; FILING DATE: 02-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,719
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD.272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-927-219-49
;
; Query Match 9.7%; Score 41; DB 4; Length 51;
; Best Local Similarity 28.2%; Pred. No. 1.8e+02;
; Matches 11; Conservative 3; Mismatches 11; Indels 14; Gaps 1;
;
; QY 51 AMRKKG-----LRLGTHGSPASSOSSAT 75
; DB 12 SNRRAGCPYASLTWCPCPSRCSRMTMTSKPSSSLT 50
;
;
; RESULT 22
; US-09-246-500B-9
; Sequence 9, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Huo, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; TITLE OF INVENTION: Using the Substrates
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mouse C4a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
; US-09-246-500B-9
;
; Query Match 9.7%; Score 41; DB 4; Length 76;
; Best Local Similarity 38.5%; Pred. No. 3.3e+02;
; Matches 10; Conservative 4; Mismatches 10; Indels 2; Gaps 1;
;
; QY 59 RLGTHGSPAS--SOSATNMAIHS 82
; DB 11 KLGQYASPTAKRCQDQVTRLPKRS 36
;
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; RESULT 23
; US-08-459-568-52
; Sequence 52, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-52

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Query Match          9.6%; Score 40.5; DB 2; Length 66;
Best Local Similarity 47.4%; Pred. No. 3.1e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

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QY 16 SISSENSLVAMDFS-GOKSR 33
Db 22 TVNKGSLVALGFSGDGEAR 40

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RESULT 24
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; Sequence 52, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-399-411-52

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Query Match          9.6%; Score 40.5; DB 2; Length 66;
Best Local Similarity 47.4%; Pred. No. 3.1e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

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QY 16 SISSENSLVAMDFS-GOKSR 33
Db 22 TVNKGSLVALGFSGDGEAR 40

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RESULT 25
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; Sequence 52, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-516-859A-52

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Query Match          9.6%; Score 40.5; DB 3; Length 66;
Best Local Similarity 47.4%; Pred. No. 3.1e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

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QY 16 SISSENSLVAMDFS-GOKSR 33
Db 22 TVNKGSLVALGFSGDGEAR 40

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Search completed: March 28, 2003, 09:09:39
Job time : 32.4724 secs

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 08:55:25 ; Search time 66.1417 Seconds  
(without alignments)  
169.228 Million cell updates/sec

Perfect score: 423.66 (US-09-936-697-6)

Sequence: 1 QCRSCSSQISPMRSISEN.....SPTASSQSSATNMAIHRSP 84

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 160864

Minimum DB seq length: 40  
Maximum DB seq length: 90

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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3	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT	2	100	0	84	Peptide derived fr
4	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT	2	100	0	84	Peptide derived fr
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15	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT	2	100	0	84	Peptide derived fr
16	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT	2	100	0	84	Peptide derived fr
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19	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT	2	100	0	84	Peptide derived fr
20	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT	2	100	0	84	Peptide derived fr
21	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT	2	100	0	84	Peptide derived fr
22	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT	2	100	0	84	Peptide derived fr
23	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT	2	100	0	84	Peptide derived fr

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
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2	3	212	50.1	43	21	Peptide derived fr
3	4	205	48.5	43	21	Peptide derived fr
4	5	191	45.2	80	21	Peptide derived fr
5	6	191	45.2	80	21	Peptide derived fr
6	7	189	44.7	82	21	Peptide derived fr
7	8	186	44.0	82	21	Peptide derived fr
8	9	179	42.3	80	21	Peptide derived fr
9	10	169	40.0	43	21	Peptide derived fr

11	162	38.3	43	21	Peptide derived fr
12	161	38.1	43	21	Peptide derived fr
13	159	37.6	43	21	Peptide derived fr
14	159	37.6	43	21	Peptide derived fr
15	65.5	15.5	47	22	Human polypeptide
16	61	14.4	77	22	Human polypeptide
17	59.5	14.1	76	22	Human polypeptide
18	58.5	13.8	51	22	Novel human diagno
19	58.5	13.8	78	22	Human polypeptide
20	56.5	13.4	48	22	Human polypeptide
21	56	13.2	72	22	Novel human secret
22	56	13.2	79	22	Human albumin fusi
23	56	13.2	79	22	Human secreted pro
24	55.5	13.1	49	22	Human polypeptide
25	55	13.0	73	22	Human polypeptide
26	54.5	12.9	53	22	Human PRO0663 homo
27	54.5	12.9	57	22	Human polypeptide
28	54.5	12.9	60	21	Human colon cancer
29	54.5	12.9	72	21	Human polypeptide
30	54	12.8	51	22	Human polypeptide
31	54	12.8	86	22	Human polypeptide
32	53	12.5	49	22	Human polypeptide
33	53	12.5	70	22	Propionibacterium
34	53	12.5	75	22	Human polypeptide
35	52.5	12.4	52	22	Human polypeptide
36	52.5	12.4	67	22	Human polypeptide
37	52.5	12.4	75	22	Human polypeptide
38	52	12.3	49	22	Human polypeptide
39	52	12.3	53	22	Human novel endocr
40	52	12.3	70	21	Human secreted pro
41	52	12.3	78	22	Human nervous syst
42	52	12.2	90	22	Novel human secret
43	51.5	12.2	61	22	Human polypeptide
44	51.5	12.2	64	22	Human polypeptide
45	51.5	12.2	68	22	Human immune/haema
46	51.5	12.2	72	21	Human secreted pro
47	51.5	12.2	74	22	Human polypeptide
48	51.5	12.2	83	22	Human reproductive
49	51.5	12.2	83	22	Human ovarian anti
50	51.5	12.2	83	23	Novel ovarian rela
51	51.5	12.2	83	23	Human ORF1560
52	51.5	12.2	88	22	Human polypeptide
53	51	12.1	67	22	Novel human secret
54	51	12.1	72	22	Human reproductive
55	51	12.1	72	22	Human polypeptide
56	51	12.1	83	22	Human polypeptide
57	51	12.1	84	23	Human peptide enco
58	51	12.1	87	22	Human polypeptide
59	51	12.1	88	22	Human secreted pro
60	50.5	11.9	55	21	Human polypeptide
61	50.5	11.9	69	22	Human polypeptide
62	50.5	11.9	71	22	Propionibacterium
63	50.5	11.9	76	22	Propionibacterium
64	50.5	11.9	81	22	Human polypeptide
65	50.5	11.9	83	23	Human ovarian anti
66	50.5	11.9	83	23	Human ORF25 protei
67	50	11.8	48	22	Human polypeptide
68	50	11.8	53	22	Human immune/haema
69	50	11.8	60	22	Novel human secret
70	50	11.8	74	22	Human polypeptide
71	50	11.8	77	22	Human immune/haema
72	50	11.8	78	22	Propionibacterium
73	49.5	11.7	45	21	Human secreted pro
74	49.5	11.7	48	22	Human polypeptide
75	49.5	11.7	49	22	Human nervous syst
76	49.5	11.7	50	22	Human polypeptide
77	49.5	11.7	56	22	Propionibacterium
78	49.5	11.7	57	22	Human polypeptide
79	49.5	11.7	74	22	Human secreted pro
80	49.5	11.7	80	23	Human albumin fusi
81	49.5	11.7	80	23	ABG64654
82	49.5	11.7	80	23	Peptide derived fr
83	49.5	11.7	80	23	Peptide derived fr

84	49.5	11.7	87	22	AAM23681	Human EST encoded	157	47	11.1	89	22	AAM23622	Human digestive sy
85	49.5	11.7	90	22	AAU62249	Propionibacterium	158	46.5	11.0	43	21	AAU27856	Protein fragment e
86	49	11.6	50	22	AAU62249	Human polypeptide	159	46.5	11.0	54	22	AAU27856	Human polypeptide
87	49	11.6	54	22	AAU62249	Human polypeptide	160	46.5	11.0	57	23	AAU27856	Human ORFX protein
88	49	11.6	67	23	AAU62249	Human ORFX protein	161	46.5	11.0	60	21	AAU27856	Arabidopsis thalia
89	49	11.6	68	21	AAU62249	Human secreted pro	162	46.5	11.0	60	22	AAU27856	Propionibacterium
90	49	11.6	69	23	AAU62249	Human ORFX protein	163	46.5	11.0	61	22	AAU27856	Human polypeptide
91	49	11.6	71	21	AAU62249	Propionibacterium	164	46.5	11.0	64	22	AAU27856	Human polypeptide
92	49	11.6	72	20	AAU62249	Human prostate tum	165	46.5	11.0	65	21	AAU27856	Arabidopsis thalia
93	49	11.6	73	22	AAU62249	Human polypeptide	166	46.5	11.0	68	22	AAU27856	Propionibacterium
94	49	11.6	78	22	AAU62249	Human polypeptide	167	46.5	11.0	73	22	AAU27856	Propionibacterium
95	49	11.6	84	22	AAU62249	Propionibacterium	168	46.5	11.0	73	22	AAU27856	Human polypeptide
96	49	11.6	84	22	AAU62249	Propionibacterium	169	46.5	11.0	74	22	AAU27856	Novel human secret
97	49	11.6	85	22	AAU62249	Novel human diagno	170	46.5	11.0	78	22	AAU27856	Propionibacterium
98	48.5	11.5	41	22	AAU62249	Human polypeptide	171	46.5	11.0	78	22	AAU27856	Human digestive sy
99	48.5	11.5	42	22	AAU62249	Human polypeptide	172	46.5	11.0	78	22	AAU27856	Human liver associ
100	48.5	11.5	60	22	AAU62249	Human reproductive	173	46.5	11.0	83	22	AAU27856	Human liver antige
101	48.5	11.5	60	22	AAU62249	Propionibacterium	174	46.5	11.0	83	22	AAU27856	Human immune/haema
102	48.5	11.5	60	22	AAU62249	Human immune/haema	175	46.5	11.0	85	22	AAU27856	Propionibacterium
103	48.5	11.5	63	22	AAU62249	Propionibacterium	176	46.5	11.0	86	23	AAU27856	Human ORFX protein
104	48.5	11.5	65	22	AAU62249	Drosophila melanog	177	46.5	11.0	87	22	AAU27856	Human foetal prote
105	48.5	11.5	65	22	AAU62249	Human polypeptide	178	46.5	11.0	90	22	AAU27856	Propionibacterium
106	48.5	11.5	73	22	AAU62249	Human colon cancer	179	46.5	11.0	90	22	AAU27856	Human polypeptide
107	48.5	11.5	75	22	AAU62249	Human polypeptide	180	46	10.9	52	23	AAU27856	Human ORFX121 prot
108	48.5	11.5	76	20	AAU62249	Human RFX-1 protei	181	46	10.9	55	22	AAU27856	Human polypeptide
109	48.5	11.5	76	23	AAU62249	Human ORFX1252 prot	182	46	10.9	55	22	AAU27856	Propionibacterium
110	48.5	11.5	82	22	AAU62249	Peptide #11838 enc	183	46	10.9	57	22	AAU27856	Human polypeptide
111	48.5	11.5	82	22	AAU62249	Protein #9191 enco	184	46	10.9	59	22	AAU27856	Propionibacterium
112	48.5	11.5	82	22	AAU62249	Human brain expres	185	46	10.9	59	22	AAU27856	Propionibacterium
113	48.5	11.5	82	22	AAU62249	Human bone marrow	186	46	10.9	61	21	AAU27856	Propionibacterium
114	48.5	11.5	82	22	AAU62249	Peptide #8990 enco	187	46	10.9	61	22	AAU27856	Human secreted pro
115	48.5	11.5	82	22	AAU62249	Peptide #12331 enc	188	46	10.9	65	22	AAU27856	Human immune/haema
116	48.5	11.5	82	22	AAU62249	Human peptide enco	189	46	10.9	65	22	AAU27856	Propionibacterium
117	48.5	11.5	84	23	AAU62249	Human uterogloblin	190	46	10.9	68	22	AAU27856	Human polypeptide
118	48	11.3	50	22	AAU62249	Novel bone marrow	191	46	10.9	68	22	AAU27856	Human lung antigen
119	48	11.3	54	22	AAU62249	Human polypeptide	192	46	10.9	68	22	AAU27856	Novel human respir
120	48	11.3	54	22	AAU62249	Human polypeptide	193	46	10.9	69	22	AAU27856	Novel human connec
121	48	11.3	64	22	AAU62249	Propionibacterium	194	46	10.9	70	22	AAU27856	Propionibacterium
122	48	11.3	64	22	AAU62249	Human polypeptide	195	46	10.9	76	20	AAU27856	S. pombe SAK1 prot
123	48	11.3	67	21	AAU62249	Human polypeptide	196	46	10.9	85	22	AAU27856	Human polypeptide
124	48	11.3	75	22	AAU62249	A. thaliana ygd p	197	46	10.9	85	22	AAU27856	Propionibacterium
125	48	11.3	76	20	AAU62249	Human immune/haema	198	46	10.9	86	22	AAU27856	Propionibacterium
126	48	11.3	76	20	AAU62249	Human endometrium	199	45.5	10.8	87	23	AAU27856	Human Mch2 protei
127	48	11.3	77	22	AAU62249	Propionibacterium	200	45.5	10.8	40	22	AAU27856	Human secreted pro
128	48	11.3	78	22	AAU62249	Propionibacterium	201	45.5	10.8	44	21	AAU27856	Human secreted pro
129	48	11.3	79	22	AAU62249	Human polypeptide	202	45.5	10.8	44	21	AAU27856	Gene 24 human secr
130	48	11.3	79	22	AAU62249	Human ORFX protein	203	45.5	10.8	45	21	AAU27856	Gene 14 human secr
131	47.5	11.2	44	22	AAU62249	Human polypeptide	204	45.5	10.8	45	22	AAU27856	Human polypeptide
132	47.5	11.2	53	21	AAU62249	Human secreted pro	205	45.5	10.8	46	21	AAU27856	Gene 35 human secr
133	47.5	11.2	59	22	AAU62249	Human polypeptide	206	45.5	10.8	49	22	AAU27856	Human polypeptide
134	47.5	11.2	60	21	AAU62249	Human secreted pro	207	45.5	10.8	50	21	AAU27856	Gene 31 human secr
135	47.5	11.2	67	22	AAU62249	Human polypeptide	208	45.5	10.8	51	21	AAU27856	Gene 6 human secr
136	47.5	11.2	69	22	AAU62249	Human polypeptide	209	45.5	10.8	56	22	AAU27856	Human colon cancer
137	47.5	11.2	77	22	AAU62249	Propionibacterium	210	45.5	10.8	56	22	AAU27856	Propionibacterium
138	47.5	11.2	86	22	AAU62249	Novel human secret	211	45.5	10.8	58	21	AAU27856	Human colon cancer
139	47.5	11.2	86	22	AAU62249	Novel human secret	212	45.5	10.8	58	21	AAU27856	Human colon cancer
140	47.5	11.2	89	22	AAU62249	Propionibacterium	213	45.5	10.8	58	21	AAU27856	Human colon cancer
141	47	11.1	50	22	AAU62249	Human polypeptide	214	45.5	10.8	58	21	AAU27856	Human cancer assoc
142	47	11.1	56	22	AAU62249	Human polypeptide	215	45.5	10.8	58	22	AAU27856	Human polypeptide
143	47	11.1	61	21	AAU62249	Human secreted pro	216	45.5	10.8	58	22	AAU27856	Gene 18 human secr
144	47	11.1	62	23	AAU62249	Human ORFX protein	217	45.5	10.8	58	22	AAU27856	Human secreted pro
145	47	11.1	63	23	AAU62249	Human polypeptide	218	45.5	10.8	60	22	AAU27856	Human musculoskele
146	47	11.1	64	22	AAU62249	Propionibacterium	219	45.5	10.8	60	22	AAU27856	Human secreted pro
147	47	11.1	64	22	AAU62249	Human novel endocr	220	45.5	10.8	66	21	AAU27856	Human secreted pro
148	47	11.1	64	22	AAU62249	Propionibacterium	221	45.5	10.8	69	21	AAU27856	Peptide #1. Homo
149	47	11.1	65	22	AAU62249	Human polypeptide	222	45.5	10.8	71	21	AAU27856	Human secreted pro
150	47	11.1	65	22	AAU62249	Human nervous syst	223	45.5	10.8	72	22	AAU27856	Peptide #5924 enco
151	47	11.1	68	22	AAU62249	Human polypeptide	224	45.5	10.8	72	22	AAU27856	Protein #5592 enco
152	47	11.1	74	22	AAU62249	Human polypeptide	225	45.5	10.8	72	22	AAU27856	Human brain expres
153	47	11.1	77	22	AAU62249	Propionibacterium	226	45.5	10.8	72	22	AAU27856	Human bone marrow
154	47	11.1	86	22	AAU62249	Propionibacterium	227	45.5	10.8	72	22	AAU27856	Peptide #5642 enco
155	47	11.1	89	22	AAU62249	Novel human colon	228	45.5	10.8	72	22	AAU27856	Peptide #5693 enco
156	47	11.1	89	22	AAU62249	Novel human secret	229	45.5	10.8	72	22	AAU27856	

230	45.5	10.8	72	22	AAG30310	C glutamicum prote	303	44	10.4	53	21	AAG02567	Human secreted pro
231	45.5	10.8	72	23	ABG41369	Human peptide enco	304	44	10.4	53	22	AAU57846	Protonibacterium
232	45.5	10.8	73	21	AA339164	Human secreted pro	305	44	10.4	54	22	AAO10611	Human polypeptide
233	45.5	10.8	75	22	AAU42093	Protonibacterium	306	44	10.4	59	22	AAO11595	Human polypeptide
234	45.5	10.8	76	22	ABBI17542	Human nervous syst	307	44	10.4	59	22	AAO11595	Human polypeptide
235	45.5	10.8	76	22	AAO08577	Human polypeptide	308	44	10.4	61	22	AAO11595	Human polypeptide
236	45.5	10.8	79	22	AAO08077	Human polypeptide	309	44	10.4	62	22	ABG05559	Human ESR encoded
237	45.5	10.8	80	22	ABG45455	Gene 49 human secr	310	44	10.4	63	20	AAI02955	Novel human diagno
238	45.5	10.8	81	22	ABG10030	Novel human diagno	311	44	10.4	64	22	AAU58893	Fragment of human
239	45.5	10.8	86	22	AAU32278	Novel human secr	312	44	10.4	64	22	ABP03147	Protonibacterium
240	45.5	10.8	87	22	AAU44670	Gene 31 human secr	313	44	10.4	64	22	AAO06933	Human ORFX protein
241	45.5	10.8	88	22	AAU58387	Novel human secr	314	44	10.4	65	22	AAO06933	Human polypeptide
242	45.5	10.8	88	22	AAU48821	Protonibacterium	315	44	10.4	66	22	AAO07539	Human polypeptide
243	45.5	10.8	90	22	AAU04881	Protonibacterium	316	44	10.4	67	21	AAI52247	Synechocystis sp.
244	45.5	10.6	52	22	AAO07771	Human polypeptide	317	44	10.4	68	21	AAI52247	Human prostate can
245	45.5	10.6	52	22	AAO06973	Human polypeptide	318	44	10.4	69	22	AAU63389	Protonibacterium
246	45.5	10.6	53	22	AAU34536	Human polypeptide	319	44	10.4	74	22	AAU63389	Novel human secr
247	45.5	10.6	55	21	AAU32815	Human polypeptide	320	44	10.4	74	22	AAU63389	Human immune/haema
248	45.5	10.6	55	21	AAU32815	Human polypeptide	321	44	10.4	77	22	AAU63389	Human colon cancer
249	45.5	10.6	55	21	AAU32815	Human polypeptide	322	44	10.4	78	22	AAU63389	Protonibacterium
250	45.5	10.6	59	23	AAU75092	Eucalyptus grandis	323	44	10.4	79	23	ABP30966	N-terminal portion
251	45.5	10.6	65	22	ABG15996	Novel human diagno	324	44	10.4	81	21	AAU77532	RSPV strain RSPA7
252	45.5	10.6	66	22	AAU45043	Novel human diagno	325	44	10.4	81	21	AAU77532	Sequences homologou
253	45.5	10.6	66	22	AAU12969	Protonibacterium	326	44	10.4	82	22	ABG08745	Drosophila melanog
254	45.5	10.6	73	22	AAU03344	Human polypeptide	327	44	10.4	84	22	ABG08745	Novel human diagno
255	45.5	10.6	73	22	AAU14572	Human polypeptide	328	44	10.4	85	22	ABG08745	Protonibacterium
256	45.5	10.6	73	22	AAU14508	Human novel protei	329	44	10.4	85	22	ABG08745	Protonibacterium
257	45.5	10.6	74	21	AAU32752	Eucalyptus grandis	330	44	10.4	86	21	AAU31059	Arabidopsis thalia
258	45.5	10.6	76	22	AAU47589	Rat CD24 peptide	331	44	10.4	86	22	AAU31059	Arabidopsis thalia
259	45.5	10.6	76	22	AAU90941	Human polypeptide	332	44	10.4	87	21	AAU31059	Arabidopsis thalia
260	45.5	10.6	77	22	AAU12367	Human polypeptide	333	44	10.4	89	22	ABG06199	Novel human diagno
261	45.5	10.6	77	22	AAU12367	Human polypeptide	334	44	10.4	90	22	AAU12367	Human polypeptide
262	45.5	10.6	77	22	AAU12367	Human polypeptide	335	44	10.4	90	22	AAU12367	Human polypeptide
263	45.5	10.6	90	17	AAU98972	Chronic hepatitis	336	43.5	10.3	45	22	AAO04574	Human protein sequ
264	44.5	10.5	43	22	AAU00375	Human polypeptide	337	43.5	10.3	50	22	AAO04574	Protonibacterium
265	44.5	10.5	43	22	AAU00375	Human polypeptide	338	43.5	10.3	51	22	AAO04574	Protonibacterium
266	44.5	10.5	51	22	ABG00853	Human ORFX protein	339	43.5	10.3	52	22	AAO04574	Human brain expres
267	44.5	10.5	51	22	ABG00853	Human ORFX protein	340	43.5	10.3	52	22	AAO04574	Human bone marrow
268	44.5	10.5	55	21	AAU34833	Human colon cancer	341	43.5	10.3	52	22	AAO07759	Human polypeptide
269	44.5	10.5	55	21	AAU34833	Human colon cancer	342	43.5	10.3	52	22	AAO07759	Human polypeptide
270	44.5	10.5	56	22	AAU53255	Protonibacterium	343	43.5	10.3	52	23	ABG44045	Peptide #816 enco
271	44.5	10.5	57	22	AAU53104	Protonibacterium	344	43.5	10.3	53	23	ABG44045	Human peptide enco
272	44.5	10.5	57	22	AAU08310	Human polypeptide	345	43.5	10.3	53	23	ABG44045	Human colon cancer
273	44.5	10.5	58	22	AAU08310	Human polypeptide	346	43.5	10.3	54	22	AAO05120	Human ORFX protein
274	44.5	10.5	58	22	AAU08310	Human polypeptide	347	43.5	10.3	54	22	AAO05120	Human polypeptide
275	44.5	10.5	58	22	AAU08310	Human ORFX protein	348	43.5	10.3	56	21	AAO10701	Human secreted pro
276	44.5	10.5	61	19	ABG06948	Novel human diagno	349	43.5	10.3	57	22	AAU51931	Protonibacterium
277	44.5	10.5	61	22	ABG17439	Human secreted pro	350	43.5	10.3	58	22	AAU51931	Protonibacterium
278	44.5	10.5	63	22	AAU61408	Human nervous syst	351	43.5	10.3	59	21	AAU51931	Human colon cancer
279	44.5	10.5	65	21	AAU53876	Protonibacterium	352	43.5	10.3	61	22	AAU51931	Human secreted pro
280	44.5	10.5	66	22	AAU53876	Human colon cancer	353	43.5	10.3	64	22	AAU51931	Protonibacterium
281	44.5	10.5	67	21	AAU34839	Human immune/haema	354	43.5	10.3	64	22	AAU51931	Human immune/haema
282	44.5	10.5	67	22	AAU08320	Human polypeptide	355	43.5	10.3	65	22	AAU51931	Protonibacterium
283	44.5	10.5	69	22	AAU08320	Human polypeptide	356	43.5	10.3	65	22	AAU51931	Human polypeptide
284	44.5	10.5	73	21	AAU33196	Novel human diagno	357	43.5	10.3	66	22	AAU51931	Human protein sequ
285	44.5	10.5	73	21	AAU33196	Novel human diagno	358	43.5	10.3	69	22	AAU51931	Human polypeptide
286	44.5	10.5	74	22	AAU87164	Gene 37 human secr	359	43.5	10.3	70	22	AAU51931	Human polypeptide
287	44.5	10.5	74	22	AAU87164	Novel central nerv	360	43.5	10.3	71	22	AAU51931	Protonibacterium
288	44.5	10.5	75	22	AAU39776	Novel central nerv	361	43.5	10.3	72	20	ABG03553	Human musculoskele
289	44.5	10.5	78	20	AAU12864	Protonibacterium	362	43.5	10.3	74	20	ABG03553	Beak and feather d
290	44.5	10.5	82	21	AAU03407	Human 5' EST secre	363	43.5	10.3	77	22	ABG03553	Human nervous syst
291	44.5	10.5	82	21	AAU03407	Human secreted pro	364	43.5	10.3	78	22	AAU57876	Protonibacterium
292	44.5	10.5	85	22	AAU68055	Human secreted pro	365	43.5	10.3	80	23	AAU07929	Human polypeptide
293	44.5	10.5	87	22	AAU75339	Human DNA mismatch	366	43.5	10.3	81	22	AAU07929	Human ORFX protein
294	44.5	10.5	90	22	AAU12344	Human secreted pro	367	43.5	10.3	81	22	AAU13035	Protonibacterium
295	44.5	10.5	90	22	AAU12344	Human polypeptide	368	43.5	10.3	82	22	AAU13035	Human polypeptide
296	44.5	10.4	43	21	AAU33944	Human secreted pro	369	43.5	10.3	82	22	AAU13035	Human colon cancer
297	44.5	10.4	43	21	AAU33944	Sequence homologou	370	43.5	10.3	84	22	ABG17731	Human nervous syst
298	44.5	10.4	47	22	AAU94366	Human reproductive	371	43.5	10.3	86	21	ABG17731	Novel human diagno
299	44.5	10.4	49	22	AAU08395	Human polypeptide	372	43.5	10.3	86	22	ABG17731	Arabidopsis thalia
300	44.5	10.4	50	21	AAU45179	Human secreted pro	373	43.5	10.3	89	21	ABG17731	Protonibacterium
301	44.5	10.4	50	22	AAU08215	Human polypeptide	374	43.5	10.2	89	22	AAU08215	Human immune/haema
302	44.5	10.4	51	22	AAU08215	Human immune/haema	375	43.5	10.2	41	22	AAU08215	Human polypeptide
			51	22	AAU04963	Human polypeptide		43	10.2	42	22	AAU04963	Human polypeptide

376	43	10.2	53	22	AA004572	Human polypeptide	449	42.5	10.0	84	23	ABP03741	Human ORFX protein
377	43	10.2	53	22	AA005347	Human polypeptide	450	42.5	10.0	86	21	ABG19836	Arabidopsis thalia
378	43	10.2	54	22	AA008646	Human polypeptide	451	42.5	10.0	87	22	ABG27850	Human peptide #501
379	43	10.2	54	22	AA023700	Human EST encoded	452	42.5	10.0	87	22	ABG33022	Peptide #528 enco
380	43	10.2	55	22	AA052453	Propionibacterium	453	42.5	10.0	87	22	ABG18494	Protein #493 enco
381	43	10.2	56	22	AA009832	Human polypeptide	454	42.5	10.0	87	22	AA053820	Human brain expres
382	43	10.2	57	22	AA048294	Propionibacterium	455	42.5	10.0	87	22	AA066206	Human bone marrow
383	43	10.2	58	22	AA009257	Human polypeptide	456	42.5	10.0	87	22	AA012987	Human polypeptide
384	43	10.2	60	22	AA009361	Human polypeptide	457	42.5	10.0	87	22	AA014076	Peptide #510 enco
385	43	10.2	61	19	AA020500	Human neurofilamen	458	42.5	10.0	87	22	AA01816	Peptide #520 enco
386	43	10.2	61	21	AA045374	Human secreted pro	459	42.5	10.0	87	22	AA026483	Peptide #498 enco
387	43	10.2	61	21	AA000552	Human secreted pro	460	42.5	10.0	87	22	AA008216	Human polypeptide
388	43	10.2	61	22	AA010476	Human polypeptide	461	42.5	10.0	89	23	AA008430	Human polypeptide
389	43	10.2	63	22	AA039397	Propionibacterium	462	42.5	10.0	89	23	ABP04430	Streptococcus poly
390	43	10.2	64	22	AA056979	Propionibacterium	463	42.5	10.0	89	23	ABP29332	Human ORFX ORF2588
391	43	10.2	64	22	AA005374	Human polypeptide	464	42.5	10.0	90	21	ABG42824	Human ovarian anti
392	43	10.2	66	22	AB003852	Human musculoskele	465	42.5	10.0	90	23	ABF41587	Human polypeptide
393	43	10.2	69	22	AA012888	Human polypeptide	466	42.5	9.9	42	22	AA005327	Peptide #8700 enco
394	43	10.2	70	22	AB017706	Human nervous syst	467	42.5	9.9	44	22	ABG41194	Protein #7209 enco
395	43	10.2	71	22	AA089187	Human immune/haema	468	42.5	9.9	44	22	ABG25210	Human brain expres
396	43	10.2	72	21	AA054855	Arabidopsis thalia	469	42.5	9.9	44	22	AA062054	Human bone marrow
397	43	10.2	72	21	ABG01031	Novel human diagno	470	42.5	9.9	44	22	AA074856	Human polypeptide
398	43	10.2	73	22	AA042235	Propionibacterium	471	42.5	9.9	44	22	AA005563	Human polypeptide
399	43	10.2	73	22	AA062648	Propionibacterium	472	42.5	9.9	44	22	AA034973	Peptide #9010 enco
400	43	10.2	74	22	AA005345	Human polypeptide	473	42.5	9.9	44	22	ABG44632	Human peptide enco
401	43	10.2	75	23	ABP34417	Human ORF3390 prot	474	42.5	9.9	45	22	AA087183	Human immune/haema
402	43	10.2	76	22	AA049885	Propionibacterium	475	42.5	9.9	46	22	AA004462	Human polypeptide
403	43	10.2	77	22	ABG06206	Novel human diagno	476	42.5	9.9	50	22	AA065179	Propionibacterium
404	43	10.2	78	22	AA006313	Human polypeptide	477	42.5	9.9	50	22	AA002589	Human polypeptide
405	43	10.2	79	22	AA055569	Propionibacterium	478	42.5	9.9	51	22	AA075662	Human colon cancer
406	43	10.2	82	22	AA061736	Propionibacterium	479	42.5	9.9	52	23	ABP08244	Human ORFX protein
407	43	10.2	82	22	ABG11875	Novel human diagno	480	42.5	9.9	52	23	ABP10658	Human ORFX protein
408	43	10.2	83	20	AA012244	Human 5' EST secre	481	42.5	9.9	53	21	AA000407	Human secreted pro
409	43	10.2	83	20	AA084441	Human immune/haema	482	42.5	9.9	53	21	AA076898	Human colon cancer
410	43	10.2	84	20	AA059177	Secreted protein 5	483	42.5	9.9	55	20	AA030860	Human secreted pro
411	43	10.2	84	22	ABG01122	Novel human diagno	484	42.5	9.9	55	21	AA042012	Human ORFX ORF1776
412	43	10.2	84	22	AA008165	Human polypeptide	485	42.5	9.9	56	22	AA058588	Propionibacterium
413	43	10.2	84	22	AA076198	Human colon cancer	486	42.5	9.9	56	22	ABG44115	Human peptide enco
414	43	10.2	85	22	AA009684	Human polypeptide	487	42.5	9.9	63	21	ABG23287	Arabidopsis thalia
415	43	10.2	86	22	AA055636	Propionibacterium	488	42.5	9.9	63	22	ABG28328	Human peptide #979
416	43	10.2	87	21	AA000354	Human secreted pro	489	42.5	9.9	63	22	ABG33505	Peptide #1011 enco
417	43	10.2	87	22	AA075668	Propionibacterium	490	42.5	9.9	63	22	ABG18964	Human brain expres
418	43	10.2	87	22	AA052229	Propionibacterium	491	42.5	9.9	63	22	AA054284	Human bone marrow
419	43	10.2	87	22	AA030956	Novel human secret	492	42.5	9.9	63	22	AA066679	Human ORFX ORF3037
420	43	10.2	87	22	AA009144	Human polypeptide	493	42.5	9.9	63	22	AA014547	Peptide #981 enco
421	43	10.2	89	22	AA041466	Human immune/haema	494	42.5	9.9	63	22	AA026965	Peptide #955 enco
422	43	10.2	90	22	AA057552	Human polypeptide	495	42.5	9.9	63	22	AA002273	Human peptide enco
423	42.5	10.0	42	22	AA008440	Human polypeptide	496	42.5	9.9	63	23	ABG36334	Human colon cancer
424	42.5	10.0	48	22	AA007940	Human polypeptide	497	42.5	9.9	64	22	AA075517	Propionibacterium
425	42.5	10.0	48	22	AA008085	Human polypeptide	498	42.5	9.9	65	22	AA049663	Human prostate tum
426	42.5	10.0	48	22	AA008088	Human polypeptide	499	42.5	9.9	68	20	AA074206	Novel human secret
427	42.5	10.0	48	22	AA048273	Propionibacterium	500	42.5	9.9	68	22	AA032254	Human ORF380 prote
428	42.5	10.0	50	22	AA046164	Propionibacterium	501	42.5	9.9	68	23	ABP31407	Human ORFX ORF3037
429	42.5	10.0	52	22	AA046164	Propionibacterium	502	42.5	9.9	69	21	AA043273	Human polypeptide
430	42.5	10.0	53	23	ABP02561	Human ORFX protein	503	42.5	9.9	69	22	AA010503	Human ORFX ORF3037
431	42.5	10.0	60	22	AA006728	Human reproductive	504	42.5	9.9	71	21	ABP08257	Human secreted pro
432	42.5	10.0	61	17	AA042422	SH3 domain B of hu	505	42.5	9.9	71	21	ABG56271	Propionibacterium
433	42.5	10.0	65	21	AA034530	Human secreted pro	506	42.5	9.9	71	22	AA049496	Propionibacterium
434	42.5	10.0	66	22	AA005171	Propionibacterium	507	42.5	9.9	71	22	AA017779	Novel human respir
435	42.5	10.0	67	22	AA009125	Human polypeptide	508	42.5	9.9	71	22	ABG69713	Novel human respir
436	42.5	10.0	69	20	ABG23240	Novel human diagno	509	42.5	9.9	72	22	ABG67450	Human immune/haema
437	42.5	10.0	69	20	AA001282	Human secreted pro	510	42.5	9.9	72	22	AA055859	Propionibacterium
438	42.5	10.0	70	21	AA001297	Human secreted pro	511	42.5	9.9	74	22	AA054326	Propionibacterium
439	42.5	10.0	70	22	AA002241	Human polypeptide	512	42.5	9.9	75	22	AA054326	Human ORFX protein
440	42.5	10.0	71	22	AA076625	Corynebacterium gl	513	42.5	9.9	75	23	ABP07854	Human ORFX protein
441	42.5	10.0	73	22	AA053960	Propionibacterium	514	42.5	9.9	76	22	AA050122	Human immune/haema
442	42.5	10.0	76	22	AA006377	Human polypeptide	515	42.5	9.9	76	22	AA050845	Human immune/haema
443	42.5	10.0	77	22	ABG09467	Novel human diagno	516	42.5	9.9	76	22	AA091838	Human immune/haema
444	42.5	10.0	78	21	AA021116	Arabidopsis thalia	517	42.5	9.9	77	22	ABP32314	Human ORF1287 prot
445	42.5	10.0	78	22	AA032264	Novel human secret	518	42.5	9.9	77	22	AA062445	Propionibacterium
446	42.5	10.0	79	23	ABG44124	Human peptide enco	519	42.5	9.9	77	22	ABG30209	Novel human diagno
447	42.5	10.0	83	22	ABG16786	Human nervous syst	520	42.5	9.9	78	17	AA099709	pKTH1798-encoded p
448	42.5	10.0	84	22	AA043383	Propionibacterium	521	42.5	9.9	78	22	AA022319	Human cardiovascular

522	42	9.9	78	22	AAE00778	Aminotransferase d	595	41.5	9.8	88	22	AAU39918	Propionibacterium
523	42	9.9	78	23	ABP38003	Staphylococcus epi	596	41.5	9.8	88	22	AAO07068	Human polypeptide
524	42	9.9	79	22	AAO10568	Human polypeptide	597	41.5	9.8	88	22	AAO10609	Human polypeptide
525	42	9.9	80	21	AAE51004	Human secreted pro	598	41.5	9.8	89	20	ABB11537	Human PRO1722 homo
526	42	9.9	80	22	AAU51996	Propionibacterium	599	41.5	9.8	90	20	AAU59864	Human normal uteru
527	42	9.9	81	20	AAU35749	Chlamydia pneumoni	600	41	9.7	43	22	ABB26793	Protein #8792 enco
528	42	9.9	81	20	AAU13495	Tissue cement prot	601	41	9.7	43	22	AAU64851	Human brain expre
529	42	9.9	82	23	AAU50376	Clone 21 tick ceme	602	41	9.7	46	22	AAO09283	Human polypeptide
530	42	9.9	82	23	ABP33716	Human ORF2689 prot	603	41	9.7	48	22	AAU32180	Novel human secret
531	42	9.9	83	22	ABP33716	Peptide #10043 enc	604	41	9.7	48	22	AAO07693	Human polypeptide
532	42	9.9	83	22	ABP33716	Protein #7935 enco	605	41	9.7	48	22	AAU63590	Human immune/haema
533	42	9.9	83	22	AAU63427	Human brain expre	606	41	9.7	49	22	AAO08165	Human polypeptide
534	42	9.9	83	22	AAU76240	Human bone marrow	607	41	9.7	50	19	AAU20772	Human neurofilamen
535	42	9.9	83	22	AAU36350	Peptide #10387 enc	608	41	9.7	50	22	AAO09169	Human polypeptide
536	42	9.9	83	22	ABG45566	Human peptide enco	609	41	9.7	51	19	AAU71570	Hepatocyte nuclear
537	42	9.9	85	21	AAU45018	Human secreted pro	610	41	9.7	52	21	AAU51893	Human polypeptide
538	42	9.9	85	22	ABU16594	Human nervous syst	611	41	9.7	52	22	AAU39844	Propionibacterium
539	42	9.9	86	23	ABU49577	Listeria monocytog	612	41	9.7	52	22	AAU52927	Human digestive sy
540	42	9.9	86	23	AAU50153	Tarantula venom pr	613	41	9.7	53	22	AAU55125	Propionibacterium
541	42	9.9	88	22	AAO09027	Human polypeptide	614	41	9.7	54	22	AAO11851	Human polypeptide
542	41.5	9.8	42	22	AAO09502	Human polypeptide	615	41	9.7	54	22	ABP01280	Human ORFX protein
543	41.5	9.8	42	22	AAO11934	Human polypeptide	616	41	9.7	54	23	ABP01280	Human ORFX protein
544	41.5	9.8	43	22	AAO12469	Human polypeptide	617	41	9.7	55	22	AAU50602	Propionibacterium
545	41.5	9.8	45	22	ABB32036	Peptide #4687 enco	618	41	9.7	58	21	AAU44194	Human cancer assoc
546	41.5	9.8	45	22	ABB32036	Peptide #4791 enco	619	41	9.7	58	21	AAO00098	Human secreted pro
547	41.5	9.8	45	22	ABB37285	Human brain expre	620	41	9.7	58	21	AAO10026	Human polypeptide
548	41.5	9.8	45	22	AAU70471	Human bone marrow	621	41	9.7	59	20	AAU11377	Human ORFX protei
549	41.5	9.8	45	22	AAU57988	Human polypeptide	622	41	9.7	59	23	ABP31870	Human 5' EST secre
550	41.5	9.8	45	22	AAU04771	Human polypeptide	623	41	9.7	60	23	ABP32751	Human ORF843 prote
551	41.5	9.8	46	21	AAU34273	Peptide #4549 enco	624	41	9.7	60	23	ABP32751	Human ORF1724 prot
552	41.5	9.8	47	22	AAO08735	Human secreted pro	625	41	9.7	61	22	AAU62940	Propionibacterium
553	41.5	9.8	49	22	AAO08735	Human polypeptide	626	41	9.7	62	20	AAU27216	Human polypeptide
554	41.5	9.8	51	21	AAU16822	Bacteriophage Do-1	627	41	9.7	63	22	ABB82192	Tobacco protox tra
555	41.5	9.8	53	22	AAO07563	Human polypeptide	628	41	9.7	63	23	ABP00735	Human ORFX protein
556	41.5	9.8	54	22	AAU54453	Propionibacterium	629	41	9.7	63	23	ABP03924	Human ORFX protein
557	41.5	9.8	54	23	AAU21787	Long-specific amin	630	41	9.7	66	22	AAU59149	Propionibacterium
558	41.5	9.8	56	22	AAU63207	Propionibacterium	631	41	9.7	66	22	AAO07830	Human polypeptide
559	41.5	9.8	59	22	AAO07258	Human polypeptide	632	41	9.7	66	23	ABP04330	Human ORFX protei
560	41.5	9.8	61	22	AAU41123	Novel human diagno	633	41	9.7	67	22	AAU81711	Human haematologic
561	41.5	9.8	63	22	ABG00882	Novel human secret	634	41	9.7	67	22	AAU81951	Human haematologic
562	41.5	9.8	63	22	AAU32267	Human polypeptide	635	41	9.7	69	22	AAO00760	Human polypeptide
563	41.5	9.8	63	22	AAU07078	Propionibacterium	636	41	9.7	69	22	AAU44591	Propionibacterium
564	41.5	9.8	65	22	AAU66833	Human polypeptide	637	41	9.7	69	22	AAU49304	Propionibacterium
565	41.5	9.8	66	22	ABG63387	Drosophila melanog	638	41	9.7	70	19	AAU98525	H. pylori GHPO 138
566	41.5	9.8	68	22	AAO12997	S. pneumoniae anti	639	41	9.7	70	22	ABB67736	Drosophila melanog
567	41.5	9.8	69	23	AAU63840	Human polypeptide	640	41	9.7	70	22	AAU43234	Propionibacterium
568	41.5	9.8	72	22	AAU58698	Propionibacterium	641	41	9.7	71	22	AAU83798	Human immune/haema
569	41.5	9.8	75	22	AAO08890	Human polypeptide	642	41	9.7	71	22	AAU13052	Human polypeptide
570	41.5	9.8	76	22	AAU41740	Propionibacterium	643	41	9.7	72	22	AAU52732	Propionibacterium
571	41.5	9.8	76	22	AAU51833	Propionibacterium	644	41	9.7	72	22	AAU60316	Propionibacterium
572	41.5	9.8	76	22	ABG16616	Novel human diagno	645	41	9.7	73	22	AAU56655	Human ORF2982 prot
573	41.5	9.8	76	22	AAU91908	Human immune/haema	646	41	9.7	73	23	ABP34009	Human secreted pro
574	41.5	9.8	77	22	AAU40298	Propionibacterium	647	41	9.7	74	21	AAO09985	Human ovarian anti
575	41.5	9.8	77	22	AAO11163	Novel human diagno	648	41	9.7	74	23	ABP41126	Propionibacterium
576	41.5	9.8	78	22	ABG19038	Human polypeptide	649	41	9.7	75	22	AAU48136	Human polypeptide
577	41.5	9.8	78	23	ABP00955	Human ORFX protei	650	41	9.7	75	22	AAO06046	Mouse C4a anaphyla
578	41.5	9.8	78	23	ABG20265	Human lung specifi	651	41	9.7	76	22	AAE05453	Human secreted pro
579	41.5	9.8	79	22	ABG23486	Novel human diagno	652	41	9.7	77	21	AAU27821	Human immune/haema
580	41.5	9.8	81	15	ABG2806	TCR alpha chain of	653	41	9.7	77	22	AAU89472	Fragment of human
581	41.5	9.8	81	22	AAU48002	Propionibacterium	654	41	9.7	78	20	AAU78240	Novel human secret
582	41.5	9.8	84	22	AAU51713	Propionibacterium	655	41	9.7	79	21	AAU85185	A. thaliana Rar1 f
583	41.5	9.8	85	22	ABG23437	Novel human diagno	656	41	9.7	79	22	AAU32647	Novel human secret
584	41.5	9.8	86	19	AAU52589	KGF-2 deletion mut	657	41	9.7	79	22	AAU32648	Human immune/haema
585	41.5	9.8	86	22	AAO07222	Human polypeptide	658	41	9.7	80	22	AAU83057	Human immune/haema
586	41.5	9.8	86	22	AAO09217	Human polypeptide	659	41	9.7	80	22	AAU84679	Human secreted pro
587	41.5	9.8	86	22	AAU60211	Human KGF-2 deleti	660	41	9.7	81	22	AAU64767	Human colon cancer
588	41.5	9.8	87	20	AAU32903	E. coli optimised	661	41	9.7	82	22	AAU87532	Human immune/haema
589	41.5	9.8	87	21	AAU44671	Human secreted pro	662	41	9.7	82	22	AAU72127	Human polypeptide
590	41.5	9.8	87	21	AAU10318	Human KGF-2 deleti	663	41	9.7	86	20	AAU27217	Human polypeptide
591	41.5	9.8	87	22	ABU11351	Human secreted pro	664	41	9.7	86	22	AAO04313	Human polypeptide
592	41.5	9.8	87	22	AAO09695	Human polypeptide	665	41	9.7	87	22	AAO04050	Human polypeptide
593	41.5	9.8	87	22	AAU61682	KGF-2 deletion con	666	41	9.7	87	22	AAO13361	Human polypeptide
594	41.5	9.8	88	20	AAU35796	Amino acid sequenc	667	41	9.7	89	22	AAU59414	Propionibacterium



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668	41	9.7	89	22	ABH11459	Human secreted pro	741	40	9.5	47	20	AAV03000	Fragment of human
669	41	9.7	90	22	AAO01665	Human polypeptide	742	40	9.5	47	22	ABG15360	Novel human diagno
670	41	9.7	90	22	AAO07298	Human polypeptide	743	40	9.5	47	22	AAO10711	Human polypeptide
671	41	9.7	90	22	ABP11857	Human ORF830 prote	744	40	9.5	49	22	ABH42761	Peptide #10267 enc
672	40.5	9.6	40	22	AAO11871	Human polypeptide	745	40	9.5	49	22	ABH26054	Protein #8053 enco
673	40.5	9.6	42	22	AAO04678	Human polypeptide	746	40	9.5	49	22	AAH63652	Human brain expres
674	40.5	9.6	45	22	AAO09192	Human polypeptide	747	40	9.5	49	22	AAH76466	Human bone marrow
675	40.5	9.6	45	22	AAO13730	Human polypeptide	748	40	9.5	49	22	AAH36573	Peptide #10610 enc
676	40.5	9.6	46	22	AAO08993	Human polypeptide	749	40	9.5	49	23	ABG45727	Human peptide enco
677	40.5	9.6	46	22	ABG62250	Human gene 5-encod	750	40	9.5	50	22	ABH15458	Human nervous syst
678	40.5	9.6	49	22	ABG11933	Novel human diagno	751	40	9.5	50	22	AAU27800	Human full-length
679	40.5	9.6	49	22	AAO02090	Human polypeptide	752	40	9.5	51	20	AAV36084	Extended human sec
680	40.5	9.6	50	22	AAO06840	Human polypeptide	753	40	9.5	51	20	AAV35945	Extended human sec
681	40.5	9.6	51	23	ABP41944	Human ovarian anti	754	40	9.5	51	22	AAO07326	Human polypeptide
682	40.5	9.6	52	23	ABP06142	Human ORFX protein	755	40	9.5	52	22	AAU45977	Protonibacterium
683	40.5	9.6	54	22	AAU061140	Human immune/haema	756	40	9.5	52	22	AAH94542	Human reproductiv
684	40.5	9.6	56	22	AAU42048	Protonibacterium	757	40	9.5	53	20	AAV13042	Human secreted pro
685	40.5	9.6	56	22	AAU01967	Human secreted pro	758	40	9.5	53	22	AAU62994	Protonibacterium
686	40.5	9.6	57	22	AAU48814	Protonibacterium	759	40	9.5	54	22	AAU40018	Protonibacterium
687	40.5	9.6	58	21	AAH56078	Arabidopsis thalia	760	40	9.5	54	22	AAO4589	Human polypeptide
688	40.5	9.6	58	21	AAH56037	Arabidopsis thalia	761	40	9.5	54	22	AAO4590	Human polypeptide
689	40.5	9.6	58	23	AAH56055	Human reproductiv	762	40	9.5	55	19	AAH80132	Nucleocapsid deriv
690	40.5	9.6	58	23	ABP09494	Human ORFX protein	763	40	9.5	55	22	AAU58679	Protonibacterium
691	40.5	9.6	60	22	AAO10479	Human polypeptide	764	40	9.5	56	17	AAH93223	Partial fibroblast
692	40.5	9.6	61	22	ABG71280	Human gene 6-encod	765	40	9.5	57	21	AAU02206	Human secreted pro
693	40.5	9.6	61	23	ABG63496	Human albumin fusi	766	40	9.5	57	22	AAU50759	Protonibacterium
694	40.5	9.6	62	22	ABH17617	Human nervous syst	767	40	9.5	57	22	AAO08564	Human polypeptide
695	40.5	9.6	62	22	AAO10289	Human polypeptide	768	40	9.5	57	22	AAH23824	Human EST encoded
696	40.5	9.6	64	22	AAH7489	Human immune/haema	769	40	9.5	58	22	AAU39860	Protonibacterium
697	40.5	9.6	66	21	AAH12066	SH3 domain from p8	770	40	9.5	58	22	AAU44219	Protonibacterium
698	40.5	9.6	67	22	AAH94815	Human reproductiv	771	40	9.5	59	21	AAH41107	Human ORFX ORF871
699	40.5	9.6	68	18	AAH09415	Human G protein ga	772	40	9.5	59	22	AAU46970	Protonibacterium
700	40.5	9.6	68	19	AAH61906	Human G protein ga	773	40	9.5	59	22	ABG25325	Novel human diagno
701	40.5	9.6	68	20	AAH17986	Human G protein ga	774	40	9.5	59	23	ABP02829	Human ORFX protein
702	40.5	9.6	68	20	AAH14069	Human CBLA07 pro	775	40	9.5	60	22	AAU56709	Protonibacterium
703	40.5	9.6	68	22	AAH92836	Human digestive sy	776	40	9.5	60	22	AAH90911	Human immune/haema
704	40.5	9.6	68	22	AAO20917	68-mer human prote	777	40	9.5	60	22	AAU24419	Human EST encoded
705	40.5	9.6	69	22	AAU46277	Protonibacterium	778	40	9.5	61	22	AAU54374	Protonibacterium
706	40.5	9.6	70	22	AAO05802	Human polypeptide	779	40	9.5	61	22	AAH88761	Human immune/haema
707	40.5	9.6	71	22	AAO12345	Human polypeptide	780	40	9.5	62	23	ABP07003	Human ORFX protein
708	40.5	9.6	71	23	ABH1379	Human prostatic spe	781	40	9.5	63	21	AAH38169	Arabidopsis thalia
709	40.5	9.6	74	21	ABG55105	Arabidopsis thalia	782	40	9.5	64	22	AAU29745	Novel human secret
710	40.5	9.6	75	22	AAU42067	Protonibacterium	783	40	9.5	64	23	ABP05590	Human ORFX protein
711	40.5	9.6	77	23	ABP11324	Human MDR1 SEQ ID	784	40	9.5	65	14	AAH38891	pF12 of nef protei
712	40.5	9.6	78	23	ABG55392	Human breast speci	785	40	9.5	65	22	AAU61257	Protonibacterium
713	40.5	9.6	79	22	AAU060635	Protonibacterium	786	40	9.5	65	22	ABG23916	Novel human diagno
714	40.5	9.6	79	22	AAH53749	Human immune/haema	787	40	9.5	65	22	AAH73221	Human bone marrow
715	40.5	9.6	79	22	AAH74258	Human colon cancer	788	40	9.5	65	22	AAH86405	Human immune/haema
716	40.5	9.6	80	21	AAH00040	Human secreted pro	789	40	9.5	65	23	ABG43068	Human peptide enco
717	40.5	9.6	80	22	AAU00148	Protonibacterium	790	40	9.5	66	22	AAU56163	Protonibacterium
718	40.5	9.6	82	22	AAU62958	Protonibacterium	791	40	9.5	67	21	AAH01922	Human secreted pro
719	40.5	9.6	82	22	AAH58547	Protonibacterium	792	40	9.5	67	22	ABH17351	Human nervous syst
720	40.5	9.6	83	21	AAH000294	Human secreted pro	793	40	9.5	67	23	ABP05628	Human ORFX protein
721	40.5	9.6	83	22	ABH08156	Novel human diagno	794	40	9.5	68	10	AAH92266	Peptide pF12 from
722	40.5	9.6	83	22	AAO12440	Mouse ICAM-1 domai	795	40	9.5	68	20	AAH67818	Human secreted pro
723	40.5	9.6	84	22	AAH48409	Human polypeptide	796	40	9.5	68	21	AAH00980	Human secreted pro
724	40.5	9.6	84	22	AAH05978	Human polypeptide	797	40	9.5	68	22	AAU53273	Protonibacterium
725	40.5	9.6	84	22	AAH08388	Human polypeptide	798	40	9.5	68	22	AAH08590	Human polypeptide
726	40.5	9.6	85	22	AAH56882	Protonibacterium	799	40	9.5	69	21	AAH51499	Human secreted pro
727	40.5	9.6	86	20	AAH13136	Human secreted pro	800	40	9.5	69	21	AAH51503	Human secreted pro
728	40.5	9.6	86	22	AAH01370	Human gene 19 enco	801	40	9.5	69	22	AAH61455	Protonibacterium
729	40.5	9.6	87	22	ABG64121	Human albumin fusi	802	40	9.5	70	21	AAH08451	Arabidopsis thalia
730	40.5	9.6	87	22	AAH58059	Protonibacterium	803	40	9.5	70	22	AAH01617	Human gene 22 enco
731	40.5	9.6	88	22	AAU82332	Protonibacterium	804	40	9.5	70	23	ABG63787	Human albumin fusi
732	40.5	9.6	88	22	ABG09992	Novel human diagno	805	40	9.5	71	21	AAH16132	Arabidopsis thalia
733	40.5	9.6	89	20	AAH75316	Human ovarian tumo	806	40	9.5	71	22	AAH41341	Protonibacterium
734	40.5	9.6	89	22	AAO02352	Human secreted pro	807	40	9.5	71	22	AAH63002	Protonibacterium
735	40.5	9.6	89	22	AAO02098	Human polypeptide	808	40	9.5	71	22	AAH65916	Protonibacterium
736	40.5	9.6	89	22	AAH99944	Human dihydroorota	809	40	9.5	71	22	AAU22574	Novel human colon
737	40.5	9.6	90	22	AAH48467	Protonibacterium	810	40	9.5	71	22	AAU92537	Human digestive sy
738	40.5	9.6	90	23	AAH07556	Human macroprotein	811	40	9.5	72	20	AAH02999	Fragment of human
739	40	9.5	41	20	AAH87807	A Bcl-2 associated	812	40	9.5	72	21	AAH26497	Human immunodefici
740	40	9.5	41	22	AAH74124	N-terminus of Baxg	813	40	9.5	72	21	AAH03435	Human secreted pro

814	40	9.5	72	22	ABG03275	Novel human diagno	887	40	9.5	90	22	AAM34203	Peptide #8240 enco
815	40	9.5	73	22	AAU41987	Propionibacterium	888	40	9.5	90	23	AAE24325	Human lung-specific
816	40	9.5	73	22	ABJ39762	Peptide #7268 enco	889	40	9.5	90	23	ABG43931	Human peptide enco
817	40	9.5	73	22	AAU60483	Human brain expres	890	39.5	9.3	43	21	AAAB27764	Protein fragment e
818	40	9.5	73	22	AAU60483	Human bone marrow	891	39.5	9.3	46	22	AAO112287	Human polypeptide
819	40	9.5	73	22	AAU33344	Peptide #7381 enco	892	39.5	9.3	48	22	ABG28738	Novel human diagno
820	40	9.5	73	22	ABG42974	Human peptide enco	893	39.5	9.3	48	22	AAO06938	Human polypeptide
821	40	9.5	73	22	ABP00756	Human ORFX protein	894	39.5	9.3	50	23	ABP04413	Human ORFX protein
822	40	9.5	74	21	AAU56258	Human secreted pro	895	39.5	9.3	51	22	AAO04105	Human polypeptide
823	40	9.5	74	21	AAU32842	Zea mays protein f	896	39.5	9.3	52	21	AAO12603	Human polypeptide
824	40	9.5	74	21	AAU61701	Arabidopsis thalia	897	39.5	9.3	52	21	AAU16816	Bacteriophage Dp-1
825	40	9.5	74	22	ABU12126	Human secreted pro	898	39.5	9.3	52	22	AAU43310	Propionibacterium
826	40	9.5	75	22	AAU44393	Propionibacterium	899	39.5	9.3	52	22	AAO08421	Human polypeptide
827	40	9.5	75	22	ABP10512	Human ORFX protein	900	39.5	9.3	52	22	AAO04988	Human ORFX protein
828	40	9.5	77	15	ABU55888	Nucleic acid trans	901	39.5	9.3	53	22	AAU14500	Human haematologic
829	40	9.5	77	22	ABU03450	Human C4a anaphyla	902	39.5	9.3	53	22	AAU17007	Human polypeptide
830	40	9.5	78	22	ABU30562	Peptide #3213 enco	903	39.5	9.3	53	22	AAO10582	Human polypeptide
831	40	9.5	78	22	ABU35727	Peptide #3233 enco	904	39.5	9.3	54	20	AAU06664	Magnaporthe grisea
832	40	9.5	78	22	ABU21153	Protein #3152 enco	905	39.5	9.3	54	21	AAU02490	Human secreted pro
833	40	9.5	78	22	AAU56336	Human brain expres	906	39.5	9.3	54	21	AAU02543	Human secreted pro
834	40	9.5	78	22	AAU68918	Human bone marrow	907	39.5	9.3	54	22	AAU31674	Novel human secret
835	40	9.5	78	22	AAU08487	Human polypeptide	908	39.5	9.3	56	22	AAU84965	Human immune/haema
836	40	9.5	78	22	AAU16741	Peptide #3175 enco	909	39.5	9.3	56	22	AAO08648	Human polypeptide
837	40	9.5	78	22	AAU29229	Peptide #3266 enco	910	39.5	9.3	56	22	AAO09380	Human polypeptide
838	40	9.5	78	22	AAU04458	Peptide #3140 enco	911	39.5	9.3	57	22	AAU41773	Propionibacterium
839	40	9.5	78	22	ABG38499	Human peptide enco	912	39.5	9.3	57	22	ABG02248	Novel human diagno
840	40	9.5	79	22	AAU91065	Human immune/haema	913	39.5	9.3	57	22	AAO10327	Human polypeptide
841	40	9.5	79	22	AAU71305	Human gene 19-enco	914	39.5	9.3	57	22	AAO11104	Human ORFX protein
842	40	9.5	79	22	ABG53472	Human albumin fusl	915	39.5	9.3	58	21	AAU02828	Human secreted pro
843	40	9.5	80	22	AAU53327	Propionibacterium	916	39.5	9.3	58	22	AAU56169	Propionibacterium
844	40	9.5	80	22	AAU91132	Human immune/haema	917	39.5	9.3	58	22	AAU0541	Human ORFX protein
845	40	9.5	80	22	ABU34764	Human structural p	918	39.5	9.3	59	22	AAU67155	Propionibacterium
846	40	9.5	81	22	AAU25621	Human structural sequ	919	39.5	9.3	59	22	AAU44620	Propionibacterium
847	40	9.5	81	22	AAU68621	Arabidopsis thalia	920	39.5	9.3	60	22	AAU57944	Propionibacterium
848	40	9.5	82	22	AAU64405	Propionibacterium	921	39.5	9.3	60	22	AAU78252	Novel human diagno
849	40	9.5	82	22	AAU49537	Propionibacterium	922	39.5	9.3	60	22	ABG05299	Human immune/haema
850	40	9.5	82	22	AAU08251	Novel human diagno	923	39.5	9.3	61	21	AAU27982	Human secreted pro
851	40	9.5	82	22	AAU08251	Human ORFX protein	924	39.5	9.3	61	22	ABU33884	Lactococcus lactis
852	40	9.5	82	22	ABU11289	Propionibacterium	925	39.5	9.3	62	22	AAU43395	Propionibacterium
853	40	9.5	83	22	AAU42599	Propionibacterium	926	39.5	9.3	63	22	AAU55294	Peptide #7381 enco
854	40	9.5	83	22	AAU42960	Propionibacterium	927	39.5	9.3	64	22	ABU39875	Human brain foetal
855	40	9.5	83	22	AAU57332	Human immune/haema	928	39.5	9.3	64	22	AAU20992	Human bone marrow
856	40	9.5	83	22	AAU66526	Human polypeptide	929	39.5	9.3	64	22	AAU60611	Human bone marrow
857	40	9.5	83	22	AAU12786	Human polypeptide	930	39.5	9.3	64	22	AAU73283	Peptide #7521 enco
858	40	9.5	84	22	AAU63652	Propionibacterium	931	39.5	9.3	64	22	AAU33484	Human secreted pro
859	40	9.5	84	22	AAU31832	Murine chisel (Csl	932	39.5	9.3	66	21	ABG43133	Human nervous syst
860	40	9.5	85	20	AAU28650	Peptide #1151 enco	933	39.5	9.3	66	21	AAU16860	Human 5' ESR seque
861	40	9.5	85	22	ABU28500	Peptide #1191 enco	934	39.5	9.3	67	20	AAU11459	Human polypeptide
862	40	9.5	85	22	ABU33685	Protein #1134 enco	935	39.5	9.3	67	20	AAU05536	Listeria monocytog
863	40	9.5	85	22	ABU19135	Human brain expres	936	39.5	9.3	67	23	ABU49652	Human bone marrow
864	40	9.5	85	22	AAU54453	Human bone marrow	937	39.5	9.3	68	22	AAU73013	Human immune/haema
865	40	9.5	85	22	AAU66858	Peptide #1154 enco	938	39.5	9.3	68	22	AAU90801	Peptide #7275 enco
866	40	9.5	85	22	AAU14720	Peptide #1129 enco	939	39.5	9.3	68	22	AAU32238	Human secreted pro
867	40	9.5	85	22	AAU27142	Peptide #1125 enco	940	39.5	9.3	68	22	ABG46408	Human polypeptide
868	40	9.5	85	22	ABG36514	Human peptide enco	941	39.5	9.3	68	22	ABG42853	Human secreted pro
869	40	9.5	86	22	AAU10325	Human polypeptide	942	39.5	9.3	69	22	AAU08659	Human polypeptide
870	40	9.5	86	22	AAU10325	Human polypeptide	943	39.5	9.3	69	22	AAU64841	Gene 24 human secr
871	40	9.5	86	22	ABU35536	Human ORF4509 prot	944	39.5	9.3	70	22	AAU51187	Propionibacterium
872	40	9.5	86	22	ABU35536	Human human diagno	945	39.5	9.3	70	22	AAU67440	Propionibacterium
873	40	9.5	87	22	AAU20301	Novel human secret	946	39.5	9.3	70	22	AAU31992	Novel human secret
874	40	9.5	87	22	AAU31894	Propionibacterium	947	39.5	9.3	71	21	AAU28757	Peptide #2. Homo
875	40	9.5	88	22	AAU43344	Human immune/haema	948	39.5	9.3	71	22	AAU33214	Novel human secret
876	40	9.5	88	22	AAU44277	Streptococcus poly	949	39.5	9.3	71	22	AAU33302	Arabidopsis thalia
877	40	9.5	88	22	ABP29439	Propionibacterium	950	39.5	9.3	72	22	AAU55776	Propionibacterium
878	40	9.5	89	22	AAU44672	Propionibacterium	951	39.5	9.3	72	22	AAU43779	Novel human diagno
879	40	9.5	89	22	AAU58480	Human heat shock f	952	39.5	9.3	72	22	ABG19310	Human polypeptide
880	40	9.5	89	22	AAU08306	Peptide #7985 enco	953	39.5	9.3	72	22	AAU42326	Peptide encoded by
881	40	9.5	89	22	AAU018169	Protein #6815 enco	954	39.5	9.3	72	22	AAU41202	Peptide encoded by
882	40	9.5	90	22	ABU40479	Human brain expres	955	39.5	9.3	73	17	AAU04190	Peptide encoded by
883	40	9.5	90	22	ABU24816	Human bone marrow	956	39.5	9.3	73	17	AAU04199	P. obesus beacon p
884	40	9.5	90	22	AAU61304	Peptide #636 enco	957	39.5	9.3	73	20	AAU08413	
885	40	9.5	90	22	AAU74035		958	39.5	9.3	73			
886	40	9.5	90	22	AAU20202		959	39.5	9.3	73			

960 39.5 9.3 73 21 AAB36290 Israeli sand rat b  
 961 39.5 9.3 73 22 AAU52874 Propionibacterium  
 962 39.5 9.3 73 22 AAM59792 Human excretory re  
 963 39.5 9.3 73 22 AAM39680 Human polypeptide  
 964 39.5 9.3 73 22 AAM42607 Human kidney relat  
 965 39.5 9.3 75 22 AAU53462 Propionibacterium  
 966 39.5 9.3 75 22 AAG75540 Human colon cancer  
 967 39.5 9.3 75 22 AAM50753 Mycobacterium tube  
 968 39.5 9.3 76 21 AAG28488 zea mays protein f  
 969 39.5 9.3 76 22 AAM87664 Human immune/haema  
 970 39.5 9.3 78 22 AAU64032 Propionibacterium  
 971 39.5 9.3 78 22 AAU12297 Human polypeptide  
 972 39.5 9.3 78 22 AAU12976 Human polypeptide  
 973 39.5 9.3 79 22 ABG26965 Novel human diagno  
 974 39.5 9.3 79 22 AAU27471 Novel bone marrow  
 975 39.5 9.3 79 22 AAU02216 Human polypeptide  
 976 39.5 9.3 80 22 AAU03929 Human polypeptide  
 977 39.5 9.3 80 22 AAU09316 Human polypeptide  
 978 39.5 9.3 80 22 AAU04270 Human gene 9 encod  
 979 39.5 9.3 80 22 AAU54520 Propionibacterium  
 980 39.5 9.3 82 22 AAU56054 Human polypeptide  
 981 39.5 9.3 82 22 AAU12587 Human polypeptide  
 982 39.5 9.3 82 22 AAU12587 Human polypeptide  
 983 39.5 9.3 83 21 AAG03392 Human secreted pro  
 984 39.5 9.3 83 22 AAG67815 Propionibacterium  
 985 39.5 9.3 83 22 ABG28281 Novel human diagno  
 986 39.5 9.3 83 22 AAB15709 Human nervous syst  
 987 39.5 9.3 84 21 AAB56588 Human prostate can  
 988 39.5 9.3 84 22 AAU12537 Propionibacterium  
 989 39.5 9.3 85 22 AAU49000 Human signal pepti  
 990 39.5 9.3 85 22 AAG78014 Human immune/haema  
 991 39.5 9.3 85 22 AAM89070 Human STAT protein  
 992 39.5 9.3 85 23 AAB28761 Peptide #6, Homo  
 993 39.5 9.3 86 21 AAB28761 Arabidopsis thalia  
 994 39.5 9.3 86 21 AAG55775 Human polypeptide  
 995 39.5 9.3 86 22 AAU02184 Peptide #6489 enco  
 996 39.5 9.3 87 22 AAB38983 Peptide #8833 enco  
 997 39.5 9.3 87 22 AAB41327 Human brain expres  
 998 39.5 9.3 87 22 AAM59635 Human brain expres  
 999 39.5 9.3 87 22 AAM62195 Human bone marrow  
 1000 39.5 9.3 87 22 AAM72208

## ALIGNMENTS

RESULT 1  
 ID AAB18942 standard; peptide: 84 AA.  
 XX  
 AC AAB18942;  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 XX  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome x.  
 XX  
 OS Homo sapiens  
 XX  
 DT 21-SEP-2000.  
 XX  
 PF 14-MAR-2000; 2000MO-FR00613.  
 XX  
 PR 15-MAR-1999; 99FR-0003159.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;

XX WPI; 2000-587566/55.  
 XX Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 XX  
 XX Claim 2; Page 26; 46pp; French.  
 XX  
 CC B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome x.  
 XX  
 XX Sequence 84 AA;  
 XX  
 XX Query Match 100.0%; Score 423; DB 21; Length 84;  
 XX Best Local Similarity 100.0%; Pred. NO. 6.2e-47; Indels 0; Gaps 0;  
 XX Matches 84; Conservative 0; Mismatches 0;  
 QY 1 QGRSGCSQSISPMRSISNSLVAMDFSGQSRVIENTALSVAVEGLAWRRKGCLRL 60  
 DB 1 QGRSGCSQSISPMRSISNSLVAMDFSGQSRVIENTALSVAVEGLAWRRKGCLRL 60  
 QY 61 GTGHSPTASSQSSTATNMAIHRSP 84  
 DB 61 GTGHSPTASSQSSTATNMAIHRSP 84  
 RESULT 2  
 ID AAB18938 standard; peptide: 84 AA.  
 XX  
 AC AAB18938;  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 XX  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome x.  
 XX  
 OS Rattus sp.  
 XX  
 DT 21-SEP-2000.  
 XX  
 PF 14-MAR-2000; 2000MO-FR00613.  
 XX  
 PR 15-MAR-1999; 99FR-0003159.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX  
 XX WPI; 2000-587566/55.  
 XX Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 XX  
 XX Claim 2; Page 23-24; 46pp; French.  
 XX  
 CC B18937-64 represent the PIR (phosphorylated insulin receptor interacting

CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 CC  
 XX  
 XX

SQ Sequence 84 AA;

Query Match 91.3%; Score 386; DB 21; Length 84;  
 Best Local Similarity 88.1%; Pred. No. 3.9e-42;  
 Matches 74; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 QGRGCSQSISPMRSISNSLVAMDFSGQSRVIENTALSVAVEGLAWRKGGLRL 60

DB 1 QARSACSQSVPMRSVNSLVAMDFSGQKTRVIDNPTALSVAVEGLAWRKGGLRL 60

QY 61 GTHGSPTASSQSATNMALHRSQP 84

DB 61 GNHGSPTAPSSAVNMLHRSQP 84

RESULT 3

ID AAB18941 standard; peptide; 43 AA.

XX AAB18941;

DT 08-FEB-2001 (first entry)

DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.

XX Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Homo sapiens.  
 XX  
 XX WO200055634-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 14-MAR-2000; 2000WO-FR00613.  
 XX  
 XX 15-MAR-1999; 99FR-0003159.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 XX  
 XX Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity  
 XX  
 XX Claim 2; Page 25; 46pp; French.

PS Claim 2; Page 25; 46pp; French.

XX BL937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.

XX  
 SQ Sequence 43 AA;  
 Query Match 50.1%; Score 212; DB 21; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-20;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 PMRSISNSLVAMDFSGQSRVIENTALSVAVEGLAWRKG 55  
 DB 1 PMRSISNSLVAMDFSGQSRVIENTALSVAVEGLAWRKG 43

RESULT 4

ID AAB18937 standard; peptide; 43 AA.

XX AAB18937;

DT 08-FEB-2001 (first entry)

DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.

XX Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Rattus sp.  
 XX  
 XX WO200055634-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 14-MAR-2000; 2000WO-FR00613.  
 XX  
 XX 15-MAR-1999; 99FR-0003159.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 XX  
 XX Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity  
 XX  
 XX Claim 2; Page 23; 46pp; French.

PS Claim 2; Page 23; 46pp; French.

XX BL937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX  
 XX Sequence 43 AA;

Query Match 48.5%; Score 205; DB 21; Length 43;  
 Best Local Similarity 93.0%; Pred. No. 4.3e-19;  
 Matches 40; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 PMRSISNSLVAMDFSGQSRVIENTALSVAVEGLAWRKG 55

DB 1 PMRSISNSLVAMDFSGQKTRVIDNPTALSVAVEGLAWRKG 43

RESULT 5

AAB18954

ID AAB18954 standard; peptide; 80 AA.  
 AC AAB18954;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 DE  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Rattus sp.  
 XX  
 PN WO200055634-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 14-MAR-2000; 2000WO-FR00613.  
 XX  
 PR 15-MAR-1999; 99FR-0003159.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 XX  
 DR Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity  
 PT  
 PT Claim 2; Page 32; 46pp; French.  
 PS  
 XX B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX  
 SQ Sequence 80 AA;  
 Query Match 45.2%; Score 191; DB 21; Length 80;  
 Best Local Similarity 59.7%; Pred. No. 6.9e-17;  
 Matches 43; Conservative 8; Mismatches 17; Indels 4; Gaps 2;  
 QY 13 PMRSISENSLVAMDFSGKSRVIENTEALSVAVEGLAWRKKGCLRLGTHGSPASSQS 72  
 DB 13 PLRSVSDNTLVAMDFSGHAGRVIDNPREALSAAMEEAQAWRKKNHRLSL---PTTCSGS 69  
 QY 73 SATNMAIHRSP 84  
 DB 70 S-LSAAIHRTP 80  
 RESULT 6  
 ID AAB18962 standard; peptide; 80 AA.  
 AC AAB18962;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 DE  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.

KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 XX Mus muris.  
 OS WO200055634-A1.  
 XX  
 PN 21-SEP-2000.  
 XX  
 PD 14-MAR-2000; 2000WO-FR00613.  
 XX  
 PR 15-MAR-1999; 99FR-0003159.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 XX  
 DR Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity  
 PT  
 PT Claim 2; Page 37; 46pp; French.  
 PS  
 XX B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX  
 SQ Sequence 80 AA;  
 Query Match 45.2%; Score 191; DB 21; Length 80;  
 Best Local Similarity 59.7%; Pred. No. 6.9e-17;  
 Matches 43; Conservative 8; Mismatches 17; Indels 4; Gaps 2;  
 QY 13 PMRSISENSLVAMDFSGKSRVIENTEALSVAVEGLAWRKKGCLRLGTHGSPASSQS 72  
 DB 13 PLRSVSDNTLVAMDFSGHAGRVIDNPREALSAAMEEAQAWRKKNHRLSL---PTTCSGS 69  
 QY 73 SATNMAIHRSP 84  
 DB 70 S-LSAAIHRTP 80  
 RESULT 7  
 ID AAB18950 standard; peptide; 82 AA.  
 AC AAB18950;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 DE  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Homo sapiens.  
 XX  
 PN WO200055634-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PR 14-MAR-2000; 2000WO-FR00613.  
 XX

PR 15-MAR-1999; 99FR-0003159.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 CC Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 XX  
 PS Claim 2; Page 30; 46pp; French.  
 CC BI8937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX  
 SQ Sequence 82 AA;  
 Query Match 44.7%; Score 189; DB 21; Length 82;  
 Best Local Similarity 53.0%; Pred. No. 1.3e-16;  
 Matches 44; Conservative 11; Mismatches 26; Indels 2; Gaps 2;  
 OY 1 QGRSGCSQISIPMSISVAVDFSGOKSRVIENTEALSVAVEGLAWRKGCRL 60  
 DB 1 QQRKALLSPSTFVRSVNSLVAVDFSGQIGRVINPAEQSALEEGHAWRRS-TRM 59  
 OY 61 GTHGSPASSQSATNMAHRSQ-83  
 DB 60 NILGQSFLHPSTLSTV-IHRTQ 81  
 RESULT 8  
 AAB18946  
 ID AAB18946 standard; peptide; 82 AA.  
 AC AAB18946;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Mus muris.  
 PN WO200055634-A1.  
 XX 21-SEP-2000.  
 XX 14-MAR-2000; 2000WO-FR00613.  
 XX 15-MAR-1999; 99FR-0003159.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 CC Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 XX

PT  
 XX  
 PS  
 CC Claim 2; Page 28; 46pp; French.  
 CC BI8937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
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 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX  
 SQ Sequence 82 AA;  
 Query Match 44.0%; Score 186; DB 21; Length 82;  
 Best Local Similarity 54.1%; Pred. No. 3.2e-16;  
 Matches 46; Conservative 6; Mismatches 23; Indels 10; Gaps 3;  
 OY 3 RGCSCSQISIPMSISVAVDFSGOKSRVIENTEALSVAVEGLAWRKGCRL 62  
 DB 3 RKGLPPFPNAPRSVNSLVAVDFSGQIGRVINPAEQSALEEGHAWR-NGSTRMN- 60  
 OY 63 HGSPASSQS-----SATNMAHRSQ 83  
 DB 61 -----ILSSQSLHPSTLSTV-IHRTQ 81  
 RESULT 9  
 AAB18958  
 ID AAB18958 standard; peptide; 80 AA.  
 AC AAB18958;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Homo sapiens.  
 PN WO200055634-A1.  
 XX 21-SEP-2000.  
 XX 14-MAR-2000; 2000WO-FR00613.  
 XX 15-MAR-1999; 99FR-0003159.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI; 2000-587566/55.  
 CC Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 XX  
 PS Claim 2; Page 34-35; 46pp; French.  
 CC BI8937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
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 CC stimulate or inhibit tyrosine kinase activity of the receptor. The

CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX  
 SQ

Sequence 80 AA;

Query Match 42.3%; Score 179; DB 21; Length 80;

Best Local Similarity 59.2%; Pred. No. 2.5e-15;

Matches 42; Conservative 8; Mismatches 17; Indels 4; Gaps 2;

OY 13 PMRSISNSLVAMDFSGKSRVIENPTEALSVAVEGLAWRKGLTGHSPTASSQS 72

DB 13 PLRSASDNTLVAMDFSGHAGRVENPREALSVALEEAQAWRKKTNRHLSL--PMPASGT 69

OY 73 SATNMAIHRSQ 83

DB 70 S-LSAAIHRQTQ 79

RESULT 10

AAB18949

ID AAB18949 standard; peptide; 43 AA.

XX AC

XX AAB18949;

XX DT

XX 08-FEB-2001 (first entry)

XX DE

XX Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.

XX KW

XX Phosphorylated insulin receptor interacting region; Grb7 family protein;

XX Insulin receptor; tyrosine kinase; insulin; insulin-associated disease;

XX KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.

XX XX

XX Homo sapiens.

XX XX

XX WO200005634-A1.

XX XX

XX 21-SEP-2000.

XX XX

XX 14-MAR-2000; 2000WO-FR00613.

XX PR

XX 15-MAR-1999; 99FR-0003159.

XX XX

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX PA

XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;

XX PI

XX WPI; 2000-587566/55.

XX DR

XX Fragments of Grb family proteins to identify compounds are useful in

XX treating insulin-associated diseases, particularly diabetes and obesity

XX PT

XX -

XX PS

XX Claim 2; Page 30; 46pp; French.

XX XX

XX BI8937-64 represent the PIR (phosphorylated insulin receptor interacting

XX region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.

XX PIR is the actual binding region but its effect is about 10 times

XX greater in presence of SH2 (which by itself is inactive). Agents that

XX affect binding between the peptides and the insulin receptor can

XX stimulate or inhibit tyrosine kinase activity of the receptor. The

XX peptides are used for screening molecules for ability to treat diseases

XX in which insulin is implicated. The peptides are used to identify agents

XX that are potentially useful for treating insulin-associated diseases,

XX particularly diabetes and obesity but also polycystic ovarian syndrome

XX and syndrome X.

XX SQ

Sequence 43 AA;

Query Match

Best Local Similarity 40.0%; Score 169; DB 21; Length 43;

Matches 32; Conservative 7; Indels 0; Gaps 0;

Matches 33; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 13 PMRSISNSLVAMDFSGKSRVIENPTEALSVAVEGLAWRK 55

DB 1 PVRSVSNSLVAMDFSGTGRVIENPFAEQSAALLEGHAWRK 43

RESULT 11

AAB18957

ID AAB18957 standard; peptide; 43 AA.

XX AC

XX AAB18957;

XX DT

XX 08-FEB-2001 (first entry)

XX DE

XX Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.

XX KW Phosphorylated insulin receptor interacting region; Grb7 family protein;

XX Insulin receptor; tyrosine kinase; insulin; insulin-associated disease;

XX KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.

XX OS

XX Homo sapiens.

XX XX

XX WO200005634-A1.

XX XX

XX 21-SEP-2000.

XX XX

XX 14-MAR-2000; 2000WO-FR00613.

XX XX

XX 15-MAR-1999; 99FR-0003159.

XX XX

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX PA

XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;

XX PI

XX WPI; 2000-587566/55.

XX DR

XX Fragments of Grb family proteins to identify compounds are useful in

XX treating insulin-associated diseases, particularly diabetes and obesity

XX PT

XX -

XX PS

XX Claim 2; Page 34; 46pp; French.

XX XX

XX BI8937-64 represent the PIR (phosphorylated insulin receptor interacting

XX region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.

XX PIR is the actual binding region but its effect is about 10 times

XX greater in presence of SH2 (which by itself is inactive). Agents that

XX affect binding between the peptides and the insulin receptor can

XX stimulate or inhibit tyrosine kinase activity of the receptor. The

XX peptides are used for screening molecules for ability to treat diseases

XX in which insulin is implicated. The peptides are used to identify agents

XX that are potentially useful for treating insulin-associated diseases,

XX particularly diabetes and obesity but also polycystic ovarian syndrome

XX and syndrome X.

XX SQ

Sequence 43 AA;

Query Match

Best Local Similarity 38.3%; Score 162; DB 21; Length 43;

Matches 32; Conservative 7; Indels 0; Gaps 0;

OY 13 PMRSISNSLVAMDFSGKSRVIENPTEALSVAVEGLAWRK 55

DB 1 PLRSASDNTLVAMDFSGHAGRVENPREALSVALEEAQAWRK 43

RESULT 12

AAB18945

ID AAB18945 standard; peptide; 43 AA.

XX AC

XX AAB18945;

XX DT

XX 08-FEB-2001 (first entry)

XX DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 XX KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 XX OS Mus muris.  
 XX PN WO200055634-A1.  
 XX PD 21-SEP-2000.  
 XX PF 14-MAR-2000; 2000WO-FR00613.  
 XX PR 15-MAR-1999; 99FR-0003159.  
 XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX DR WPI; 2000-587566/55.  
 XX XX Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 PT  
 XX PS Claim 2; Page 27-28; 46pp; French.  
 XX CC B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX SQ Sequence 43 AA;  
 XX Query Match 38.1%; Score 161; DB 21; Length 43;  
 XX Best Local Similarity 78.0%; Pred. No. 2.2e-13;  
 XX Matches 32; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 13 PMRSISENSLVAMDFSGQKSRVIENPTSEALSVAVEEGLAWR 53  
 DB 1 PMRSISENSLVAMDFSGQIGRVIDNPALAEQSALEBHWAR 41  
 RESULT 13  
 AAB18953  
 ID AAB18953 standard; peptide; 43 AA.  
 AC AAB18953;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 XX Rattus sp.  
 XX OS  
 XX PN WO200055634-A1.  
 XX PD 21-SEP-2000.  
 XX PF 14-MAR-2000; 2000WO-FR00613.

XX PR 15-MAR-1999; 99FR-0003159.  
 XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX DR WPI; 2000-587566/55.  
 XX XX Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 PT  
 XX PS Claim 2; Page 32; 46pp; French.  
 XX CC B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX SQ Sequence 43 AA;  
 XX Query Match 37.6%; Score 159; DB 21; Length 43;  
 XX Best Local Similarity 69.8%; Pred. No. 4e-13;  
 XX Matches 30; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 13 PMRSISENSLVAMDFSGQKSRVIENPTSEALSVAVEEGLAWRKK 55  
 DB 1 PLRSVSNLTVMDFSGHAGRVIDNPALAEQSALEQAWRKK 43  
 RESULT 14  
 AAB18961  
 ID AAB18961 standard; peptide; 43 AA.  
 AC AAB18961;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 XX Mus muris.  
 XX OS  
 XX PN WO200055634-A1.  
 XX PD 21-SEP-2000.  
 XX PF 14-MAR-2000; 2000WO-FR00613.  
 XX PR 15-MAR-1999; 99FR-0003159.  
 XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PI Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX DR WPI; 2000-587566/55.  
 XX XX Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 PT  
 XX PS Claim 2; Page 36; 46pp; French.



Sequence 47 AA;

Query Match	15.5%	Score 65.5;	DB 22;	Length 47;
Best Local Similarity	38.58;	Pred. No. 0.6;		

```

Db      4 DGVPRNPGSLOPPSPGSSDPPTSAOESGTTGAHHTR 42
      :|:| | | | | : | | | | | | | | | |

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RESULT 16  
AA013559  
ID AA013559 standard; Protein: 77 AA.

ID	AA013559 standard; Protein; 77 AA.
XX	
AC	AA013559;
XX	
DT	06-NOV-2001 (first entry)

XX  
DE  
Human polypeptide SEQ ID NO 27451.

XX  
KW  
Human; cytokine; cell proliferation

KW vaccine;  
KW tissue gr

KW nervous system disorders;  
XX

OS Homo sapiens.  
XX

PN WO200164835-A2.  
XX  
XX  
PD 07-SEP-2001.  
XX  
XX  
PD 26-FEB-2001: 2001WO-0504927

XX  
PR 28-FEB-2000;

PR 18-MAY-2000; 2000US-0577409.  
XX

PA (HYSE-) HYSE  
XX

Pi Tang YT, Liu C, Drmanac RT;  
XX

DR WPI; 2001-514838/56.  
DR N-PSDB: AAT93490.

DR N-PSDB; AAI93490.  
XX

PT Isolated nucleic acids and polypeptides, useful for preventing  
PT diagnosing and treating e.g. leukaemia, inflammation and immune

PT disorders -  
XX

PS Claim 20; SEQ ID NO  
XX

The invention relates to the encoded proteins

the encoded proteins (AA000010-AA013910) that exhibit activity cytokine, cell proliferation or cell differentiation or which m production of other cytokines in other cell populations. The polypeptides and polynucleotides are useful for the treatment

peptide therapy. The polypeptides have various cytokine-like activity, e.g. stem cell growth factor activity, haematopoiesis regulating

activity, tissue growth factor activity, immunomodulatory activity and  
 activity/inhibin activity and may be useful in the diagnosis and/or  
 treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 inflammation.

Note: the sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

Query Match 14.48; Score 61; DB 22; Length 77;



Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.	Human sapiens.	WO200164835-A2.	07-SEP-2001.	26-FEB-2001; 2001WO-US04927.	28-FEB-2000; 2000US-0515126.	18-MAY-2000; 2000US-0577409.	(HYSE-) HYSEQ INC.	Tang YT, Liu C, Drmanac RT; WPI; 2001-514838/56. N-FSDS; AAI84507.	Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -	Claim 20: SEQ ID NO 18468; 1399pp + Sequence Listing; English.	The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibitin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	Query Match 13.4%; Score 56.5; DB 22; Length 48; Best Local Similarity 48.4%; Pred.No. 9.1; 12: Indels 1; Caps 1; Matches 13; Conservative 3; Mismatches 12	QY 55 KGCLRLTGCSPTAS-SQSSATNMAIHRSP 84 :                6 QGSELLTSGDPASASQAEITGVSHRTQP 36	Db	RESULT 21 AAU30892 ID AAU30892 standard: Protein; 72 AA.	AAU30892; 18-DEC-2001 (first entry) Novel human secreted protein #1383.	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.	Human sapiens.	WO200179449-A2.
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PD 25-OCT-2001.  
 XX 16-APR-2001; 2001WO-US08656.  
 XX 18-APR-2000; 2000US-0552929.  
 PR 26-JAN-2001; 2001US-0770160.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI; 2001-611725/70.  
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy -  
 XX Claim 20; Page 366; 765pp; English.  
 XX The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising  
 CC the nucleic acids encoding the polypeptides and cells genetically  
 CC engineered to express them are also useful for producing the proteins.  
 CC The proteins are useful in genetic vaccination, testing and  
 CC therapy, and can be used as nutritional supplements. They may be used to  
 CC increase stem cell proliferation; to regulate haematopoiesis; and in  
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;  
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and  
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid  
 CC sequences of novel human secreted proteins of the invention.  
 XX SQ Sequence 72 AA;  
 Query Match 13.2%; Score 56; DB 22; Length 72;  
 Best Local Similarity 27.9%; Pred. No. 19;  
 Matches 17; Conservative 14; Mismatches 16; Indels 14; Gaps 3;  
 OY 8 SQSIPMRISISLVNDFSGKSRV-----TENPEALSV-----VEEGLAWRK 54  
 DB 11 SSSNPLSSXLLNKIPSLPSSWEXWIPPNKNCLSLLNFPSP-SUAPSLDDIKEGLSWKK 69  
 OY 55 K 55  
 DB 70 K 70  
 RESULT 22  
 ID ABG65212 standard; Protein; 79 AA.  
 AC ABG65212;  
 XX 27-AUG-2002 (first entry)  
 DT Human albumin fusion protein #1887.  
 DE Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytostatic; antifertility; antiinflammatory; antiulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neutropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX

PN WO200177137-A1.  
 XX 18-OCT-2001.  
 XX 12-APR-2001; 2001WO-US11988.  
 XX 12-APR-2000; 2000US-229358P.  
 PR 25-APR-2000; 2000US-199384P.  
 PR 21-DEC-2000; 2000US-256931P.  
 XX (HUNA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Haseltine WA;  
 PI WPI; 2002-010886/01.  
 XX New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -  
 XX Claim 1; Page 1828-1829; 2102pp; English.  
 XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X, and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.  
 XX SQ Sequence 79 AA;  
 Query Match 13.2%; Score 56; DB 23; Length 79;  
 Best Local Similarity 39.3%; Pred. No. 22;  
 Matches 11; Conservative 3; Mismatches 14; Indels 0; Gaps 0;  
 OY 57 CLRGLTGHTASSQSSATNMAIHRSP 84  
 DB 45 CLSIGQHELPSYSCPGKRRLPHHSQP 72  
 RESULT 23  
 ID AAU91124 standard; Protein; 79 AA.  
 AC AAU91124;  
 XX 05-JUN-2002 (first entry)  
 DT Human secreted protein sequence #44.  
 DE Human secreted protein; autoimmune disease; hyperproliferative disorder;  
 KW cardiovascular disorder; cerebrovascular disorder; infection; cancer;  
 KW nervous system disorder; ocular disorder; epithelial cell proliferation;  
 KW wound healing; skin aging; sunburn; transplantation; chemotaxis;  
 KW tissue regeneration; food additive; preservative; cytostatic; cardiant;  
 KW antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.  
 XX Homo sapiens.  
 OS WO200218412-A1.  
 XX 07-MAR-2002.  
 PD 17-JAN-2001; 2001WO-US01384.  
 PF 28-AUG-2000; 2000US-228086P.  
 PR

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PR 04-JAN-2001; 2001US-259516P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
PI Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH, Fiscella M;
PI Ni J;
XX WPI; 2002-269525/31.
DR N-PSDB; ABK54162.
XX Seventeen nucleic acid molecules encoding human secreted proteins,
PT useful in the prevention, treatment and diagnosis of cancer, immune
PT disorders, cardiovascular disorders and neurological diseases -
XX
XX Claim 11; Page 478-479; 505pp; English.
XX The present invention relates to the isolation of novel human secreted
CC proteins and the polynucleotide sequences encoding them. The secreted
CC proteins are useful to prevent, treat or ameliorate a medical condition
CC in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or
CC sheep. The secreted proteins are also useful in diagnosing a pathological
CC condition or susceptibility to a pathological condition. Antibodies to
CC the secreted proteins can also be used in alleviating symptoms associated
CC with disorders and in diagnostic immunoassays e.g. radioimmunoassays or
CC enzyme linked immunosorbent assays (ELISA). Disorders which can be
CC diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. cancer, cardiovascular
CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
CC ischaemia, angioneurosis, nervous system disorders e.g. Parkinson's
CC disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting the culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities.
CC AAU91081-AAU91148 represent human secreted protein sequences.
XX
XX Sequence 79 AA;
SQ
Query Match 13.2%; Score 56; DB 23; Length 79;
Best Local Similarity 39.3%; Pred. No. 22;
Matches 11; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 57 CLRIGTSGPTASSQSATNMATHRSQP 84
DB 45 CLSIGQHELPSYSCQGRKLLPHHSQP 72
RESULT 24
AAO00883
ID AAO00883 standard; Protein; 49 AA.
XX
XX AAO00883;
AC
XX 06-NOV-2001 (first entry)
DT
XX Human polypeptide SEQ ID NO 14775.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
OS
XX WO200164835-A2.
PN
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US04927.
PF
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-514838/56.
DR N-PSDB; AAI80814.
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 20; SEQ ID NO 14775; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO1310) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 49 AA;
SQ
Query Match 13.1%; Score 55.5; DB 22; Length 49;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 13; Conservative 8; Mismatches 15; Indels 3; Gaps 1;
QY 48 EGLAWKKGCLRLCTHGS---PTASSQSATNMATHRSQ 83
DB 6 DGVPRNFGSLKPPSGSDPPFISASQECGIGAHHTR 44
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PR 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-514838/56.
DR N-PSDB; AAI80814.
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 20; SEQ ID NO 14775; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO1310) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 49 AA;
SQ
Query Match 13.1%; Score 55.5; DB 22; Length 49;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 13; Conservative 8; Mismatches 15; Indels 3; Gaps 1;
QY 48 EGLAWKKGCLRLCTHGS---PTASSQSATNMATHRSQ 83
DB 6 DGVPRNFGSLKPPSGSDPPFISASQECGIGAHHTR 44
RESULT 25
AAO06915
ID AAO06915 standard; Protein; 73 AA.
XX
XX AAO06915;
AC
XX 06-NOV-2001 (first entry)
DT
XX Human polypeptide SEQ ID NO 20807.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
OS
XX WO200164835-A2.
PN
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US04927.
PF
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-514838/56.
DR
```

DR N-PSDB: AAI86846.  
 XX Isolated nucleic acids and polypeptides, useful for preventing  
 PT diagnosing and treating e.g. leukaemia, inflammation and immune  
 PT disorders -  
 XX  
 PS  
 XX Claim 20: SEQ ID NO 20807; 1399pp + Sequence Listing: English.  
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 73 AA:

Query Match 13.0%; Score 55; DB 22; Length 73;  
 Best Local Similarity 44.4%; Pred. NO. 26;  
 Matches 12; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 58 LRLGTHGSPATASOSSATNMAIHRSP 84  
 ||||| : : : : :  
 Db 23 LRLGLSDPPASASESTGTCMHCSP 49

Search completed: March 28, 2003, 09:05:51  
 Job time : 87.1417 secs

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 09:01:30 ; Search time 35,2126 seconds  
(without alignments)  
251.615 Million cell updates/sec

Title: us-09-936-697-5  
Sequence: 1 PMSISENSILVAMDFSGOKS.....ENPTSEALSVAVEGLAMRKK 43

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 74486

Minimum DB seq length: 40  
Maximum DB seq length: 90

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database: us-09-936-697-5  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_mhc:  
9: sp\_mhc:  
10: sp\_mhc:  
11: sp\_mhc:  
12: sp\_mhc:  
13: sp\_mhc:  
14: sp\_mhc:  
15: sp\_mhc:  
16: sp\_mhc:  
17: sp\_mhc:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45.5	21.5	73	5	P91302 caenorhabdi
2	45	21.2	77	17	O28902 archaeoglob
3	45	21.2	82	17	O27686 methanobact
4	44	20.8	60	17	O8ttk0 methanosarc
5	44	20.8	79	2	O9rcd4 xanthomonas
6	44	20.8	82	5	O9vxc1 drosophila
7	43.5	20.5	69	15	O9wmc6 human immun
8	43.5	20.5	88	10	O9lml1 arabidopsis
9	42.5	20.0	80	3	O9hgr8 chloanthephora
10	42	19.8	53	16	O9pfg5 xyliella fas
11	42	19.8	58	9	O80316 bacterioph
12	42	19.8	76	12	O64944 avian infec
13	42	19.8	76	12	O64947 avian infec
14	42	19.8	79	16	O928x5 chlamydia p
15	42	19.8	79	16	O9jsh8 chlamydia p
16	42	19.8	81	16	O9k247 chlamydia p

P72094 neisseria m  
O40019 hordeum vul  
O41693 vigna radia  
Q9nrp2 homo sapien  
Q9wcl1 xanthomonas  
O8r9d7 thermoanaer  
O8tr24 methanosarc  
O74620 human immun  
O74630 human immun  
Q9wmr4 human immun  
Q9wmc5 human immun  
Q936t5 pseudomonas  
Q98kz6 rhizobium l  
Q9yv28 human immun  
Q97is7 clostridium  
P71998 mycobacteri  
Q02288 coccidioid  
Q9wkh1 encephalomy  
Q9akh7 rickettsia  
Q9kk61 mycobacteri  
Q27193 tetrahymena  
Q9chz4 lactococcus  
Q92em1 listeria in  
Q9l0t9 streptomyce  
Q69533 human immun  
Q9wmr3 human immun  
Q9bz11 homo sapien  
Q9epv8 mus musculu  
Q8yxu8 anabaena sp  
Q9gst4 human immun  
Q9lmm9 arabidopsis  
O22414 oryza sativ  
Q9yv38 human immun  
Q9yv37 human immun  
Q9yv35 human immun  
Q9yv25 human immun  
Q9yv24 human immun  
Q9wa05 human immun  
Q9w8f1 human immun  
Q9yjk2 human immun  
Q9y141 human immun  
Q9w8s7 human immun  
Q9w8s2 human immun  
O18852 macaca radi  
Q96g13 homo sapien  
Q9y775 arabidopsis  
Q9t0n2 arabidopsis  
Q9hll3 homo sapien  
P9120 bos taurus  
Q8yjd3 bruceella me  
Q9ypl4 encephalomy  
Q64948 avian infec  
Q9hzj7 pseudomonas  
Q9k4k2 streptomyce  
Q91726 grapevine r  
Q91903 rupestris s  
Q9phk1 xyliella fas  
Q92854 chlamydia p  
Q9x7n4 streptomyce  
Q8y9v4 listeria mo  
Q8y4m8 listeria mo  
Q74093 human immun  
Q74545 human immun  
O51902 proteus mir  
Q9cw15 mus musculu  
Q9wmt2 human immun  
Q9yiv0 uncultured  
Q90q66 human immun  
Q9yiv9 mus musculu  
Q90x98 meleagris g  
Q9lgw8 oryza sativ  
Q27909 drosophila  
Q92j17 rickettsia

17 42 19.8 90 2 P72094  
18 41.5 19.6 87 10 O40019  
19 41 19.3 69 10 O41693  
20 41 19.3 79 4 Q9nrp2  
21 41 19.3 85 2 Q9wcl1  
22 41 19.3 85 16 O8r9d7  
23 41 19.3 87 17 O8tr24  
24 40.5 19.1 68 15 O74620  
25 40.5 19.1 68 15 O74630  
26 40.5 19.1 69 15 Q9wmr4  
27 40.5 19.1 69 15 Q9wmc5  
28 40.5 19.1 79 2 Q936t5  
29 40.5 19.1 88 16 Q98kz6  
30 40.5 19.1 89 15 Q9yv28  
31 40 18.9 67 16 Q97is7  
32 40 18.9 70 16 P71998  
33 40 18.9 73 3 Q02288  
34 40 18.9 84 12 Q9wkh1  
35 40 18.9 89 2 Q9akh7  
36 39.5 18.6 56 2 Q9kk61  
37 39.5 18.6 58 5 Q27193  
38 39.5 18.6 61 16 Q9chz4  
39 39.5 18.6 67 16 Q92em1  
40 39.5 18.6 67 16 Q9l0t9  
41 39.5 18.6 68 15 Q69533  
42 39.5 18.6 69 15 Q9wmr3  
43 39.5 18.6 73 4 Q9bz11  
44 39.5 18.6 73 11 Q9epv8  
45 39.5 18.6 77 16 O8yxu8  
46 39.5 18.6 80 15 Q9gst4  
47 39.5 18.6 82 10 Q9lmm9  
48 39.5 18.6 89 15 O22414  
49 39.5 18.6 89 15 Q9yv38  
50 39.5 18.6 89 15 Q9yv37  
51 39.5 18.6 89 15 Q9yv35  
52 39.5 18.6 89 15 Q9yv25  
53 39.5 18.6 89 15 Q9yv24  
54 39.5 18.6 89 15 Q9wa05  
55 39.5 18.6 89 15 Q9w8f1  
56 39.5 18.6 89 15 Q9yjk2  
57 39.5 18.6 89 15 Q9y141  
58 39.5 18.6 89 15 Q9w8s7  
59 39.5 18.6 89 15 Q9w8s2  
60 39 18.4 41 6 O18852  
61 39 18.4 52 4 Q96g13  
62 39 18.4 54 10 Q9y775  
63 39 18.4 62 10 Q9t0n2  
64 39 18.4 67 4 Q9hll3  
65 39 18.4 68 6 P9120  
66 39 18.4 72 16 O8yjd3  
67 39 18.4 73 12 Q9ypl4  
68 39 18.4 76 12 Q64948  
69 39 18.4 77 16 Q9hzj7  
70 39 18.4 77 16 Q9k4k2  
71 39 18.4 80 12 Q91726  
72 39 18.4 80 12 Q91903  
73 39 18.4 87 16 Q9phk1  
74 39 18.4 90 16 Q92854  
75 38.5 18.2 67 16 Q9x7n4  
76 38.5 18.2 68 16 Q8y9v4  
77 38.5 18.2 67 16 Q8y4m8  
78 38.5 18.2 68 15 Q74093  
79 38.5 18.2 68 15 Q74545  
80 38.5 18.2 69 2 O51902  
81 38.5 18.2 69 11 Q9cw15  
82 38.5 18.2 69 15 Q9wmt2  
83 38.5 18.2 80 14 Q9yiv0  
84 38.5 18.2 81 15 Q90q66  
85 38.5 18.2 86 11 Q9yiv9  
86 38.5 18.2 87 13 Q90x98  
87 38.5 18.2 89 10 Q9lgw8  
88 38 17.9 53 5 Q27909  
89 38 17.9 64 16 Q92j17

90	38	17.9	67	12	O90745	O90745 encephalomy	163	37.5	17.7	83	16	O9KK50	O9KK50 vibrio chol
91	38	17.9	68	12	O9YRD4	O9YRD4 largemouth	164	37.5	17.7	83	15	O9WFE3	O9WFE3 human immun
92	38	17.9	69	12	O9XXH1	O9XXH1 caenorhabdit	165	37	17.5	53	17	O9EXV5	O9EXV5 sulfolobus
93	38	17.9	70	12	O8VN29	O8VN29 helicobacte	166	37	17.5	59	12	O39817	O39817 encephalomy
94	38	17.9	71	12	O6A946	O6A946 avian infec	167	37	17.5	61	2	O9EVR8	O9EVR8 streptococc
95	38	17.9	72	12	O6A950	O6A950 avian infec	168	37	17.5	63	2	O9RNM8	O9RNM8 camomonas t
96	38	17.9	73	12	O4O808	O4O808 hepatitis c	169	37	17.5	63	2	O9R9T3	O9R9T3 pseudomonas
97	38	17.9	74	12	O4O809	O4O809 hepatitis c	170	37	17.5	66	16	O8ZCR3	O8ZCR3 yersinia pe
98	38	17.9	75	12	O8U014	O8U014 methanopyru	171	37	17.5	72	17	O8Z257	O8Z257 pyrobaculum
99	38	17.9	76	12	O9SR21	O9SR21 streptomyce	172	37	17.5	73	10	O9RLS6	O9RLS6 arabidopsis
100	38	17.9	77	12	O57347	O57347 xenopus lae	173	37	17.5	73	11	O8R4G4	O8R4G4 rattus norv
101	37.5	17.7	78	12	O73724	O73724 human immun	174	37	17.5	73	11	O8RLH0	O8RLH0 mus musculu
102	37.5	17.7	79	12	O73726	O73726 human immun	175	37	17.5	74	12	O9W8B2	O9W8B2 encephalomy
103	37.5	17.7	80	12	O73728	O73728 human immun	176	37	17.5	75	12	O9WK35	O9WK35 encephalomy
104	37.5	17.7	81	12	O73729	O73729 human immun	177	37	17.5	76	12	O6A943	O6A943 avian infec
105	37.5	17.7	82	12	O73731	O73731 human immun	178	37	17.5	80	3	O9HGR5	O9HGR5 mucor pirif
106	37.5	17.7	83	12	O73733	O73733 human immun	179	37	17.5	81	12	O9YPK9	O9YPK9 encephalomy
107	37.5	17.7	84	12	O73763	O73763 human immun	180	37	17.5	81	12	O9W8J1	O9W8J1 encephalomy
108	37.5	17.7	85	12	O73765	O73765 human immun	181	37	17.5	83	12	O9YPK3	O9YPK3 porcine enc
109	37.5	17.7	86	12	O73767	O73767 human immun	182	37	17.5	83	12	O9YPL3	O9YPL3 encephalomy
110	37.5	17.7	87	12	O73769	O73769 human immun	183	37	17.5	83	12	O9WK36	O9WK36 encephalomy
111	37.5	17.7	88	12	O73771	O73771 human immun	184	37	17.5	86	11	O9JIK6	O9JIK6 mus musculu
112	37.5	17.7	89	12	O73773	O73773 human immun	185	37	17.5	88	16	O9PF17	O9PF17 xylella fas
113	37.5	17.7	90	12	O73811	O73811 human immun	186	37	17.5	88	16	O8RA79	O8RA79 thermoanaer
114	37.5	17.7	91	12	O73813	O73813 human immun	187	37	17.5	89	2	O9AQL6	O9AQL6 pseudomonas
115	37.5	17.7	92	12	O73815	O73815 human immun	188	37	17.5	89	16	O9K781	O9K781 bacillus ha
116	37.5	17.7	93	12	O73817	O73817 human immun	189	37	17.5	90	10	O9H8Y8	O9H8Y8 rhizobium l
117	37.5	17.7	94	12	O73827	O73827 human immun	190	37	17.5	90	10	O9KH05	O9KH05 ipomoea bat
118	37.5	17.7	95	12	O43656	O43656 homo sapien	191	36.5	17.2	53	10	O9XGU2	O9XGU2 arabidopsis
119	37.5	17.7	96	12	O90584	O90584 human immun	192	36.5	17.2	53	10	O9XGU2	O9XGU2 arabidopsis
120	37.5	17.7	97	12	O910X3	O910X3 streptomyce	193	36.5	17.2	53	10	O9XGU2	O9XGU2 arabidopsis
121	37.5	17.7	98	12	O80094	O80094 staphylococ	194	36.5	17.2	53	10	O9WMO0	O9WMO0 human immun
122	37.5	17.7	99	12	O80617	O80617 human immun	195	36.5	17.2	72	10	O93258	O93258 arabidopsis
123	37.5	17.7	100	12	O89619	O89619 human immun	196	36.5	17.2	72	10	O93258	O93258 arabidopsis
124	37.5	17.7	101	12	O89619	O89619 human immun	197	36.5	17.2	76	2	O8VN31	O8VN31 helicobacte
125	37.5	17.7	102	12	O74091	O74091 human immun	198	36.5	17.2	80	3	O9HGR0	O9HGR0 poitrasiac c
126	37.5	17.7	103	12	O74249	O74249 human immun	199	36.5	17.2	80	3	O96090	O96090 neurospora
127	37.5	17.7	104	12	O74256	O74256 human immun	200	36.5	17.2	80	15	O905E6	O905E6 human immun
128	37.5	17.7	105	12	O74258	O74258 human immun	201	36.5	17.2	80	15	O905E6	O905E6 human immun
129	37.5	17.7	106	12	O74258	O74258 human immun	202	36.5	17.2	81	15	O91893	O91893 human immun
130	37.5	17.7	107	12	O74289	O74289 human immun	203	36.5	17.2	81	15	O905E4	O905E4 human immun
131	37.5	17.7	108	12	O74296	O74296 human immun	204	36.5	17.2	81	15	O982V4	O982V4 human immun
132	37.5	17.7	109	12	O74298	O74298 human immun	205	36.5	17.2	81	15	O8UPP8	O8UPP8 human immun
133	37.5	17.7	110	12	O74298	O74298 human immun	206	36.5	17.2	81	15	O8UPP8	O8UPP8 human immun
134	37.5	17.7	111	12	O74103	O74103 human immun	207	36.5	17.2	81	15	O8UPM1	O8UPM1 human immun
135	37.5	17.7	112	12	O74245	O74245 human immun	208	36.5	17.2	81	15	O8UPM2	O8UPM2 human immun
136	37.5	17.7	113	12	O74294	O74294 human immun	209	36.5	17.2	81	15	O8UNM0	O8UNM0 human immun
137	37.5	17.7	114	12	O74247	O74247 human immun	210	36.5	17.2	84	9	O9W6P6	O9W6P6 bacterioph
138	37.5	17.7	115	12	O74616	O74616 human immun	211	36.5	17.2	84	17	O29898	O29898 archaeoglob
139	37.5	17.7	116	12	O74618	O74618 human immun	212	36.5	17.2	86	15	O90V10	O90V10 human immun
140	37.5	17.7	117	12	O74632	O74632 human immun	213	36.5	17.2	87	15	O9FL25	O9FL25 bacillus ci
141	37.5	17.7	118	12	O74632	O74632 human immun	214	36.5	17.2	87	16	O9AA08	O9AA08 caulobacter
142	37.5	17.7	119	12	O74640	O74640 human immun	215	36.5	17.2	87	2	O52972	O52972 rhizobium m
143	37.5	17.7	120	12	O74647	O74647 human immun	216	36.5	17.2	89	15	O9YV34	O9YV34 human immun
144	37.5	17.7	121	12	O74649	O74649 human immun	217	36.5	17.2	89	15	O9YV34	O9YV34 human immun
145	37.5	17.7	122	12	O74670	O74670 human immun	218	36.5	17.2	89	15	O9YV33	O9YV33 human immun
146	37.5	17.7	123	12	O59647	O59647 human immun	219	36.5	17.2	89	15	O9YV32	O9YV32 human immun
147	37.5	17.7	124	12	O74672	O74672 human immun	220	36.5	17.2	89	15	O9YV31	O9YV31 human immun
148	37.5	17.7	125	12	O74259	O74259 human immun	221	36.5	17.2	89	15	O9YV29	O9YV29 human immun
149	37.5	17.7	126	12	O74261	O74261 human immun	222	36.5	17.2	89	15	O9YV26	O9YV26 human immun
150	37.5	17.7	127	12	O74263	O74263 human immun	223	36.5	17.2	89	15	O9WA13	O9WA13 human immun
151	37.5	17.7	128	12	O74265	O74265 human immun	224	36	17.0	89	16	O9A015	O9A015 streptococc
152	37.5	17.7	129	12	O74267	O74267 human immun	225	36	17.0	89	16	O9M3T0	O9M3T0 betula verr
153	37.5	17.7	130	12	O74269	O74269 human immun	226	36	17.0	55	12	O96728	O96728 equid herpe
154	37.5	17.7	131	12	O74271	O74271 human immun	227	36	17.0	56	17	O9YCB1	O9YCB1 aeropyrum p
155	37.5	17.7	132	12	O9WU02	O9WU02 human immun	228	36	17.0	63	2	O9Z431	O9Z431 pseudomonas
156	37.5	17.7	133	12	O9WMT1	O9WMT1 human immun	229	36	17.0	65	16	O92XZ8	O92XZ8 rhizobium m
157	37.5	17.7	134	12	O9WMT1	O9WMT1 human immun	230	36	17.0	67	6	O9MZQ6	O9MZQ6 cryptotolagu
158	37.5	17.7	135	12	O9WMT1	O9WMT1 human immun	231	36	17.0	67	4	O9MD78	O9MD78 homo sapien
159	37.5	17.7	136	12	O9WFE1	O9WFE1 human immun	232	36	17.0	69	16	O98JL2	O98JL2 rhizobium l
160	37.5	17.7	137	12	O9L2P5	O9L2P5 arabidopsis	233	36	17.0	71	10	O22336	O22336 stellaria l
161	37.5	17.7	138	12	O9IF12	O9IF12 human immun	234	36	17.0	71	12	O9WK37	O9WK37 encephalomy
162	37.5	17.7	139	12	O95P56	O95P56 leishmania	235	36	17.0	71	12	O91ET4	O91ET4 cydia pomon
					O905F4	O905F4 human immun						O99SP6	O99SP6 staphylococ





382	34	16.0	51	15	073751	073751 human immun	455	34	16.0	84	16	098N19	098n19 rhizobium l
383	34	16.0	51	15	073752	073752 human immun	456	34	16.0	84	16	08XP02	08xp02 raistonia s
384	34	16.0	51	15	073753	073753 human immun	457	34	16.0	85	11	08VDG4	08vdg4 mus musculus
385	34	16.0	51	15	073754	073754 human immun	458	34	16.0	85	16	08XSR8	08xsr8 raistonia s
386	34	16.0	51	15	073755	073755 human immun	459	34	16.0	87	15	08Q663	08q663 human immun
387	34	16.0	51	15	073756	073756 human immun	460	34	16.0	87	17	097X20	097x20 sulfobolus
388	34	16.0	51	15	073757	073757 human immun	461	34	16.0	88	2	09S0R9	09s0r9 streptococc
389	34	16.0	51	15	073758	073758 human immun	462	34	16.0	88	17	026775	026775 methanobact
390	34	16.0	51	15	073759	073759 human immun	463	34	16.0	90	2	093DU8	093du8 unidentified
391	34	16.0	51	15	073760	073760 human immun	464	34	16.0	90	4	09H4J2	09h4j2 homo sapien
392	34	16.0	51	15	073761	073761 human immun	465	34	16.0	90	12	091U88	091u88 grapevine l
393	34	16.0	51	15	073762	073762 human immun	466	34	16.0	90	17	09H0T6	09h0t6 halobacteri
394	34	16.0	51	15	073763	073763 human immun	467	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
395	34	16.0	51	15	073764	073764 human immun	468	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
396	34	16.0	51	15	073765	073765 human immun	469	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
397	34	16.0	51	15	073766	073766 human immun	470	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
398	34	16.0	51	15	073767	073767 human immun	471	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
399	34	16.0	51	15	073768	073768 human immun	472	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
400	34	16.0	51	15	073769	073769 human immun	473	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
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402	34	16.0	51	15	073771	073771 human immun	475	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
403	34	16.0	51	15	073772	073772 human immun	476	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
404	34	16.0	51	15	073773	073773 human immun	477	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
405	34	16.0	51	15	073774	073774 human immun	478	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
406	34	16.0	51	15	073775	073775 human immun	479	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
407	34	16.0	51	15	073776	073776 human immun	480	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
408	34	16.0	51	15	073777	073777 human immun	481	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
409	34	16.0	51	15	073778	073778 human immun	482	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
410	34	16.0	51	15	073779	073779 human immun	483	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
411	34	16.0	51	15	073780	073780 human immun	484	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
412	34	16.0	51	15	073781	073781 human immun	485	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
413	34	16.0	51	15	073782	073782 human immun	486	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
414	34	16.0	51	15	073783	073783 human immun	487	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
415	34	16.0	51	15	073784	073784 human immun	488	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
416	34	16.0	51	15	073785	073785 human immun	489	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
417	34	16.0	51	15	073786	073786 human immun	490	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
418	34	16.0	51	15	073787	073787 human immun	491	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
419	34	16.0	51	15	073788	073788 human immun	492	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
420	34	16.0	51	15	073789	073789 human immun	493	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
421	34	16.0	51	15	073790	073790 human immun	494	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
422	34	16.0	51	15	073791	073791 human immun	495	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
423	34	16.0	51	15	073792	073792 human immun	496	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
424	34	16.0	51	15	073793	073793 human immun	497	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
425	34	16.0	51	15	073794	073794 human immun	498	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
426	34	16.0	51	15	073795	073795 human immun	499	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
427	34	16.0	51	15	073796	073796 human immun	500	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
428	34	16.0	51	15	073797	073797 human immun	501	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
429	34	16.0	51	15	073798	073798 human immun	502	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
430	34	16.0	51	15	073799	073799 human immun	503	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
431	34	16.0	51	15	073800	073800 human immun	504	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
432	34	16.0	51	15	073801	073801 human immun	505	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
433	34	16.0	51	15	073802	073802 human immun	506	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
434	34	16.0	51	15	073803	073803 human immun	507	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
435	34	16.0	51	15	073804	073804 human immun	508	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
436	34	16.0	51	15	073805	073805 human immun	509	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
437	34	16.0	51	15	073806	073806 human immun	510	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
438	34	16.0	51	15	073807	073807 human immun	511	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
439	34	16.0	51	15	073808	073808 human immun	512	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
440	34	16.0	51	15	073809	073809 human immun	513	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
441	34	16.0	51	15	073810	073810 human immun	514	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
442	34	16.0	51	15	073811	073811 human immun	515	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
443	34	16.0	51	15	073812	073812 human immun	516	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
444	34	16.0	51	15	073813	073813 human immun	517	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
445	34	16.0	51	15	073814	073814 human immun	518	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
446	34	16.0	51	15	073815	073815 human immun	519	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
447	34	16.0	51	15	073816	073816 human immun	520	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
448	34	16.0	51	15	073817	073817 human immun	521	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
449	34	16.0	51	15	073818	073818 human immun	522	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
450	34	16.0	51	15	073819	073819 human immun	523	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
451	34	16.0	51	15	073820	073820 human immun	524	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
452	34	16.0	51	15	073821	073821 human immun	525	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
453	34	16.0	51	15	073822	073822 human immun	526	34	16.0	90	17	08ZU13	08zu13 pyrobaculum
454	34	16.0	51	15	073823	073823 human immun	527	34	16.0	90	17	08ZU13	08zu13 pyrobaculum

528	33.5	15.8	86	15	Q994R6	Q994r6 human immun	601	33	15.6	66	12	Q8QIW5	Q8QIW5 hepatitis c
529	33.5	15.8	86	15	Q994K6	Q994k6 human immun	602	33	15.6	66	12	Q8QIW4	Q8QIW4 hepatitis c
530	33.5	15.8	86	15	Q91V98	Q91V98 human immun	603	33	15.6	66	12	Q8QIW3	Q8QIW3 hepatitis c
531	33.5	15.8	86	15	Q90VG8	Q90VG8 human immun	604	33	15.6	66	12	Q8QIW2	Q8QIW2 hepatitis c
532	33.5	15.8	86	15	Q8UTM7	Q8UTM7 human immun	605	33	15.6	66	12	Q8QIW1	Q8QIW1 hepatitis c
533	33.5	15.8	86	15	Q8UTF5	Q8UTF5 human immun	606	33	15.6	66	12	Q8QIV9	Q8QIV9 hepatitis c
534	33.5	15.8	87	17	Q8ZUG3	Q8ZUG3 pyrobaculum	607	33	15.6	66	12	Q8QIV8	Q8QIV8 hepatitis c
535	33.5	15.8	88	9	Q9GXI1	Q9GXI1 caenorhabdi	608	33	15.6	66	12	Q8QIV7	Q8QIV7 hepatitis c
536	33.5	15.8	88	9	Q9B065	Q9B065 mycobacteri	609	33	15.6	66	12	Q8QIV6	Q8QIV6 hepatitis c
537	33.5	15.8	88	17	Q8U180	Q8U180 pyrococcus	610	33	15.6	66	12	Q8QIV5	Q8QIV5 hepatitis c
538	33.5	15.8	90	15	Q90V14	Q90V14 human immun	611	33	15.6	66	12	Q8QIV4	Q8QIV4 hepatitis c
539	33	15.6	41	12	Q8QNS8	Q8QNS8 cotton leaf	612	33	15.6	66	12	Q8QIV3	Q8QIV3 hepatitis c
540	33	15.6	44	12	Q8QY08	Q8QY08 streptococc	613	33	15.6	66	12	Q8QIV2	Q8QIV2 hepatitis c
541	33	15.6	45	12	Q8QY17	Q8QY17 hepatitis c	614	33	15.6	66	12	Q8QIV0	Q8QIV0 hepatitis c
542	33	15.6	47	16	Q8FL22	Q8FL22 salmonella	615	33	15.6	66	12	Q8QI09	Q8QI09 hepatitis c
543	33	15.6	49	16	Q8VJ10	Q8VJ10 mycobacteri	616	33	15.6	66	12	Q8QI08	Q8QI08 hepatitis c
544	33	15.6	50	10	Q8S4Y4	Q8S4Y4 zea mays (m	617	33	15.6	66	12	Q8QI06	Q8QI06 hepatitis c
545	33	15.6	51	3	Q9HGX8	Q9HGX8 arthroderma	618	33	15.6	66	12	Q8QI01	Q8QI01 hepatitis c
546	33	15.6	54	2	Q32688	Q32688 helicobacte	619	33	15.6	66	12	Q8QI00	Q8QI00 hepatitis c
547	33	15.6	54	8	Q9MDP2	Q9MDP2 puma concol	620	33	15.6	66	12	Q8QI99	Q8QI99 hepatitis c
548	33	15.6	54	8	Q9MG35	Q9MG35 acinonyx ju	621	33	15.6	66	12	Q8QI98	Q8QI98 hepatitis c
549	33	15.6	54	8	Q9MG31	Q9MG31 puma concol	622	33	15.6	66	12	Q8QI90	Q8QI90 hepatitis c
550	33	15.6	54	8	Q9MG30	Q9MG30 puma concol	623	33	15.6	67	4	Q9UDF8	Q9UDF8 homo sapien
551	33	15.6	55	12	Q9WPG9	Q9WPG9 zebra herpe	624	33	15.6	67	13	Q42599	Q42599 xenopus lae
552	33	15.6	55	12	Q8V0G5	Q8V0G5 asinine her	625	33	15.6	67	16	Q8UJ23	Q8UJ23 agrobacteri
553	33	15.6	55	12	Q8V0G4	Q8V0G4 asinine her	626	33	15.6	68	12	Q65022	Q65022 aleutian m
554	33	15.6	55	12	Q8V0G3	Q8V0G3 asinine her	627	33	15.6	69	12	Q8QWD8	Q8QWD8 human echov
555	33	15.6	56	12	Q9WPH2	Q9WPH2 equine herp	628	33	15.6	71	9	Q8VSE9	Q8VSE9 shigella fl
556	33	15.6	56	12	Q8V0G1	Q8V0G1 asinine her	629	33	15.6	71	9	Q8QI46	Q8QI46 bacterioph
557	33	15.6	56	12	Q8V0G0	Q8V0G0 asinine her	630	33	15.6	71	16	Q8ZKD0	Q8ZKD0 salmonella
558	33	15.6	56	12	Q8V0F9	Q8V0F9 asinine her	631	33	15.6	72	2	Q07693	Q07693 mycobacteri
559	33	15.6	56	12	Q9RFW6	Q9RFW6 asinine her	632	33	15.6	72	2	Q8X0V0	Q8X0V0 neurospora
560	33	15.6	56	12	Q9RFW6	Q9RFW6 streptococc	633	33	15.6	72	16	Q8XU54	Q8XU54 raietonia s
561	33	15.6	57	12	Q9WPH0	Q9WPH0 wild ass he	634	33	15.6	72	16	Q8XU54	Q8XU54 raietonia s
562	33	15.6	58	9	Q9MCF3	Q9MCF3 bacterioph	635	33	15.6	73	2	Q99Q03	Q99Q03 corynebacte
563	33	15.6	58	11	Q91ZM0	Q91ZM0 mus musculu	636	33	15.6	73	10	Q9ZV16	Q9ZV16 arabidopsis
564	33	15.6	58	17	Q9RMU2	Q9RMU2 halobacteri	637	33	15.6	73	17	Q8UJ23	Q8UJ23 pyrococcus
565	33	15.6	59	12	Q8QI40	Q8QI40 sulfolobus	638	33	15.6	76	5	Q95XA1	Q95XA1 caenorhabdi
566	33	15.6	59	16	Q8Y0U0	Q8Y0U0 anabaena sp	639	33	15.6	76	15	Q99IR9	Q99IR9 human immun
567	33	15.6	60	16	Q9RJE2	Q9RJE2 streptomyce	640	33	15.6	76	15	Q99IR8	Q99IR8 human immun
568	33	15.6	60	2	Q9Z383	Q9Z383 escherichia	641	33	15.6	77	9	Q15810	Q15810 homo sapien
569	33	15.6	60	4	Q14546	Q14546 homo sapien	642	33	15.6	77	9	Q38381	Q38381 bacterioph
570	33	15.6	61	9	Q48431	Q48431 lactobacill	643	33	15.6	78	2	Q9F755	Q9F755 uncultured
571	33	15.6	62	15	Q12081	Q12081 caprine art	644	33	15.6	78	16	Q92P82	Q92P82 rhizobium m
572	33	15.6	62	15	Q12083	Q12083 caprine art	645	33	15.6	78	17	Q972N2	Q972N2 sulfolobus
573	33	15.6	62	15	Q12085	Q12085 caprine art	646	33	15.6	79	4	Q12938	Q12938 homo sapien
574	33	15.6	62	15	Q12087	Q12087 caprine art	647	33	15.6	79	12	Q9YPL7	Q9YPL7 encephalomy
575	33	15.6	62	15	Q12091	Q12091 caprine art	648	33	15.6	79	16	Q9RTC5	Q9RTC5 deinococcus
576	33	15.6	62	15	Q12115	Q12115 caprine art	649	33	15.6	79	16	Q9EXU7	Q9EXU7 rhizobium m
577	33	15.6	62	15	Q12117	Q12117 caprine art	650	33	15.6	79	17	Q8TTP8	Q8TTP8 methanosarc
578	33	15.6	62	15	Q12119	Q12119 caprine art	651	33	15.6	80	9	Q64261	Q64261 mycobacteri
579	33	15.6	63	17	Q9ZU22	Q9ZU22 pyrobaculum	652	33	15.6	80	16	Q8XBA0	Q8XBA0 escherichia
580	33	15.6	64	17	Q91960	Q91960 gallus gall	653	33	15.6	81	5	Q8S846	Q8S846 encephalito
581	33	15.6	66	12	Q91JH7	Q91JH7 hepatitis c	654	33	15.6	81	7	Q15683	Q15683 homo sapien
582	33	15.6	66	12	Q91JH4	Q91JH4 hepatitis c	655	33	15.6	81	15	Q982V3	Q982V3 human immun
583	33	15.6	66	12	Q91JF9	Q91JF9 hepatitis c	656	33	15.6	81	12	Q9YPL6	Q9YPL6 encephalomy
584	33	15.6	66	12	Q91JF6	Q91JF6 hepatitis c	657	33	15.6	84	2	Q9SLK6	Q9SLK6 streptococc
585	33	15.6	66	12	Q91JF4	Q91JF4 hepatitis c	658	33	15.6	84	16	P96913	P96913 mycobacteri
586	33	15.6	66	12	Q91DD3	Q91DD3 hepatitis c	659	33	15.6	85	13	Q9PUB9	Q9PUB9 astyanax fa
587	33	15.6	66	12	Q91DD2	Q91DD2 hepatitis c	660	33	15.6	87	5	Q9NM36	Q9NM36 leishmania
588	33	15.6	66	12	Q91DC0	Q91DC0 hepatitis c	661	33	15.6	87	12	Q65025	Q65025 aleutian m
589	33	15.6	66	12	Q91DB8	Q91DB8 hepatitis c	662	33	15.6	87	16	Q93GR2	Q93GR2 salmonella
590	33	15.6	66	12	Q8QI22	Q8QI22 hepatitis c	663	33	15.6	88	2	Q91U00	Q91U00 rhizobium m
591	33	15.6	66	12	Q8QI15	Q8QI15 hepatitis c	664	33	15.6	88	12	Q914K3	Q914K3 sulfolobus
592	33	15.6	66	12	Q8QI14	Q8QI14 hepatitis c	665	33	15.6	88	16	Q982D4	Q982D4 rhizobium l
593	33	15.6	66	12	Q8QI13	Q8QI13 hepatitis c	666	33	15.6	89	2	Q8YRE7	Q8YRE7 anabaena sp
594	33	15.6	66	12	Q8QI12	Q8QI12 hepatitis c	667	33	15.6	89	15	Q74886	Q74886 agrobacteri
595	33	15.6	66	12	Q8QI11	Q8QI11 hepatitis c	668	33	15.6	89	15	Q74887	Q74886 human immun
596	33	15.6	66	12	Q8QI10	Q8QI10 hepatitis c	669	33	15.6	90	2	Q45787	Q45787 bacillus th
597	33	15.6	66	12	Q8QI09	Q8QI09 hepatitis c	670	32.5	15.3	46	16	Q9CHS4	Q9CHS4 lactococcus
598	33	15.6	66	12	Q8QI08	Q8QI08 hepatitis c	671	32.5	15.3	57	8	Q94YF5	Q94YF5 pollicipes
599	33	15.6	66	12	Q8QI07	Q8QI07 hepatitis c	672	32.5	15.3	58	8	Q94ZH2	Q94ZH2 chthamalus
600	33	15.6	66	12	Q8QI06	Q8QI06 hepatitis c	673	32.5	15.3	58	8	Q94ZF2	Q94ZF2 chthamalus

674	32.5	15.3	60	6	062782	062782 isocodon mac	747	32.5	15.3	81	15	Q905G6	Q905g6 human immun
675	32.5	15.3	62	2	066909	066909 frankia sp.	748	32.5	15.3	81	15	Q905G2	Q905g2 human immun
676	32.5	15.3	63	16	Q9J027	Q9J027 neisseria m	749	32.5	15.3	81	15	Q71877	Q71877 human immun
677	32.5	15.3	64	9	064169	064169 bacterioph	750	32.5	15.3	81	15	Q71883	Q71883 human immun
678	32.5	15.3	64	16	082574	082574 anabaena sp	751	32.5	15.3	81	15	Q71893	Q71893 human immun
679	32.5	15.3	64	16	08Y0U5	08Y0U5 anabaena sp	752	32.5	15.3	81	15	Q71976	Q71976 human immun
680	32.5	15.3	64	16	Q31879	Q31879 bacillus su	753	32.5	15.3	81	15	Q71982	Q71982 human immun
681	32.5	15.3	65	2	Q35713	Q35713 streptomyce	754	32.5	15.3	81	15	Q79302	Q79302 human immun
682	32.5	15.3	65	6	Q9TSA2	Q9TSA2 sus scrofa	755	32.5	15.3	81	15	Q8G721	Q8G721 human immun
683	32.5	15.3	66	12	06Q011	06Q011 hepatitis c	756	32.5	15.3	82	6	002782	002782 bubalus bub
684	32.5	15.3	67	16	Q92168	Q92168 rickettsia	757	32.5	15.3	82	15	Q9W177	Q9W177 human immun
685	32.5	15.3	68	15	Q74285	Q74285 human immun	758	32.5	15.3	82	16	Q8VJ56	Q8VJ56 mycobacteri
686	32.5	15.3	69	12	Q8O8G3	Q8O8G3 human coxsa	759	32.5	15.3	82	16	Q25501	Q25501 helicobacte
687	32.5	15.3	69	12	Q8QWQ0	Q8QWQ0 human coxsa	760	32.5	15.3	84	10	Q9FGV6	Q9FGV6 arabidopsi
688	32.5	15.3	69	15	Q9WMT9	Q9WMT9 human immun	761	32.5	15.3	84	15	Q90CH4	Q90CH4 human immun
689	32.5	15.3	69	15	Q9WMT6	Q9WMT6 human immun	762	32.5	15.3	85	6	Q95MA6	Q95MA6 equus cabal
690	32.5	15.3	69	15	Q9WMT5	Q9WMT5 human immun	763	32.5	15.3	85	12	Q99DR0	Q99DR0 chilli leaf
691	32.5	15.3	69	15	Q9WMT8	Q9WMT8 human immun	764	32.5	15.3	85	16	Q9L5F4	Q9L5F4 salmonella
692	32.5	15.3	69	15	Q9WMT7	Q9WMT7 human immun	765	32.5	15.3	86	15	Q90D25	Q90D25 human immun
693	32.5	15.3	69	15	Q9WMT8	Q9WMT8 human immun	766	32.5	15.3	87	16	P73973	P73973 synochocyst
694	32.5	15.3	69	15	Q9WMT9	Q9WMT9 human immun	767	32.5	15.3	88	2	Q86876	Q86876 bacillus me
695	32.5	15.3	69	15	Q9WMT8	Q9WMT8 human immun	768	32.5	15.3	88	2	Q8RJP9	Q8RJP9 xanthomonas
696	32.5	15.3	69	15	Q9WMT9	Q9WMT9 human immun	769	32.5	15.3	89	12	Q89852	Q89852 budgerigar
697	32.5	15.3	69	15	Q9WMT9	Q9WMT9 human immun	770	32.5	15.3	89	15	Q9W9P8	Q9W9P8 human immun
698	32.5	15.3	69	15	Q9WMT9	Q9WMT9 human immun	771	32.5	15.3	89	16	Q50462	Q50462 mycobacteri
699	32.5	15.3	69	16	Q9WMT9	Q9WMT9 human immun	772	32.5	15.3	89	16	Q911T3	Q911T3 pseudomonas
700	32.5	15.3	72	2	Q3N80	Q3N80 thermotoga	773	32.5	15.3	90	11	P70443	P70443 mus musculu
701	32.5	15.3	73	16	Q9KAK6	Q9KAK6 bacillus ha	774	32.5	15.3	90	16	P82253	P82253 salmonella
702	32.5	15.3	75	16	Q9JY21	Q9JY21 neisseria m	775	32.5	15.3	91	17	Q9H035	Q9H035 halobacteri
703	32.5	15.3	75	16	Q49558	Q49558 mycobacteri	776	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
704	32.5	15.3	76	2	Q9VN34	Q9VN34 helicobacte	777	32.5	15.3	91	2	P95771	P95771 staphylococ
705	32.5	15.3	76	17	Q96283	Q96283 sulfolobus	778	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
706	32.5	15.3	77	6	Q8G895	Q8G895 atthobacte	779	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
707	32.5	15.3	77	6	Q8G895	Q8G895 atthobacte	780	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
708	32.5	15.3	77	17	Q97P99	Q97P99 sulfolobus	781	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
709	32.5	15.3	78	15	Q93AN2	Q93AN2 human immun	782	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
710	32.5	15.3	78	15	Q93AN1	Q93AN1 human immun	783	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
711	32.5	15.3	81	15	Q91V01	Q91V01 human immun	784	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
712	32.5	15.3	81	15	Q91V01	Q91V01 human immun	785	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
713	32.5	15.3	81	15	Q91V01	Q91V01 human immun	786	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
714	32.5	15.3	81	15	Q91V01	Q91V01 human immun	787	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
715	32.5	15.3	81	15	Q91V01	Q91V01 human immun	788	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
716	32.5	15.3	81	15	Q91V01	Q91V01 human immun	789	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
717	32.5	15.3	81	15	Q91V01	Q91V01 human immun	790	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
718	32.5	15.3	81	15	Q91V01	Q91V01 human immun	791	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
719	32.5	15.3	81	15	Q91V01	Q91V01 human immun	792	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
720	32.5	15.3	81	15	Q91V01	Q91V01 human immun	793	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
721	32.5	15.3	81	15	Q91V01	Q91V01 human immun	794	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
722	32.5	15.3	81	15	Q91V01	Q91V01 human immun	795	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
723	32.5	15.3	81	15	Q91V01	Q91V01 human immun	796	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
724	32.5	15.3	81	15	Q91V01	Q91V01 human immun	797	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
725	32.5	15.3	81	15	Q91V01	Q91V01 human immun	798	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
726	32.5	15.3	81	15	Q91V01	Q91V01 human immun	799	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
727	32.5	15.3	81	15	Q91V01	Q91V01 human immun	800	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
728	32.5	15.3	81	15	Q91V01	Q91V01 human immun	801	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
729	32.5	15.3	81	15	Q91V01	Q91V01 human immun	802	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
730	32.5	15.3	81	15	Q91V01	Q91V01 human immun	803	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
731	32.5	15.3	81	15	Q91V01	Q91V01 human immun	804	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
732	32.5	15.3	81	15	Q91V01	Q91V01 human immun	805	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
733	32.5	15.3	81	15	Q91V01	Q91V01 human immun	806	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
734	32.5	15.3	81	15	Q91V01	Q91V01 human immun	807	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
735	32.5	15.3	81	15	Q91V01	Q91V01 human immun	808	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
736	32.5	15.3	81	15	Q91V01	Q91V01 human immun	809	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
737	32.5	15.3	81	15	Q91V01	Q91V01 human immun	810	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
738	32.5	15.3	81	15	Q91V01	Q91V01 human immun	811	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
739	32.5	15.3	81	15	Q91V01	Q91V01 human immun	812	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
740	32.5	15.3	81	15	Q91V01	Q91V01 human immun	813	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
741	32.5	15.3	81	15	Q91V01	Q91V01 human immun	814	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
742	32.5	15.3	81	15	Q91V01	Q91V01 human immun	815	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
743	32.5	15.3	81	15	Q91V01	Q91V01 human immun	816	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
744	32.5	15.3	81	15	Q91V01	Q91V01 human immun	817	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
745	32.5	15.3	81	15	Q91V01	Q91V01 human immun	818	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri
746	32.5	15.3	81	15	Q91V01	Q91V01 human immun	819	32.5	15.3	91	2	Q9K521	Q9K521 mycobacteri

820	32	15.1	66	16	Q92J00	Q92100 rickettsia	893	32	15.1	89	10	Q8W119	Q8W119 solanum pin
821	32	15.1	68	12	Q8QMS7	Q8QMS7 cowpox viru	894	32	15.1	89	10	Q8W118	Q8W118 solanum pin
822	32	15.1	69	12	Q92E72	Q92E72 listeria in	895	32	15.1	89	11	Q8VCL5	Q8VCL5 mus musculus
823	32	15.1	69	16	Q8Y9F0	Q8Y9F0 listeria mo	896	32	15.1	89	16	Q8FC08	Q8FC08 streptomyce
824	32	15.1	69	16	Q8XZG3	Q8XZG3 rickettsia	897	32	15.1	90	9	Q8SBL2	Q8SBL2 bacterioph
825	32	15.1	71	2	Q8S924	Q8S924 sphingomon	898	32	15.1	90	12	Q9J721	Q9J721 pariacoto v
826	32	15.1	71	10	Q8YAT6	Q8YAT6 vigna ungui	899	32	15.1	90	12	Q912S1	Q912S1 cowpox viru
827	32	15.1	72	16	Q8VJA7	Q8VJA7 mycobacteri	900	32	15.1	90	15	Q901K8	Q901K8 human immun
828	32	15.1	72	2	Q8AN03	Q8AN03 bradyrhizob	901	32	15.1	90	16	Q8ZAT5	Q8ZAT5 versinia pe
829	32	15.1	72	6	Q8I888	Q8I888 streptococ	902	32	15.1	90	17	Q97AF2	Q97AF2 sulfolobus
830	32	15.1	72	16	Q8CEP3	Q8CEP3 lactococcus	903	31.5	14.9	47	2	Q934J1	Q934J1 carnobacter
831	32	15.1	72	16	Q8CEY3	Q8CEY3 brucella me	904	31.5	14.9	48	2	Q45783	Q45783 bacillus th
832	32	15.1	73	8	Q8NEZ2	Q8NEZ2 caenorhabdi	905	31.5	14.9	50	1	Q16095	Q16095 homo sapien
833	32	15.1	73	8	Q8S311	Q8S311 oryza sativ	906	31.5	14.9	51	11	Q925A8	Q925A8 castor cana
834	32	15.1	73	16	Q8ZEP2	Q8ZEP2 yersinia pe	907	31.5	14.9	51	11	Q925A7	Q925A7 castor fi
835	32	15.1	74	2	Q8I909	Q8I909 proteus mar	908	31.5	14.9	52	5	Q17465	Q17465 schistosoma
836	32	15.1	74	2	Q8R2X0	Q8R2X0 borrelia bu	909	31.5	14.9	57	13	Q91999	Q91999 xenopus lae
837	32	15.1	76	2	Q8VN30	Q8VN30 helicobacte	910	31.5	14.9	57	16	Q8RPF6	Q8RPF6 fusobacteri
838	32	15.1	76	3	Q8Y868	Q8Y868 aspergillus	911	31.5	14.9	58	9	Q8S502	Q8S502 bacterioph
839	32	15.1	76	12	Q8EML4	Q8EML4 amastax mo	912	31.5	14.9	59	2	Q8E2P5	Q8E2P5 burkholderi
840	32	15.1	76	16	Q8EML4	Q8EML4 amastax mo	913	31.5	14.9	59	10	Q9STQ3	Q9STQ3 arabidopsis
841	32	15.1	76	16	Q8EML4	Q8EML4 amastax mo	914	31.5	14.9	62	16	Q98KJ0	Q98KJ0 rhizobium l
842	32	15.1	76	16	Q8EML4	Q8EML4 amastax mo	915	31.5	14.9	62	16	Q928W7	Q928W7 listeria mo
843	32	15.1	77	12	Q9QTM7	Q9QTM7 thermotoga	916	31.5	14.9	63	10	Q42162	Q42162 arabidopsis
844	32	15.1	78	2	Q8AF88	Q8AF88 anaplasma m	917	31.5	14.9	63	10	Q9XEX1	Q9XEX1 dendrobium
845	32	15.1	78	4	Q8ET74	Q8ET74 homo sapien	918	31.5	14.9	63	17	Q8U465	Q8U465 pyrococcus
846	32	15.1	78	4	Q8Z45	Q8Z45 homo sapien	919	31.5	14.9	64	12	Q8VAV7	Q8VAV7 white spot
847	32	15.1	78	5	Q8Z45	Q8Z45 homo sapien	920	31.5	14.9	64	12	Q8VAV7	Q8VAV7 white spot
848	32	15.1	78	10	Q8SWZ2	Q8SWZ2 lycopersico	921	31.5	14.9	65	15	Q9J120	Q9J120 human immun
849	32	15.1	78	16	Q9R0K5	Q9R0K5 delinococcus	922	31.5	14.9	65	15	Q9J120	Q9J120 human immun
850	32	15.1	78	16	Q9R0K5	Q9R0K5 delinococcus	923	31.5	14.9	65	16	Q9CG03	Q9CG03 rhizobium m
851	32	15.1	78	16	Q9R0K5	Q9R0K5 delinococcus	924	31.5	14.9	65	16	Q9CG03	Q9CG03 rhizobium m
852	32	15.1	79	16	Q9R0K5	Q9R0K5 delinococcus	925	31.5	14.9	66	12	Q8Q136	Q8Q136 mycobacteri
853	32	15.1	80	2	Q9K25	Q9K25 xanthomonas	926	31.5	14.9	67	2	Q8RSP8	Q8RSP8 hepatitis c
854	32	15.1	80	16	Q9K25	Q9K25 xanthomonas	927	31.5	14.9	67	2	Q8RSP8	Q8RSP8 hepatitis c
855	32	15.1	81	17	Q8TIS5	Q8TIS5 methanosa	928	31.5	14.9	68	2	Q9L3P1	Q9L3P1 uncultured
856	32	15.1	81	17	Q8TIS5	Q8TIS5 methanosa	929	31.5	14.9	68	2	Q9L3P1	Q9L3P1 uncultured
857	32	15.1	81	2	Q8S044	Q8S044 thiobacilli	930	31.5	14.9	68	5	Q9NME9	Q9NME9 leishmania
858	32	15.1	81	2	Q9S257	Q9S257 helicobacte	931	31.5	14.9	68	5	Q9VW42	Q9VW42 drosophila
859	32	15.1	81	2	Q9RM30	Q9RM30 helicobacte	932	31.5	14.9	68	16	Q8R8B8	Q8R8B8 thermoaer
860	32	15.1	81	2	Q9RM30	Q9RM30 helicobacte	933	31.5	14.9	69	2	Q52569	Q52569 pseudomonas
861	32	15.1	81	2	Q94624	Q94624 clostridium	934	31.5	14.9	69	15	Q9WMS2	Q9WMS2 human immun
862	32	15.1	81	2	Q92365	Q92365 helicobacte	935	31.5	14.9	69	15	Q9WMS1	Q9WMS1 human immun
863	32	15.1	81	2	Q9R428	Q9R428 helicobacte	936	31.5	14.9	69	15	Q9WMS1	Q9WMS1 human immun
864	32	15.1	81	2	Q9R428	Q9R428 helicobacte	937	31.5	14.9	71	10	Q8XL00	Q8XL00 clostridium
865	32	15.1	81	2	Q93115	Q93115 streptococ	938	31.5	14.9	71	10	Q9M4R1	Q9M4R1 zea mays (m
866	32	15.1	81	6	Q9CL92	Q9CL92 mesoplodon	939	31.5	14.9	71	16	Q8YV24	Q8YV24 anabaena sp
867	32	15.1	81	10	Q8L711	Q8L711 arabidopsis	940	31.5	14.9	72	4	Q75961	Q75961 homo sapien
868	32	15.1	81	10	Q8L711	Q8L711 arabidopsis	941	31.5	14.9	72	4	Q75961	Q75961 homo sapien
869	32	15.1	81	15	Q8VWR9	Q8VWR9 narcisus p	942	31.5	14.9	73	5	Q9V998	Q9V998 drosophila
870	32	15.1	81	15	Q8VWR9	Q8VWR9 narcisus p	943	31.5	14.9	73	5	Q9V998	Q9V998 drosophila
871	32	15.1	82	2	Q8R0V1	Q8R0V1 human immun	944	31.5	14.9	73	17	Q8TQ84	Q8TQ84 methanosarc
872	32	15.1	82	2	Q8R0V1	Q8R0V1 human immun	945	31.5	14.9	74	10	Q93939	Q93939 hedyarum a
873	32	15.1	82	7	Q8XFP4	Q8XFP4 macaca mula	946	31.5	14.9	74	12	Q66059	Q66059 canine herp
874	32	15.1	82	7	Q8XFP4	Q8XFP4 macaca mula	947	31.5	14.9	74	12	Q66059	Q66059 canine herp
875	32	15.1	82	9	Q8XFP4	Q8XFP4 macaca mula	948	31.5	14.9	74	16	Q91293	Q91293 pseudomonas
876	32	15.1	82	9	Q8XFP4	Q8XFP4 macaca mula	949	31.5	14.9	74	16	Q91293	Q91293 pseudomonas
877	32	15.1	82	16	Q9JVB0	Q9JVB0 neisseria m	950	31.5	14.9	75	9	Q9A0Z0	Q9A0Z0 streptococ
878	32	15.1	82	16	Q9JVB0	Q9JVB0 neisseria m	951	31.5	14.9	75	9	Q9A0Z0	Q9A0Z0 streptococ
879	32	15.1	83	16	Q9JVB0	Q9JVB0 neisseria m	952	31.5	14.9	75	16	Q9RFP6	Q9RFP6 xylella fas
880	32	15.1	83	16	Q9JVB0	Q9JVB0 neisseria m	953	31.5	14.9	75	16	Q9RFP6	Q9RFP6 xylella fas
881	32	15.1	84	5	Q95PY2	Q95PY2 caenorhabdi	954	31.5	14.9	79	2	Q9ACR9	Q9ACR9 rickettsia
882	32	15.1	84	11	Q97618	Q97618 rattus norv	955	31.5	14.9	79	2	Q9ACR9	Q9ACR9 rickettsia
883	32	15.1	84	12	Q96418	Q96418 alcelaphine	956	31.5	14.9	80	6	Q9GLL7	Q9GLL7 streptomyce
884	32	15.1	85	3	Q9UB7	Q9UB7 schizosacch	957	31.5	14.9	80	9	Q8W150	Q8W150 bacterioph
885	32	15.1	86	7	Q9XK5	Q9XK5 barbus inte	958	31.5	14.9	80	15	Q9W150	Q9W150 human immun
886	32	15.1	86	16	Q8XHK5	Q8XHK5 clostridium	959	31.5	14.9	81	15	Q90508	Q90508 human immun
887	32	15.1	86	16	Q8XHK5	Q8XHK5 clostridium	960	31.5	14.9	81	15	Q90508	Q90508 human immun
888	32	15.1	87	2	Q8CHT9	Q8CHT9 lactococcus	961	31.5	14.9	81	15	P91610	P91610 drosophila
889	32	15.1	87	4	Q8TDS2	Q8TDS2 homo sapien	962	31.5	14.9	81	15	Q998E6	Q998E6 human immun
890	32	15.1	87	4	Q8TDS2	Q8TDS2 homo sapien	963	31.5	14.9	81	15	Q998E6	Q998E6 human immun
891	32	15.1	87	17	Q980S8	Q980S8 sulfolobus	964	31.5	14.9	81	15	Q998E6	Q998E6 human immun
892	32	15.1	89	2	Q9ZGD5	Q9ZGD5 streptomyce	965	31.5	14.9	81	15	Q998E6	Q998E6 human immun

966 31.5 14.9 81 15 Q8UMD5  
 967 31.5 14.9 81 16 Q92HE6  
 968 31.5 14.9 81 17 Q2TNC3  
 969 31.5 14.9 82 9 Q8W6E1  
 970 31.5 14.9 82 9 Q92LL16  
 971 31.5 14.9 82 16 Q9PC03  
 972 31.5 14.9 83 10 Q9SFV2  
 973 31.5 14.9 83 16 Q8YK68  
 974 31.5 14.9 83 16 Q8XAC1  
 975 31.5 14.9 84 4 Q98Q27  
 976 31.5 14.9 85 4 Q961N8  
 977 31.5 14.9 86 16 Q24902  
 978 31.5 14.9 86 16 Q92N03  
 979 31.5 14.9 86 16 Q92CF9  
 980 31.5 14.9 86 16 Q8Y7M9  
 981 31.5 14.9 86 16 Q92RH4  
 982 31.5 14.9 89 15 Q994H6  
 983 31.5 14.9 89 16 Q96HK4  
 984 31.5 14.9 90 2 P72475  
 985 31.5 14.9 90 10 Q92R50  
 986 31.5 14.9 90 16 Q8ZLE7  
 987 31 14.6 40 5 Q952I3  
 988 31 14.6 43 16 Q9PE48  
 989 31 14.6 44 6 Q9GKJ5  
 990 31 14.6 44 12 Q91F67  
 991 31 14.6 47 8 Q95BY9  
 992 31 14.6 47 16 Q9K248  
 993 31 14.6 48 11 Q9JL46  
 994 31 14.6 49 15 Q69906  
 995 31 14.6 49 15 Q69907  
 996 31 14.6 49 16 Q9JX04  
 997 31 14.6 50 10 Q9XIB0  
 998 31 14.6 50 10 Q82764  
 999 31 14.6 51 15 Q73757  
 1000 31 14.6 52 4 Q9UJH5

## ALIGNMENTS

## RESULT 1

ID P91302 PRELIMINARY; PRT: 73 AA.  
 AC P91302;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 GN F46F11.4 protein.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Pauley A., Gattung S.;  
 RT "The sequence of C. elegans cosmid F46F11.";  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DE EMBL; U88173; AAK21382.1; ..

DR InterPro: IPR000626; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR PROSITE: PS0053; UBIQUITIN\_2; 1.  
 SQ SEQUENCE 73 AA; 8738 MW; 61CA839BBA4006A4 CRC64;  
 Query Match 21.5%; Score 45.5; DB 5; Length 73;  
 Best Local Similarity 29.4%; Pred. No. 1.2e+02;  
 Matches 10; Conservative 7; Mismatches 12; Indels 5; Gaps 1;  
 QY 14 DFGSGKSRVIENTPEALS-----VAVEEGLAWRK 42  
 DB 8 DRLGRVRIKCNPSDTIGDLKKLIAAQTGRWER 41  
 RESULT 2  
 ID O28902 PRELIMINARY; PRT: 77 AA.  
 AC O28902;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Hydrogenase expression/format protein (HYPC).  
 GN AF1369.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 OX NCBI\_TaxID=2234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C., Gill S.,  
 Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
 Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,  
 Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 Venter J.C.;  
 RA "The complete genome sequence of the hyperthermophilic, sulphate-  
 reducing archaeon Archaeoglobus fulgidus.";  
 RT Nature 390:364-370 (1997).  
 RL EMBL; AE001009; AAB89878.1; ..  
 DR TIGR; AF1369;  
 DR InterPro: IPR001109; HupF\_HypC.  
 DR Pfam; PF01455; HupF\_HypC; 1.  
 DR ProDom; PD003112; HupF\_HypC; 1.  
 DR TIGRFAMS; TIGR00074; hupC\_hupF; 1.  
 DR PROSITE; PS01097; HUPF\_HYPC; UNKNOWN.1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 77 AA; 8783 MW; 669179CCB544D027 CRC64;  
 Query Match 21.2%; Score 45; DB 17; Length 77;  
 Best Local Similarity 35.1%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 5; Mismatches 15; Indels 4; Gaps 1;  
 QY 10 LVAMDFSGKSRV-----IENPTEALSVAVEEGLAWRK 42  
 DB 16 IATVDFGLKREVRIDLENPOIGDYVLVHVGMATOK 52  
 RESULT 3  
 ID O27686 PRELIMINARY; PRT: 82 AA.  
 AC O27686;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Hydrogenase expression/format protein HYPC.  
 GN MTH1649.

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OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Harridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.,
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH; functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000924; AAB86122.1;
DR InterPro: IPR001109; HupF_HypC.
DR Pfam: PF01455; HupF_HypC; 1.
DR PRODOM: PD003112; HupF_HypC; 1.
DR TIGRFXMS: TIGR00074; hupC_hupF; 1.
KW Complete proteome.
SQ SEQUENCE 82 AA; 9082 MW; B6EGAED010FB562D CRC64;

Query Match 21.2%; Score 45; DB 17; Length 82;
Best Local Similarity 28.9%; Pred. No. 1.6e+02;
Matches 11; Conservative 9; Mismatches 14; Indels 4; Gaps 1;

QY 6 SENSILVADFSGOKSRV---IENPTEALSVAVEGLA 39
DB 14 SEDNIATVDEGGVROQKLDLVDVDEGGYVLVHSGVA 51

RESULT 4
Q8TTKO PRELIMINARY; PRT; 60 AA.
AC Q8TTKO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Ferredoxin.
GN MA0431.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W., Birren B.,
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:332-342(2002).
DR EMBL: AE010703; AM03878.1;
KW Complete proteome.
SQ SEQUENCE 60 AA; 6265 MW; 6D75EBDB4460C21F CRC64;

Query Match 20.8%; Score 44; DB 17; Length 60;
Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 13 MDFSOGKSRVIE-NPTEA-LSVAVEGLAWRRKK 43
DB 46 LELSAEQAKAVNAHLSEALTDVDEALAWASK 78

RESULT 6
Q9VXCI PRELIMINARY; PRT; 82 AA.
AC Q9VXCI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE CG9644 protein.
GN CG9644.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.E., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaisei R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

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RT RT Resensitization and dual HIV-1 resistance to zidovudine and lamivudine in the Delta lamivudine roll-over study.\*; RT Antivir. Ther. 4:69-77(1999).  
 RL EMBL: AJ239270; CAB51518.1; .  
 DR InterPro: IPR000477; RVTSE.  
 DR Pfam: PF00078; rvt; 1.  
 KW RNA-directed DNA polymerase.  
 FT NON\_TER 1  
 FT NON\_TER 69  
 SQ SEQUENCE 69 AA: 8089 MW; 5BD8FF800A16A70C CRC64;

Query Match 20.5%; Score 43.5; DB 15; Length 69;  
 Best Local Similarity 33.3%; Pred. No. 2.1e+02;  
 Matches 11; Conservative 8; Mismatches 11; Indels 3; Gaps

QY 13 MDFSQKSRV--IENP--TEALSVAVEEGLAWRK 42  
 DB 15 LEKEGKISKIGPENYPYTPVFAIKKCKGCKWRK 47

RESULT 8  
 O9LM11 PRELIMINARY;  
 ID Q9LM11 PRT: 88 AA.  
 AC Q9LM11  
 AD Q9LM11  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DE TELIS.2.  
 DE TELIS.2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsidae.  
 ON NCBI\_TaxID=3702;  
 RX [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Kim C., Alonso J., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Shinn P., Altafi H., Bei O., Chin C., Chlou J., Choi E.,  
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,  
 RA Theologis A., Ecker J.R.;  
 RT Telomere associated sequence for Arabidopsis thaliana TELS from  
 RT chromosome 1.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Ecker J.R.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei O., Chin C., Chlou J., Choi E.,  
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.,  
 RA Theologis A., Ecker J.R.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC074299; AAF89109.1;  
 SQ SEQUENCE 88 AA: 10232 MW; B24F705FE24C581 CRC64;

Query Match 20.5%; Score 43.5; DB 10; Length 88;  
 Best Local Similarity 43.3%; Pred. No. 2.8e+02;  
 Matches 13; Conservative 6; Mismatches 8; Indels 3; Gaps

QY 6 SENSIVAMDFSQ---GKSRVIENTEALSV 32  
 DB 50 SENSIVAMDFSQGITWVIFKTKYTV 79

RA Balaw R.M., Basu A., Boxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhanderi D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlie C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson G.M., Nixon K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodgett T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RT Science 287:2185-2195 (2000).  
 CC -I- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC IONS.  
 CC EMBL: AEO03503; AAF48655.1; .  
 CC FlyBase; FBgn0030781; CG9644.  
 DR InterPro: IPR001781; LIM.  
 DR Pfam: PF00412; LIM; 2.  
 DR ProDom: PD0000094; LIM; 1.  
 DR SMART: SM00132; LIM; 1.  
 DR PROSITE; PS00478; LIM DOMAIN.1; 1.  
 DR PROSITE; PS00023; LIM DOMAIN.2; 1.  
 DR LIM domain; Metal-binding; Zinc.  
 KW LIM domain; Metal-binding; Zinc.  
 SQ SEQUENCE 82 AA; 9207 MW; 94AB7BEFF7150AD7 CRC64;

Query Match 20.8%; Score 44; DB 5; Length 82;  
 Best Local Similarity 33.3%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 5 ISESLVAMDFSQ----KSRVIENTEALSVAVEE 36  
 DB 37 ITENAIVLADAKWHRCEFKCKKCKPTITASSFVVED 72

RESULT 7  
 Q9WM06 PRELIMINARY; PRT: 69 AA.  
 ID Q9WM06  
 AD Q9WM06  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Reverse transcriptase (Fragment).  
 OS Human immunodeficiency virus.  
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 ON NCBI\_TaxID=12721;  
 RX [1]  
 RC STRAIN=DRO22/MO;  
 RC MEDLINE=20146732; PubMed=10682151;  
 RX Masquelier B., Descamps D., Carriere I., Ferchal F., Collin G.,  
 RA Denayrolles M., Ruffault A., Chanzy B., Izobet J.,  
 RA Buffet-Janvresse C., Schmitt M.P., Race E., Fleury H.J.A.,  
 RA Aboulker J.P., Yeni P., Brun-Vezinet F.



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RESULT 9
O9HGR8 PRELIMINARY; PRT; 80 AA.
AC O9HGR8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
DE (fragment).
DE GPD.
GN CHOANEPHORA INFUNDIBULIFERA.
OS Eukaryota; Fungi; Zygomycota; Mucorales; Choanephoraceae;
OC Choanephora.
OC NCBI_TaxID=127959;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NRRL 2560;
RA Tamas P.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RC STRAIN=NRRL 2560;
RA Papp T., Vastag M., Acs K., Vagvolgyi C.;
RT Phylogenetic relationships among Mucoraceae, Choanephoraceae and
RT Gilbertellaceae based on rDNA and glyceraldehyde-3-phosphate
RT dehydrogenase sequences.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE +
CC NAD(+) = 3-PHOSPHO-D-GLYCEROL PHOSPHATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL: AJ278315; CAC05662.1;
DR InterPro: IPR000173; GAP_dhdrogenase.
DR Pfam: PF02800; gpdh_C.1;
KW Glycolysis; NAD; Oxidoreductase.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 8504 MW; 4ECCBEAE035943D0 CRC64;

Query Match 20.0%; Score 42.5; DB 3; Length 80;
Best Local Similarity 42.9%; Pred. No. 3.4e+02;
Matches 9; Conservative 6; Mismatches 3; Indels 3; Gaps 1;

OY 1 PMSI---SENSLVAMDFSGQ 18
DB 37 PMKGILGYTNAVYSTDFIGE 57

RESULT 10
O9PFG5 PRELIMINARY; PRT; 53 AA.
AC O9PFG5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein xF0694.
GN xF0694.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OC NCBI_TaxID=2371;
RN SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Boye J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinchi A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

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RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Miracca E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL: AE003912; AAF83504.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 53 AA; 5958 MW; 4B1AF832900832B CRC64;

Query Match 19.8%; Score 42; DB 16; Length 53;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 30 LSVAVEEGLAWR 41
DB 21 LGVGVERGYAWR 32

RESULT 11
O80316 PRELIMINARY; PRT; 58 AA.
ID O80316;
AC O80316;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OF52 (Fragment).
GN H.
OS Bacteriophage 186.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P2-like Viruses.
OC NCBI_TaxID=29252;
RN [1]
RP SEQUENCE FROM N.A.
RA Xue Q.;
RT "Studies on the tail region of the temperate coliphage 186 genome.";
RL Thesis (1993), University of Adelaide.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98371265; PubMed=9705261;
RA Portelli R., Dodd I.B., Xue Q., Egan J.B.;
RT "The late-expressed region of the temperate coliphage 186 genome.";
RL Virology 248:117-130(1998).
DR EMBL: U32222; AAC34169.1;
FT NON_TER 1
FT VARIANT 15 15 S -> *
FT VARIANT 51 51 Q -> *
SQ SEQUENCE 58 AA; 6491 MW; 1199113D8CDEB8E6 CRC64;

Query Match 19.8%; Score 42; DB 9; Length 58;
Best Local Similarity 38.9%; Pred. No. 2.7e+02;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 26 PTEALSVAVEEGLAWRK 43
DB 31 PSELYSLSLTELITWREK 48

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## RESULT 12

Q64944 PRELIMINARY; PRT; 76 AA.  
 ID O64944  
 AC O64944  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Spike protein (Fragment).  
 GN S1.  
 OS Avian infectious bronchitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=11120;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AL1960;  
 RC MEDLINE=97049060; PubMed=8893790;  
 RA Wang C.H., Tsai C.T.;  
 RA "Genetic grouping for the isolates of avian infectious bronchitis  
 RT virus in Taiwan."  
 RL Arch. Virol. 141:1677-1688(1996).  
 DR EMBL: U38678; AAB47436.1; -  
 DR InterPro: IPR002551; Corona\_S1.  
 DR Pfam: PF01600; Corona\_S1; 1.  
 FT NON\_TER 1 76  
 FT NON\_TER 76  
 SQ SEQUENCE 76 AA; 7861 MW; 9DA97501A9CB4FD1 CRC64;

Query Match 19.8%; Score 42; DB 12; Length 76;  
 Best Local Similarity 31.8%; Pred. No. 3.7e+02;

Matches 7; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 21 RVIENTEALSVAVEEGLAWRK 42

DB 36 RIVNASSIAMTPVPGQGMQSK 57

## RESULT 13

Q64947 PRELIMINARY; PRT; 76 AA.  
 ID O64947  
 AC O64947  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Spike protein (Fragment).  
 GN S1.  
 OS Avian infectious bronchitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=11120;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AL1955;  
 RC MEDLINE=97049060; PubMed=8893790;  
 RA Wang C.H., Tsai C.T.;  
 RA "Genetic grouping for the isolates of avian infectious bronchitis  
 RT virus in Taiwan."  
 RL Arch. Virol. 141:1677-1688(1996).  
 DR EMBL: U38681; AAB47439.1; -  
 DR InterPro: IPR002551; Corona\_S1.  
 DR Pfam: PF01600; Corona\_S1; 1.  
 FT NON\_TER 1 76  
 FT NON\_TER 76  
 SQ SEQUENCE 76 AA; 7903 MW; 271F114FD4078521 CRC64;

Query Match 19.8%; Score 42; DB 12; Length 76;  
 Best Local Similarity 36.4%; Pred. No. 3.7e+02;

Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 21 RVIENTEALSVAVEEGLAWRK 42

DB 36 RIVNASSIAMTPVPGQGMQSK 57

## RESULT 14

Q928X5 PRELIMINARY; PRT; 79 AA.  
 ID Q928X5  
 AC Q928X5  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein CPN0209.  
 GN CPN0209.  
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CWL029;  
 RC MEDLINE=99206606; PubMed=10192388;  
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."  
 RL Nat. Genet. 21:385-389(1999).  
 DR EMBL: AF001607; AAD18362.1; -  
 DR EMBL: AF001607; AAD18362.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 79 AA; 9196 MW; 2813A36311D4A49A CRC64;

Query Match 19.8%; Score 42; DB 16; Length 79;  
 Best Local Similarity 33.3%; Pred. No. 3.9e+02;

Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 15 FSGOKSRVIENPTALSVAVEEGL 38

DB 28 FQKTRVIAITPAGLAIAVEQNI 51

## RESULT 15

Q9JSH8 PRELIMINARY; PRT; 79 AA.  
 ID Q9JSH8  
 AC Q9JSH8  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE Hypothetical protein CPJ0209.  
 GN CPJ0209.  
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JL18;  
 RC MEDLINE=2030349; PubMed=10871362;  
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 RL from Japan and CWL029 from USA."  
 DR Nucleic Acids Res. 28:2311-2314(2000).  
 DR EMBL: AF002545; BAA98419.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 79 AA; 9212 MW; C70CA36311C3AFF7 CRC64;

Query Match 19.8%; Score 42; DB 16; Length 79;  
 Best Local Similarity 33.3%; Pred. No. 3.9e+02;

Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 15 FSGOKSRVIENPTALSVAVEEGL 38

DB 28 FQKTRVIAITPAGLAIAVEQNI 51

## RESULT 16

Q9K247 PRELIMINARY; PRT; 81 AA.  
 ID Q9K247  
 AC Q9K247  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 GN Hypothetical protein CP0557.  
 OS Chlamydia pneumoniae (Chlamydia pneumoniae)  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AR39;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linner K., Weidman J., Knouri H., Craven B., Bowman C., Dodson R.,  
 RA Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 DR EMBL; AE002214; AAP38377.1; -;  
 DR TIGR; CP0557; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 81 AA; 9455 MW; C6A6483DA44594C2 CRC64;  
 Query Match 19.8%; Score 42; DB 16; Length 81;  
 Best Local Similarity 33.3%; Pred. No. 4e+02; Mismatches 9; Indels 0; Gaps 0;  
 Matches 8; Conservative 7;  
 QY 15 FSGQKSRVNPTEALSVAVEGL 38  
 Db 30 FGGKRRVIAITPAGIAIYEONI 53  
 RESULT 17  
 P72094  
 ID P72094 PRELIMINARY; PRT; 90 AA.  
 AC P72094;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Transposase homolog (Fragment).  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491;  
 RX MEDLINE=97008141; PubMed=8855317;  
 RA Tinsley C.R., Nassif X.;  
 RT "Analysis of the genetic differences between Neisseria meningitidis  
 RT and Neisseria gonorrhoeae: two closely related bacteria expressing two  
 RT different pathogenicities.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11109-11114(1996).  
 DR EMBL; U58765; AAC44489.1; -;  
 FT NON-TER 90  
 FT NON-TER 90  
 SQ SEQUENCE 90 AA; 10285 MW; 80FAA15ABF1F53AF CRC64;  
 Query Match 19.8%; Score 42; DB 2; Length 90;  
 Best Local Similarity 41.7%; Pred. No. 4.6e+02;  
 Matches 10; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 13 MDFSQKSRVNPTEALSVAVEE 36  
 Db 2 LDYSSQKRVAYDIHDADHIVKD 25  
 RESULT 18  
 Q40019  
 ID Q40019 PRELIMINARY; PRT; 87 AA.  
 AC Q40019;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE B12D mRNA.  
 GN HVBI2D OR B12DGI.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. BOMI;  
 RX MEDLINE=94236153; PubMed=8180622;  
 RA Aalen R.B., Opsahl-Ferstad H.G., Lindestad C., Olsen O.A.;  
 RT "Transcripts encoding an oleosin and a dormancy-related protein are  
 RT present in both the aleurone layer and the embryo of developing barley  
 RT (Hordeum vulgare L.) seeds.";  
 RL Plant J. 5:385-396(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. BOMI;  
 RX Steinum T.M., Berner H., Stacy R.A.P., Salehian Z., Aalen R.B.;  
 RT "Differential regulation of the barley (Hordeum vulgare) transcripts  
 RT B22E and B12D in mature aleurone layers.";  
 RL Physiol. Plantarum 102:337-345(1998).  
 DR EMBL; X76604; CAA34065.1; -;  
 DR EMBL; X09805; CAA70936.1; -;  
 SQ SEQUENCE 87 AA; 9648 MW; ECE117231E51046 CRC64;  
 Query Match 19.6%; Score 41.5; DB 10; Length 87;  
 Best Local Similarity 35.1%; Pred. No. 5.1e+02;  
 Matches 13; Conservative 7; Mismatches 16; Indels 1; Gaps 1;  
 QY 2 MRSISESLVAMDFSGKSRVNPTEALSVAVEGL 38  
 Db 29 LRNITGNPEVRVSKMGAGVLENHEGRRYA-EHGL 64  
 RESULT 19  
 Q41693  
 ID Q41693 PRELIMINARY; PRT; 69 AA.  
 AC Q41693;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE 1-aminocyclopropane 1-carboxylate synthase (Fragment).  
 OS Vigna radiata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
 OX NCBI\_TaxID=157791;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HYPOCOTYL;  
 RX MEDLINE=92216056; PubMed=1588953;  
 RA Botella J.R., Schlaghauser C.D., Arteca R.N., Phillips A.T.;  
 RT "Identification and characterization of three putative genes for 1-  
 RT aminocyclopropane-1-carboxylate synthase from etiolated mung bean  
 RT hypocotyl segments.";  
 RL Plant Mol. Biol. 18:793-797(1992).  
 DR EMBL; M80555; AAK38750.1; -;  
 DR HSSP; P37821; 1B8G. 1  
 FT NON-TER 69  
 FT NON-TER 69  
 SQ SEQUENCE 69 AA; 8057 MW; EAD4BDE7D47735D CRC64;  
 Query Match 19.3%; Score 41; DB 10; Length 69;  
 Best Local Similarity 28.9%; Pred. No. 4.6e+02;  
 Matches 11; Conservative 9; Mismatches 14; Indels 4; Gaps 2;  
 QY 5 ISESLVAMDFSGKSRVNPTEALSVAVEGLAWRK 42  
 Db 27 LAENPQLTDLI--QDWINKNP--QASVCTPEGVKWK 60

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RESULT 20
Q9NRP2 PRELIMINARY; PRT; 79 AA.
ID AC Q9NRP2
AC Q9NRP2
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE DC13.
DE DC13.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Y., Peng Y., Li N., Gu W., Han Z., Fu G., Chen Z.;
RT "Novel genes expressed in human dentritic cell.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201935; AAF86871.1;
SQ SEQUENCE 79 AA; 9460 MW; 783381BD5DAFB7AA CRC64;

Query Match 19.3%; Score 41; DB 4; Length 79;
Best Local Similarity 40.0%; Pred. No. 5.4e+02;
Matches 10; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 19 KSRVIENPTALSVAVVEGLAMRK 43
DB 49 KNEYVENTKSR-----EHGIAMRK 69

RESULT 21
Q9WVG1 PRELIMINARY; PRT; 85 AA.
ID AC Q9WVG1
AC Q9WVG1
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DE HRPD6.
DE HRPD6.
GN Xanthomonas campestris (pv. vesicatoria).
OS Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas;
OX NCBI_TaxID=341;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-75-3;
RX MEDLINE=98453137; PubMed=9781876;
RA Huguet E., Hahn K., Wengelnik K., Bonas U.;
RT "hpaA mutants of Xanthomonas campestris pv. vesicatoria are affected
RT in pathogenicity but retain the ability to induce host-specific
RT hypersensitive reaction.";
RL Mol. Microbiol. 29:1379-1390(1998).
DR EMBL; AF056246; AAD21324.1;
SQ SEQUENCE 85 AA; 9420 MW; 6180906387986E71 CRC64;

Query Match 19.3%; Score 41; DB 2; Length 85;
Best Local Similarity 44.4%; Pred. No. 5.8e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 12 ANDFSGOKSRVIENPTA 29
DB 26 ANDLSGERLNRVETALDA 43

RESULT 22
Q8R9D7 PRELIMINARY; PRT; 85 AA.
ID AC Q8R9D7
AC Q8R9D7
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Hypothetical protein TTE1677.

GN Thermoanaerobacter tengcongensis.
OS Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-MBAT / JCM11007;
RX MEDLINE=21592816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Tang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013122; AAM24878.1;
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 9722 MW; 03DAGADE30EDE71C CRC64;

Query Match 19.3%; Score 41; DB 16; Length 85;
Best Local Similarity 30.0%; Pred. No. 5.8e+02;
Matches 9; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 3 RSISENSLVAMDFSGOKSRVIENPTALSV 32
DB 35 RSISEGCSHLKFGLESILKVVQNLQIRNV 64

RESULT 23
Q8TKZ4 PRELIMINARY; PRT; 87 AA.
ID AC Q8TKZ4
AC Q8TKZ4
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Predicted protein.
DE Predicted protein.
GN MA3249.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Perry J.G., Jarrell K.F., White O., White R.H., de Macario E.C.,
RA Pritchett W., Sowers K.R., Jing H., Macario A.J.L., Paulsen I.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011028; AAM06620.1;
RW Complete proteome.
SQ SEQUENCE 87 AA; 10125 MW; 1A970190E4B5CD2D CRC64;

Query Match 19.3%; Score 41; DB 17; Length 87;
Best Local Similarity 22.7%; Pred. No. 6e+02;
Matches 10; Conservative 13; Mismatches 17; Indels 4; Gaps 1;

QY 4 SISENSLVAMDFSGOKSRV----IENPTALSVAVVEGLAMRK 43
DB 5 SLKRTSLTIIRFSTOESSISOKNLKKKEAKIMTIEDSIELKRE 48

RESULT 24
Q74620

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ID O74630 PRELIMINARY; PRT; 68 AA.
AC Q74630;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Reverse transcriptase (Fragment).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P18;
RX MEDLINE=95074869; PubMed=7983713;
RA Najera I., Holguin A., Quinones-Mateu M.E., Munoz-Fernandez M.A.,
RT "Pol gene quasiespecies of human immunodeficiency virus: mutations
RT associated with drug resistance in virus from patients undergoing no
RT drug therapy."
RL J. Virol. 69:23-31(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=P13;
RX MEDLINE=97000986; PubMed=8844016;
RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
RT "Point mutant frequencies in the pol gene of human immunodeficiency
RT virus type 1 are two- to threefold lower than those of env."
RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
DR EMBL; U14846; AAC55753.1; -.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7910 MW; 187F11C0FCE674C8 CRC64;

Query Match 19.1%; Score 40.5; DB 15; Length 68;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
Matches 11; Conservative 7; Mismatches 12; Indels 3; Gaps 2;

QY 13 MDFSQKSRV-IENP--TEALSVAVEEGLAWRK 42
   | : | : | | | | : : : | | |
Db 1 MEKEGKISRGIPENYPNTPVFAIKKDKSTKWK 33

RESULT 25
Q74630
ID O74630 PRELIMINARY; PRT; 68 AA.
AC Q74630;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Reverse transcriptase (Fragment).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P18;
RX MEDLINE=95074869; PubMed=7983713;
RA Najera I., Holguin A., Quinones-Mateu M.E., Munoz-Fernandez M.A.,
RT "Pol gene quasiespecies of human immunodeficiency virus: mutations
RT associated with drug resistance in virus from patients undergoing no
RT drug therapy."
RL J. Virol. 69:23-31(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=P18;
RX MEDLINE=97000986; PubMed=8844016;
RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
RT "Point mutant frequencies in the pol gene of human immunodeficiency

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RT virus type 1 are two- to threefold lower than those of env."
RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
DR EMBL; U14856; AAC55763.1; -.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7938 MW; 18678049FCE674C8 CRC64;

Query Match 19.1%; Score 40.5; DB 15; Length 68;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
Matches 11; Conservative 7; Mismatches 12; Indels 3; Gaps 2;

QY 13 MDFSQKSRV-IENP--TEALSVAVEEGLAWRK 42
   | : | : | | | | : : : | | |
Db 1 MEKEGKISRGIPENYPNTPVFAIKKDKSTKWK 33

Search completed: March 28, 2003, 09:08:02
Job time : 66.2126 secs

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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 08:56:00 ; Search time 9.48032 seconds  
(without alignments)  
188.125 Million cell updates/sec

Title: US-09-936-697-5  
RefSeq score: 212  
Sequence: 1 PRRSISENSLVAMDFSCOKS.....ENPTAUSVAEGLAWRK 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 7863

Minimum DB seq length: 40  
Maximum DB seq length: 90

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database: SwissProt 40.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46.5	21.9	62	1	YZ05_METJA
2	46	21.7	73	1	RPON_METJA
3	42	19.8	82	1	Y567_METJA
4	40	18.9	82	1	RADC_STAAU
5	39	18.4	45	1	RS22_ECOLI
6	39	18.4	71	1	Y16K_BPT4
7	38.5	18.2	67	1	CSPE_STRCO
8	38.5	18.2	74	1	NIFH_NGSSN
9	38.5	18.2	78	1	CINA_STREGV
10	38	17.9	59	1	FER_METEA
11	38	17.9	63	1	FER2_DESM
12	38	17.9	72	1	RPON_THEAC
13	38	17.9	72	1	RPON_THEVO
14	38	17.9	83	1	TMOR_PSEME
15	37	17.5	88	1	VS85_BPML5
16	36.5	17.2	88	1	RS19_CHLPN
17	36.5	17.2	88	1	RS19_CHLTR
18	36	17.0	59	1	YH13_ARCFU
19	36	17.0	66	1	CSPT_STRCL
20	36	17.0	76	1	IPKG_HUMAN
21	36	17.0	76	1	IPKG_MOUSE
22	36	17.0	80	1	GCHI_MUCHA
23	36	17.0	83	1	TRBC_ECOLI
24	35.5	16.7	69	1	GBGU_BOVIN
25	35.5	16.7	75	1	ATP9_PARTE
26	35	16.5	58	1	SINI_BACLI
27	35	16.5	67	1	HFBC_METFO
28	35	16.5	70	1	ICIC_HTRME
29	35	16.5	79	1	NSGQ_HUMAN
30	34.5	16.3	80	1	VPUL_HV1MA
31	34	16.0	51	1	VG62_BPM2D
32	34	16.0	67	1	HWT2_METFO
33	34	16.0	67	1	HWT1_METTH

34	34	16.0	68	1	V07K_PMV
35	34	16.0	78	1	Y8K2_SSV1
36	34	16.0	79	1	YH65_SYNV3
37	33.5	15.8	82	1	YHVD_ANACY
38	33	15.6	45	1	CYC6_PROHO
39	33	15.6	55	1	FER_BUTME
40	33	15.6	75	1	YODD_ECOLI
41	33	15.6	84	1	RL23_HALMA
42	33	15.6	87	1	IM08_YEAST
43	33	15.6	90	1	DBHL_RICRI
44	32.5	15.3	45	1	VPUL_HV1J3
45	32.5	15.3	81	1	VPUL_HV1J3
46	32.5	15.3	81	1	VPUL_HV1S1
47	32.5	15.3	90	1	PTSO_ECOLI
48	32	15.1	41	1	BAXC_HUMAN
49	32	15.1	52	1	SRY_AKOAZ
50	32	15.1	60	1	NXSL_DENJA
51	32	15.1	60	1	NXSL_DENJA
52	32	15.1	62	1	V452_BPT4
53	32	15.1	64	1	YBEM_ECOLI
54	32	15.1	66	1	CADO_BUNCA
55	32	15.1	66	1	RPON_SULSO
56	32	15.1	67	1	YDFZ_ECOLI
57	32	15.1	71	1	ACAL_ACAIU
58	32	15.1	71	1	YOGC_ECOLI
59	32	15.1	72	1	HAFI_ARCFU
60	32	15.1	73	1	VF14_VARV
61	32	15.1	75	1	RPOK_ARCFU
62	32	15.1	75	1	RPOZ_PORPU
63	32	15.1	83	1	YCX1_PINTH
64	32	15.1	87	1	NXLH_BUNMU
65	32	15.1	89	1	YHHL_ECOLI
66	31.5	14.9	53	1	LECA_LATAP
67	31.5	14.9	57	1	V3A_IBVU4
68	31.5	14.9	72	1	CCA2_ECOLI
69	31.5	14.9	74	1	YC65_LISIN
70	31.5	14.9	79	1	Y124_AQUAE
71	31.5	14.9	87	1	RS19_MYCGA
72	31	14.6	43	1	CC3_CARCN
73	31	14.6	46	1	V11_BPT3
74	31	14.6	46	1	RPON_METTH
75	31	14.6	55	1	UCRX_BOVIN
76	31	14.6	62	1	YJEB_TRINI
77	31	14.6	63	1	YH1A_ECOLI
78	31	14.6	63	1	YH1A_ECOLI
79	31	14.6	63	1	YH1A_ECOLI
80	31	14.6	66	1	COPP_HELPFJ
81	31	14.6	66	1	DM55_PACDA
82	31	14.6	67	1	IFIA_MOUSE
83	31	14.6	72	1	Y541_BORBU
84	31	14.6	76	1	RPON_ARCFU
85	31	14.6	77	1	RL28_HAEIN
86	31	14.6	78	1	XD80_METJA
87	31	14.6	80	1	AKA7_MOUSE
88	31	14.6	85	1	THIO_METJA
89	31	14.6	87	1	NAPD_ECOLI
90	31	14.6	88	1	PTHP_TREPA
91	31	14.6	89	1	V45_BPT7
92	31	14.6	90	1	RPOZ_VIBCH
93	30.5	14.4	45	1	VPUL_HV1N5
94	30.5	14.4	57	1	V3A_IBVU5
95	30.5	14.4	57	1	V3A_IBVU5
96	30.5	14.4	57	1	V3A_IBVU5
97	30.5	14.4	63	1	Y083_ARCFU
98	30.5	14.4	63	1	CSRA_HAEIN
99	30.5	14.4	63	1	RS21_BURMA
100	30.5	14.4	70	1	RS21_BURPS
101	30.5	14.4	76	1	CD24_RAT
102	30.5	14.4	80	1	VPUL_HV1J3
103	30.5	14.4	80	1	YDMC_SCHPO
104	30.5	14.4	81	1	UL11_HSV62
105	30.5	14.4	82	1	VPUL_HV1B1
106	30.5	14.4	87	1	RS19_MYCPN

1620554	papaya mosa
1620205	sulfolobus
162913	synchocyst
161420	anabaena cy
161274	prochloroth
161073	butylobacte
160328	eschericchia
161732	haiaorcula
167744	saccharomyc
168451	rickettsia
168805	human immun
168882	human immun
169554	human immun
163996	eschericchia
167815	homo sapien
163688	akodon azar
161417	dendroaspis
161418	dendroaspis
167878	bacterioph
167666	eschericchia
161783	bungarus ca
168028	sulfolobus
167613	eschericchia
161592	acalolepta
168878	eschericchia
162910	archaeoglob
163872	ariola vir
1629134	archaeoglob
161376	porphyra pu
160865	pinus thub
165818	bungarus mu
167614	eschericchia
167441	lathyrus ap
163039	avian infec
164695	eschericchia
16260	listeria in
166524	aquifex aeo
162336	mycoplasma
163956	carica cand
163957	carica cand
162833	bacterioph
162617	methanobact
160130	bos taurus
1630810	trichoplusi
168366	eschericchia
160721	eschericchia
162m70	helicobacte
163455	pachymedusa
160872	mus musculus
161491	borrelia bu
1629135	archaeoglob
164364	haemophilus
1658775	methanococc
165074	mus musculus
167755	methanococc
163938	eschericchia
163598	treponema p
163785	bacterioph
169km3	vibrio chol
168804	human immun
165137	avian infec
1630238	avian infec
1630240	avian infec
164879	baemophilus
164879	baemophilus
1670943	burkholderi
1670943	burkholderi
167459	rattus norv
162517	human immun
163916	schizosacch
162459	human herpe
162516	human immun
1675576	mycoplasma

107	30.5	14.4	88	1	Y67_BPT7	P03801 bacterioph	180	29	13.7	76	1	YNGJ_ECOLI	P76105 escherichia
108	30.5	14.4	89	1	RS19_XYLFA	Q9pe72 xyliella fas	181	29	13.7	76	1	YQAF_BACSU	P45903 bacillus su
109	30	14.2	45	1	RS34_CYACA	O19912 cyanidium c	182	29	13.7	77	1	YCNB_CVAPA	P48332 cyanophora
110	30	14.2	52	1	YQAO_CAEEL	P05116 caenorhabdi	183	29	13.7	77	1	YG17_ARCFU	P28656 archaeoglob
111	30	14.2	54	1	YOVO_DRONO	P05560 dromaius no	184	29	13.7	80	1	ATPD_PIG	Q92312 sus scrofa
112	30	14.2	54	1	YOVO_RHEAM	P05558 thea americ	185	29	13.7	80	1	S61G_YEAST	P33179 saccharomyc
113	30	14.2	56	1	VG36_BPML5	Q05246 mycobacteri	186	29	13.7	80	1	Y509_ECO57	P58092 escherichia
114	30	14.2	60	1	YAB7_ARCFU	O29178 archaeoglob	187	29	13.7	81	1	YAHK_ECOLI	P73692 escherichia
115	30	14.2	61	1	Y667_ARCFU	Q29590 archaeoglob	188	29	13.7	82	1	ATPH_CHLIE	Q73304 chlamydomon
116	30	14.2	62	1	UCRX_HUMAN	Q9udw1 homo sapien	189	29	13.7	83	1	RI17_PORPU	Q06842 halobacteri
117	30	14.2	62	1	XYLH_PSEPU	Q01468 pseudomonas	190	29	13.7	83	1	RI17_PORPU	P13397 tremyella d
118	30	14.2	70	1	REGI_BOVIN	P82943 bos taurus	191	29	13.7	83	1	PS1L_FREDI	P13305 porphyra pu
119	30	14.2	71	1	BDM_ECOLI	Q8xat7 escherichia	192	29	13.7	85	1	PS1L_FREDI	P13397 tremyella d
120	30	14.2	71	1	BDM_ECOLI	P76127 escherichia	193	29	13.7	85	1	ACPX_STRCN	P47406 mycoplasma
121	30	14.2	72	1	NXL4_OPHRA	P80156 ophiophagus	194	29	13.7	86	1	MYSF_DICDI	Q02570 streptomyce
122	30	14.2	72	1	NXL5_OPHRA	P80965 ophiophagus	195	29	13.7	86	1	YFHL_HAEIN	P54695 dictyosteli
123	30	14.2	74	1	CBQO_CHRVI	P56540 chromatium	196	29	13.7	86	1	YFJL_ECOLI	P44746 haemophilus
124	30	14.2	74	1	COLE_ZOPAT	P80032 zophobas at	197	29	13.7	87	1	YFJL_ECOLI	P52128 escherichia
125	30	14.2	77	1	CSME_CHLTE	O68986 chlorobium	198	29	13.7	88	1	RS16_BACST	P58190 sulfolobus
126	30	14.2	77	1	YHR2_VACCV	P17358 vaccinia vi	199	29	13.7	88	1	DBH_HAEIN	P81290 bacillus st
127	30	14.2	78	1	R28B_STRCO	Q9x8x8 streptomyce	200	28.5	13.4	50	1	SY05_PIG	P43722 haemophilus
128	30	14.2	78	1	PER_BACTJ	Q84433 methanococc	201	28.5	13.4	53	1	LEC1_LATOC	Q29288 sus scrofa
129	30	14.2	82	1	PER_BACTJ	P02122 bacillus st	202	28.5	13.4	53	1	LEC2_LATOC	P12306 lathyrus oc
130	30	14.2	82	1	S6B1_YEAST	P28702 saccharomyc	203	28.5	13.4	53	1	LEC2_LATOC	P12307 lathyrus oc
131	30	14.2	83	1	VP39_BRAPS	Q9t1q9 bacterioph	204	28.5	13.4	57	1	Y05L_BPT4	P07442 lathyrus ar
132	30	14.2	86	1	RS18_CAMJE	O69301 campylobact	205	28.5	13.4	60	1	Y569_ARCFU	O9cd69 mycobacteri
133	30	14.2	86	1	YABE_ESCFE	P28243 escherichia	206	28.5	13.4	60	1	GRG_CAEEL	P39237 bacterioph
134	30	14.2	87	1	RL26_ARATH	P51414 arabidopsis	207	28.5	13.4	62	1	Y569_ARCFU	O13199 archaeoglob
135	29.5	13.9	42	1	GIP_BOVIN	P09680 bos taurus	208	28.5	13.4	63	1	BO03_MOUSE	P54406 caenorhabdi
136	29.5	13.9	47	1	FPG_SYNP6	Q08079 synechococc	209	28.5	13.4	63	1	BO03_MOUSE	Q9wcl0 mus musculu
137	29.5	13.9	69	1	GBGU_HUMAN	O14610 homo sapien	210	28.5	13.4	66	1	YFBL_CAEEL	Q32620 helicobacte
138	29.5	13.9	72	1	Y003_ARCFU	Q30268 archaeoglob	211	28.5	13.4	66	1	YFBL_CAEEL	P35074 caenorhabdi
139	29.5	13.9	81	1	YFVX_HV12	P35966 human immun	212	28.5	13.4	67	1	YFBL_CAEEL	Q51384 pseudomonas
140	29.5	13.9	82	1	YFVX_PLEBO	P46043 plectonema	213	28.5	13.4	67	1	YFBL_CAEEL	P43882 methanobact
141	29.5	13.9	83	1	RT19_PLASU	P50893 plafonemas	214	28.5	13.4	67	1	YFBL_CAEEL	Q92e04 rickettsia
142	29.5	13.9	84	1	RL24_SULAC	O05633 sulfolobus	215	28.5	13.4	69	1	Y158_RICFR	Q92s36 thizobium m
143	29.5	13.9	86	1	ACP_CYACA	O19921 cyanidium c	216	28.5	13.4	80	1	EX7S_RICCN	Q92ies rickettsia
144	29.5	13.9	87	1	RS19_MYCGE	P47401 mycoplasma	217	28.5	13.4	81	1	YFBL_CAEEL	P05925 human immun
145	29.5	13.9	88	1	EX7S_STRCO	Q9f8m4 streptomyce	218	28.5	13.4	81	1	YFBL_CAEEL	P18806 human immun
146	29.5	13.9	88	1	YFVX_LISMO	O31148 listeria mo	219	28.5	13.4	82	1	EX7B_YEAST	P12515 human immun
147	29.5	13.9	88	1	YFVX_LISMO	P10132 mycoplasma	220	28.5	13.4	83	1	EX7S_RHIME	P38711 saccharomyc
148	29.5	13.9	88	1	RS19_UREPA	Q9p936 ureaplasma	221	28.5	13.4	84	1	RS16_RALSO	Q92r19 rhizobium m
149	29.5	13.9	90	1	PTSN_BRAJA	P33032 bradyrhizob	222	28.5	13.4	84	1	Y101_SSV1	Q9y0w0 talstonia s
150	29	13.7	44	1	DERM_PIG	P43846 sus scrofa	223	28.5	13.4	85	1	YFBL_CAEEL	P20212 sulfolobus
151	29	13.7	49	1	YLDH_MYCHY	P46188 mycoplasma	224	28.5	13.4	85	1	YFBL_CAEEL	P44228 haemophilus
152	29	13.7	51	1	YLDH_MYCHY	P80105 ectothiorho	225	28.5	13.4	85	1	YFBL_CAEEL	P50438 caenorhabdi
153	29	13.7	51	1	YLDH_MYCHY	P05559 casuarus c	226	28.5	13.4	88	1	YFBL_CAEEL	P04490 human adeno
154	29	13.7	55	1	YQAO_CAEEL	Q9xy35 drosophila	227	28.5	13.4	88	1	YFBL_CAEEL	O07125 lactobacill
155	29	13.7	55	1	YQAO_CAEEL	P81161 lycopersico	228	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
156	29	13.7	57	1	YQAO_CAEEL	P57484 buchnera ap	229	28.5	13.4	89	1	YFBL_CAEEL	O28885 archaeoglob
157	29	13.7	57	1	YQAO_CAEEL	P41462 autographa	230	28.5	13.4	89	1	YFBL_CAEEL	O28498 archaeoglob
158	29	13.7	58	1	YQAO_CAEEL	P00209 desulfovibr	231	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
159	29	13.7	60	1	YH14_ARCFU	O28559 archaeoglob	232	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
160	29	13.7	61	1	YH14_ARCFU	Q28559 archaeoglob	233	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
161	29	13.7	61	1	YH14_ARCFU	Q28559 archaeoglob	234	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
162	29	13.7	62	1	YH14_ARCFU	Q28559 archaeoglob	235	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
163	29	13.7	62	1	YH14_ARCFU	Q28559 archaeoglob	236	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
164	29	13.7	62	1	YH14_ARCFU	Q28559 archaeoglob	237	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
165	29	13.7	65	1	YH14_ARCFU	Q28559 archaeoglob	238	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
166	29	13.7	66	1	YH14_ARCFU	Q28559 archaeoglob	239	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
167	29	13.7	66	1	YH14_ARCFU	Q28559 archaeoglob	240	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
168	29	13.7	67	1	YH14_ARCFU	Q28559 archaeoglob	241	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
169	29	13.7	67	1	YH14_ARCFU	Q28559 archaeoglob	242	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
170	29	13.7	68	1	YH14_ARCFU	Q28559 archaeoglob	243	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
171	29	13.7	69	1	YH14_ARCFU	Q28559 archaeoglob	244	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
172	29	13.7	70	1	YH14_ARCFU	Q28559 archaeoglob	245	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
173	29	13.7	71	1	YH14_ARCFU	Q28559 archaeoglob	246	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
174	29	13.7	72	1	YH14_ARCFU	Q28559 archaeoglob	247	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
175	29	13.7	72	1	YH14_ARCFU	Q28559 archaeoglob	248	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
176	29	13.7	73	1	YH14_ARCFU	Q28559 archaeoglob	249	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
177	29	13.7	74	1	YH14_ARCFU	Q28559 archaeoglob	250	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
178	29	13.7	74	1	YH14_ARCFU	Q28559 archaeoglob	251	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma
179	29	13.7	76	1	YH14_ARCFU	Q28559 archaeoglob	252	28.5	13.4	89	1	YFBL_CAEEL	P47684 mycoplasma

253	26	13.2	70	1	YVAK_VACC	P20520	vaccinia vi	326	27.5	13.0	50	1	VKIL_BPHK0	P18682	bacteriophag
254	28	13.2	71	1	ST1E_XENLA	O90005	xenopus lae	327	27.5	13.0	54	1	SN25_BARIT	P55820	oryctolagus
255	28	13.2	72	1	IF1_CAUCR	O9a5v4	caulobacter	328	27.5	13.0	56	1	NINE_BPR21	O9xJg3	pseudomonas
256	28	13.2	73	1	PACA_PIG	P41535	s pituitary	329	27.5	13.0	61	1	CSRW_PSEAE	O69076	bacteriophag
257	28	13.2	73	1	RL24_HELPJ	O92j38	helicobacte	330	27.5	13.0	65	1	YBFI_ECOLI	P39901	escherichia
258	28	13.2	73	1	RL24_HELPJ	P56049	helicobacte	331	27.5	13.0	65	1	YBFI_ECOLI	P39289	escherichia
259	28	13.2	74	1	ATPL_RICPR	O92ec2	rickettsia	332	27.5	13.0	65	1	YBFI_ECOLI	P39289	escherichia
260	28	13.2	74	1	CSMB_CHLTE	O46383	chlorobium	333	27.5	13.0	72	1	UFON_HALNI	P36001	chlamydia t
261	28	13.2	74	1	MTL_ORYSA	O40633	oryza sativ	334	27.5	13.0	77	1	ULL1_HSV6U	P24448	human herpe
262	28	13.2	74	1	NKLA_BUNMU	P01378	bungarus mu	335	27.5	13.0	77	1	ACPL_CHLPN	P24448	human herpe
263	28	13.2	75	1	PSK3_ORYSA	O9f1f9	oryza sativ	336	27.5	13.0	79	1	MT2_MALDO	Q24883	chlamydia p
264	28	13.2	75	1	R17E_THEAC	O9f1f9	oryza sativ	337	27.5	13.0	81	1	FTSL_BUCAP	Q24058	malus domes
265	28	13.2	75	1	YVAF_VACC	P20515	thermoplasm	338	27.5	13.0	82	1	RS27A_YEAST	O85296	buchnera api
266	28	13.2	76	1	MTL_MATZE	P30571	zea mays (m	339	27.5	13.0	83	1	RS27A_YEAST	P35997	saccharomyc
267	28	13.2	76	1	RUXG_HUMAN	G15357	homo sapien	340	27.5	13.0	83	1	RS27A_YEAST	P42677	homo sapien
268	28	13.2	77	1	RL28_ECOLI	G82428	escherichia	341	27.5	13.0	83	1	RS27A_YEAST	P24051	rattus norv
269	28	13.2	77	1	RL28_FALSO	O9xw93	methanococc	342	27.5	13.0	83	1	RS27A_YEAST	P47904	xenopus lae
270	28	13.2	77	1	Y660_METJA	G58074	methanococc	343	27.5	13.0	83	1	YF24_ARCFU	Q28748	archaeoglob
271	28	13.2	77	1	ACR_SHIDY	G58274	cyanophora	344	27.5	13.0	83	1	YQ19_BACAN	Q38748	archaeoglob
272	28	13.2	78	1	DLAC_STAXY	Q53372	shigella dy	345	27.5	13.0	84	1	YB72_METJA	Q38748	archaeoglob
273	28	13.2	78	1	YHSG_ECOLI	O9x2n6	staphylococ	346	27.5	13.0	86	1	RS27A_YEAST	Q38748	archaeoglob
274	28	13.2	78	1	YHSG_ECOLI	O9x2n6	staphylococ	347	27.5	13.0	86	1	RS27A_YEAST	Q38748	archaeoglob
275	28	13.2	78	1	C590_THADE	O98448	escherichia	348	27.5	13.0	87	1	YSCF_YEREN	O01247	yersinia en
276	28	13.2	80	1	CD24_HUMAN	P25063	homo sapien	349	27.5	13.0	88	1	PTHP_ENTFA	P07515	enterococcu
277	28	13.2	80	1	PSAC_ANTSP	O06439	antithamnio	350	27.5	13.0	88	1	PTHP_LACCA	Q9KjV3	lactobacill
278	28	13.2	80	1	PSAC_CHLRE	Q00914	chlamydomon	351	27.5	13.0	88	1	S108_MOUSE	P27005	mus musculus
279	28	13.2	80	1	PSAC_CHLUV	P56301	chlorella v	352	27.5	13.0	88	1	Y216_LISMO	Q924m1	listeria mo
280	28	13.2	80	1	PSAC_EGGRV	P31556	euglena gra	353	27.5	13.0	88	1	Y248_LISIN	Q92f59	listeria en
281	28	13.2	80	1	PSAC_GOUTH	P31556	euglena gra	354	27.5	13.0	89	1	XHLA_BACSU	P39798	bacillus su
282	28	13.2	80	1	PSAC_GAIZE	O78443	guillardia								



399	27	12.7	75	1	FTRV_SYNY3	Q55781	synchocyst	472	26.5	12.5	60	1	RL30_THETH	p74909	thermus the
400	27	12.7	75	1	MCHB_ECOLI	Q9ms3	escherichia	473	26.5	12.5	62	1	CSRA_PASMU	P57934	pasteurella
401	27	12.7	75	1	MTL_CICAR	Q30458	cicer ariet	474	26.5	12.5	62	1	GVPA_OSCAG	P80996	oscillatoria
402	27	12.7	75	1	Y14E_BPW6	P39508	bacterioph	475	26.5	12.5	65	1	RS10_DESMO	P41207	desulfuroc
403	27	12.7	75	1	Y14E_BPW6	Q36168	bacterioph	476	26.5	12.5	66	1	GVPA_AMOPE	P80998	anoebobacte
404	27	12.7	75	1	Y14E_BPW6	P33014	escherichia	477	26.5	12.5	66	1	YVED_VACCC	P20556	vaccinia vi
405	27	12.7	76	1	Y14E_BPW6	Q28983	helicobacte	478	26.5	12.5	69	1	CL28_AQUAE	O66492	aquifex aeo
406	27	12.7	76	1	CSNA_HELPY	Q28463	macaca fasc	479	26.5	12.5	69	1	CSPG_ECOLI	O47130	escherichia
407	27	12.7	76	1	TPX4_LPTSC	P49269	apostichus	480	26.5	12.5	70	1	YAJM_RHISN	P55513	rhizobium s
408	27	12.7	77	1	MEED_ECOLI	P33660	escherichia	481	26.5	12.5	70	1	YVAN_VACCC	P20523	vaccinia v
409	27	12.7	77	1	RU28_SALTY	Q54325	salmonella	482	26.5	12.5	71	1	YG27_ARCFU	O28646	archaeoglob
410	27	12.7	77	1	YAML_STRVL	P33822	streptomyce	483	26.5	12.5	72	1	IF12_RALSO	Q8xx77	ralstonia s
411	27	12.7	77	1	YDCE_ECOLI	P31992	escherichia	484	26.5	12.5	73	1	PSAE_SYNY3	P12975	synchocyst
412	27	12.7	77	1	YOR2_FIVSD	P31903	celline immu	485	26.5	12.5	74	1	YOB0_BPP2	Q06422	bacterioph
413	27	12.7	78	1	DLTC_STAAM	Q33663	staphylococ	486	26.5	12.5	75	1	YH56_CLOAB	Q87196	clostridium
414	27	12.7	78	1	HOLI_BPW1	P51727	bacterioph	487	26.5	12.5	77	1	Y16S_SYNP6	Q8tx34	methanopyru
415	27	12.7	78	1	HXA5_SALSA	P09637	salmo salar	488	26.5	12.5	77	1	ACP_AZOBK	P05676	synchococc
416	27	12.7	78	1	MULI_MORMO	P02940	morganella	489	26.5	12.5	78	1	DLTC_LISIN	P94123	azospirillu
417	27	12.7	79	1	HFQ_RALSO	Q8y025	ralstonia s	490	26.5	12.5	78	1	DLTC_LISIN	Q93d49	listeria in
418	27	12.7	80	1	COXK_MOUSE	P56392	mus musculus	491	26.5	12.5	78	1	R320_STRPN	Q97rh7	streptococ
419	27	12.7	80	1	KORB_STRLI	P22404	streptomyce	492	26.5	12.5	78	1	VG63_BPM2	O64255	mycobacteri
420	27	12.7	80	1	PSAC_ANASP	P23392	anabaena sp	493	26.5	12.5	78	1	YKFF_ECOLI	P75677	escherichia
421	27	12.7	80	1	PSAC_ARATH	P07136	arabidopsis	494	26.5	12.5	79	1	RUXX_METTH	O26745	methanobact
422	27	12.7	80	1	PSAC_CVACA	Q19905	cyanidium c	495	26.5	12.5	81	1	RANA_RANPI	P08950	rana pipien
423	27	12.7	80	1	PSAC_CVACA	P31173	cyanophora	496	26.5	12.5	82	1	RS27_SCHPO	O74330	schizosacch
424	27	12.7	80	1	PSAC_GNEGN	P23810	freneyella d	497	26.5	12.5	83	1	ACTO_ENTHI	O15602	entamoeba h
425	27	12.7	80	1	PSAC_GNEGN	Q9mri1	gnecum gnem	498	26.5	12.5	85	1	YME3_THIFE	P22904	thiobacillu
426	27	12.7	80	1	PSAC_PEA	O07112	mastigoclad	499	26.5	12.5	85	1	YFBS_BACSU	P54160	bacillus su
427	27	12.7	80	1	PSAC_PEA	P10793	pisum sativ	500	26.5	12.5	85	1	YQAH_BACSU	P45905	bacillus su
428	27	12.7	80	1	PSAC_SPIOL	P10098	spinacia ol	501	26.5	12.5	85	1	YV22_SYNY3	P73055	synchocyst
429	27	12.7	80	1	PSAC_SNYEN	P18083	synchococcc	502	26.5	12.5	86	1	REV_HV123	Q57716	methanococ
430	27	12.7	80	1	PSAC_SYPN2	P31087	synchococcc	503	26.5	12.5	86	1	PORT_METJA	P05867	human immun
431	27	12.7	80	1	PSAC_SYPN6	P31085	synchococcc	504	26.5	12.5	86	1	R31B_RALSO	Q8y062	ralstonia s
432	27	12.7	80	1	PSAC_SYPN3	O69195	synchococcc	505	26.5	12.5	87	1	PTHF_BACST	P23404	cyanobacter
433	27	12.7	81	1	PER_BACSU	P32422	synchococcc	506	26.5	12.5	88	1	RR17_CVAPA	P58091	caulobacter
434	27	12.7	81	1	PER_BACSU	P50727	bacillus th	507	26.5	12.5	88	1	Y874_CAUCR	Q9ydv9	aeropyrum p
435	27	12.7	81	1	YXIS_ECOLI	P10245	bacillus th	508	26.5	12.5	88	1	RPOK_AERPE	Q9z6g9	chlamydia p
436	27	12.7	81	1	ATPH_ECOLI	P75970	escherichia	509	26.5	12.5	89	1	RS15_CHLPN	Q9z6g9	chlamydia p
437	27	12.7	82	1	ATPH_ECOLI	P56297	chlorella v	510	26.5	12.5	89	1	RS15_CHLTR	O84850	enterococcu
438	27	12.7	82	1	RS16_PASMU	P58123	pasteurella	511	26.5	12.5	89	1	NTPR_ENTHR	Q48433	klebsiella
439	27	12.7	82	1	VSMF_CVCAI	P36696	canine ente	512	26	12.3	42	1	ARAA_KLEPN	P49865	enterococcu
440	27	12.7	82	1	Y200_METJA	Q9zcm7	rickettsia	513	26	12.3	43	1	PSBN_ARATH	P12172	arabidopsis
441	27	12.7	82	1	Y697_RICPR	Q9zcm7	rickettsia	514	26	12.3	43	1	Y352_RICPR	O9zdh6	rickettsia
442	27	12.7	82	1	YFTD_METFE	P56509	methanother	515	26	12.3	43	1	LANA_STRSL	P36500	streptococ
443	27	12.7	83	1	PCGA_PIG	Q29011	sus scrofa	516	26	12.3	48	1	TPX2_STRPN	P42365	streptococ
444	27	12.7	83	1	RL23_MYCTU	O28356	archaeoglob	517	26	12.3	49	1	CC10_CANPG	P81588	cancer pagu
445	27	12.7	83	1	TATA_MYCTU	Q10703	mycobacteri	518	26	12.3	50	1	IOVO_RHYFU	P52251	leishmania
446	27	12.7	84	1	ACPH_MYCTU	Q11014	mycobacteri	519	26	12.3	51	1	RL40_LETMA	O85551	leishmania
447	27	12.7	85	1	MTRE_METVA	Q50830	methanococ	520	26	12.3	52	1	SODD_DEBHA	P82902	debaromyce
448	27	12.7	85	1	RS20_BORBU	P49394	borrelia bu	521	26	12.3	52	1	Y039_TREPA	O81081	treponema p
449	27	12.7	86	1	AMP_AMACA	P27275	amaranthus	522	26	12.3	55	1	RLX_HALMA	P14125	haloarcu
450	27	12.7	86	1	ONGI_VIBCH	Q8kuh2	vibrio chol	523	26	12.3	55	1	SRY_MELME	P36390	halichoer
451	27	12.7	87	1	SF19_METJA	Q8kuh2	methanococ	524	26	12.3	55	1	Y057_NPVAC	P36392	meles meles
452	27	12.7	87	1	RPOZ_HREIN	P43740	haemophilus	525	26	12.3	56	1	G559_BPSPI	O48413	bacterioph
453	27	12.7	88	1	YFIS_BPMU	Q9ctix4	bacterioph	526	26	12.3	56	1	Y097_NPVAC	P44657	autographa
454	27	12.7	89	1	YALI_BACLI	P33670	pseudomonas	527	26	12.3	58	1	GSRR_SPISP	P11804	spirulina s
455	27	12.7	89	1	YALI_BACLI	Q99164	bacillus li	528	26	12.3	58	1	Y0AH_ECOLI	P76260	escherichia
456	27	12.7	90	1	DBHA_ECOLI	P02342	escherichia	529	26	12.3	59	1	Y0AH_ECOLI	P01416	dendroaspis
457	27	12.7	90	1	DBHA_VIBPR	P15148	salmonella	530	26	12.3	60	1	NXS1_DENPO	P01406	dendroaspis
458	27	12.7	90	1	DBHA_VIBPR	P28080	vibrio prot	531	26	12.3	60	1	TX54_DENJA	P01420	naja naja
459	27	12.7	90	1	RS16_BACHD	Q8kall	bacillus ha	532	26	12.3	61	1	NXS4_NAJHA	P01421	naja naja
460	27	12.7	90	1	RS20_FUSNN	Q8rhwl	fusobacteri	533	26	12.3	61	1	NXS4_NAJHA	P12867	actinoplan
461	27	12.7	90	1	YOCB_BACSU	P45937	synchocyst	534	26	12.3	62	1	CSRA_PSEFL	Q9x6d6	pseudomonas
462	27	12.7	90	1	YV77_SYNY3	P73455	synchocyst	535	26	12.3	62	1	ITHP_HIRMA	P26631	hirudina
463	26.5	12.5	43	1	MEMI_SCHPO	P34068	schizosacch	536	26	12.3	62	1	Y57M_ECOLI	P00430	bos taurus
464	26.5	12.5	43	1	PSBN_ORYSA	P12171	oryza sativ	537	26	12.3	63	1	COXO_BOVIN	P05287	escherichia
465	26.5	12.5	45	1	YH33_ARCFU	O28541	archaeoglob	538	26	12.3	63	1	RL35_CHLTR	O84841	chlamydia t
466	26.5	12.5	46	1	COAT_BPW75	P82889	bacterioph	539	26	12.3	64	1	R17E_ARCFU	O29351	archaeoglob
467	26.5	12.5	52	1	YAAB_BACSU	P37525	bacillus su	540	26	12.3	65	1	COFF_HELPY	Q48271	helicobacte
468	26.5	12.5	53	1	Y525_METJA	O57945	methanococ	541	26	12.3	66	1	GLGS_EC057	P58613	escherichia
469	26.5	12.5	54	1	LECA_LATTI	P07444	lathyrus ti	542	26	12.3	66	1	GLGS_EC057	P58613	escherichia
470	26.5	12.5	55	1	PER_CLOSP	P00197	clostridium	543	26	12.3	66	1	GLGS_EC057	P58613	escherichia
471	26.5	12.5	58	1	PER_METFE	Q01700	methanosarc	544	26	12.3	66	1	GLGS_EC057	P58613	escherichia





837	25	11.8	88	1	RS21_CAEEL	P49197 caenorhabdi	910	24.5	11.6	87	1	PTHP_STRSL	P24366 streptococc
838	25	11.8	88	1	Y002_NPVOP	O10355 oxygia pseu	911	24.5	11.6	87	1	RS21_CANAL	Q9P644 candida alb
839	25	11.8	89	1	ALB1_PHAAR	Q9fr18 phaseolus a	912	24.5	11.6	88	1	ECU1_HALMO	P25331 bombyx mori
840	25	11.8	89	1	FLIQ_ECOLI	P31134 escherichia	913	24.5	11.6	88	1	EFIB_HALMO	Q9hg66 halobacteri
841	25	11.8	89	1	FLIQ_SALTY	P47701 salmonella	914	24.5	11.6	88	1	MK31_YEAST	P23059 saccharomyc
842	25	11.8	89	1	HV02_HEFFR	P04215 heterodontu	915	24.5	11.6	88	1	PTHP_LACLA	Q9cJ83 lactococcus
843	25	11.8	89	1	RL28_CHLMO	Q9PKV0 chlamydia m	916	24.5	11.6	88	1	PTHP_LACLA	Q9Zad9 lactococcus
844	25	11.8	89	1	R228_CHLTR	O84088 chlamydia t	917	24.5	11.6	89	1	RL31_METAC	Q8tin3 methanosarc
845	25	11.8	89	1	YN12_MYCTU	P19000 mycobacteri	918	24.5	11.6	90	1	DBHB_VIBCH	Q9Kgs9 vibrio chol
846	25	11.8	89	1	YRR8_MYCCA	P43047 mycoplasma	919	24.5	11.6	90	1	LPFA_HUMAN	Q95968 homo sapien
847	25	11.8	90	1	AC6B_MANSE	P31824 manduca sex	920	24	11.3	42	1	YADH_CLOBE	P25981 clostridium
848	25	11.8	90	1	AX6B_SOYBN	P33083 glycine max	921	24	11.3	43	1	CYTA_THETS	P81063 thieromyzon
849	25	11.8	90	1	DBH_THEAC	P02345 rhizobium m	922	24	11.3	43	1	P8BN_ANASP	Q8YyK1 anabaena sp
850	25	11.8	90	1	NOLS_RHIME	Q52975 rhizobium m	923	24	11.3	44	1	TISR_HUMAN	Q9Y5m6 homo sapien
851	25	11.8	90	1	PTHP_PSEAE	Q8hvv2 pseudomonas	924	24	11.3	45	1	AT12_HSVF4	Q00041 equine herp
852	25	11.8	90	1	R35A_METAE	Q8hvv2 pseudomonas	925	24	11.3	46	1	CSPA_YEREN	Q56922 escherichia
853	25	11.8	90	1	RS16_STRPN	Q97tm8 streptococc	926	24	11.3	48	1	YK82_ARCFU	Q28197 archaeoglob
854	25	11.8	90	1	YAWF_SCHPO	Q10189 schizosacch	927	24	11.3	49	1	RL16_AQUPY	Q9a143 aquilex pyr
855	25	11.8	90	1	YEGX_ECOLI	P76231 escherichia	928	24	11.3	51	1	LANB_STRFY	P36501 streptococc
856	25	11.8	90	1	YJG3_MYCTU	P52065 escherichia	929	24	11.3	51	1	SURE_HAESO	Q54557 streptococc
857	25	11.8	90	1	YV9A_ECOLI	Q10865 mycobacteri	930	24	11.3	51	1	YDFA_ECOLI	P36686 haemophilus
858	25	11.8	90	1	VIL1_BPW7	P75992 escherichia	931	24	11.3	52	1	LHA_ROSDE	P29008 escherichia
859	24.5	11.6	45	1	CSPA_PHOMO	P03779 bacteriophia	932	24	11.3	52	1	SRY_CROSU	P26273 roseobacter
860	24.5	11.6	47	1	AEPL_ERWCA	Q51929 photobacter	933	24	11.3	52	1	SRY_NEOAN	Q95175 crocidura s
861	24.5	11.6	55	1	ANDP_DROME	P36391 maceca fasc	934	24	11.3	52	1	YQAE_ECOLI	Q95202 neomys anom
862	24.5	11.6	58	1	VPUL_HV12H	P21663 drosophila	935	24	11.3	52	1	INS_ANGAN	P77240 escherichia
863	24.5	11.6	59	1	NAPE_PARPIN	P08806 human immun	936	24	11.3	53	1	LA_RABIT	P41522 anguilla an
864	24.5	11.6	63	1	CECC_CERCA	Q56348 paracoccus	937	24	11.3	53	1	APR_HUMAN	Q04504 mycobacteri
865	24.5	11.6	63	1	HIG2_HUMAN	Q29561 drosophila	938	24	11.3	54	1	IOVO_LARRI	Q05304 mycobacteri
866	24.5	11.6	63	1	Y07K_CVB	Q95512 homo sapien	939	24	11.3	54	1	IOVO_POLPL	P05614 larus sapien
867	24.5	11.6	65	1	RY7E_PYRAB	P37990 chrysanthem	940	24	11.3	54	1	IOVO_STRCA	P52265 polyborus p
868	24.5	11.6	67	1	W373_ARCFU	Q51282 porphyra pu	941	24	11.3	54	1	IOVO_STRCA	P05557 struthio ca
869	24.5	11.6	69	1	HMFA_METFE	O29531 archaeoglob	942	24	11.3	55	1	VG87_BPND2	O64268 mycobacteri
870	24.5	11.6	70	1	CSPA_VIBCH	Q9a143 aquilex pyr	943	24	11.3	55	1	FIXS_RHIME	P18399 rhizobium m
871	24.5	11.6	70	1	RV1E_METRA	Q8u412 microcystis	944	24	11.3	56	1	MT_SYNVU	P30565 synecococc
872	24.5	11.6	71	1	ARRO_RAT	P36577 rattus norv	945	24	11.3	57	1	COAE_BURPS	Q9af69 burkholderi
873	24.5	11.6	71	1	GVPA_PSEAN	P22453 pseudanabae	946	24	11.3	57	1	RYOK_PYRHO	Q9af93 pyrococcus
874	24.5	11.6	71	1	HP12_ECTVA	P38524 ectothiorho	947	24	11.3	58	1	YAS9_ARCFU	P29203 archaeoglob
875	24.5	11.6	71	1	HMFA_METFE	Q9a143 aquilex pyr	948	24	11.3	58	1	FER_THEMA	P46797 thermotoga
876	24.5	11.6	70	1	CSPA_VIBCH	Q9a143 aquilex pyr	949	24	11.3	60	1	CPAL_ECOLI	P03834 escherichia
877	24.5	11.6	70	1	GVPA_VIBCH	O9a143 aquilex pyr	950	24	11.3	61	1	PSAE_ERWHE	O54457 erwinia her
878	24.5	11.6	70	1	RV1E_METRA	P08412 microcystis	951	24	11.3	61	1	RI4A_LACLA	Q9cdx5 lactococcus
879	24.5	11.6	70	1	RV1E_METRA	Q8u412 microcystis	952	24	11.3	61	1	RI4A_LACLA	Q9cdx5 lactococcus
880	24.5	11.6	71	1	ARRO_RAT	P36577 rattus norv	953	24	11.3	61	1	YW98_PYRAB	Q9s34 staphylococ
881	24.5	11.6	71	1	GVPA_PSEAN	P22453 pseudanabae	954	24	11.3	62	1	COXC_HORVU	Q9uzf0 pyrococcus
882	24.5	11.6	71	1	HP12_ECTVA	P38524 ectothiorho	955	24	11.3	62	1	NXSC_LATCR	Q42841 hordeum vul
883	24.5	11.6	71	1	HMFA_METFE	Q9a143 aquilex pyr	956	24	11.3	62	1	SCX2_TITBA	P10458 laticauda c
884	24.5	11.6	71	1	CSPA_VIBCH	O9a143 aquilex pyr	957	24	11.3	62	1	YCF9_CHLRE	P56609 titius bahi
885	24.5	11.6	72	1	YH12_ARCFU	C28561 archaeoglob	958	24	11.3	62	1	COXO_HUMAN	P92276 chlamydomon
886	24.5	11.6	72	1	CCDA_ECOLI	P56702 escherichia	959	24	11.3	63	1	RL7E_METAC	P15954 homo sapien
887	24.5	11.6	72	1	YH12_ARCFU	O28561 archaeoglob	960	24	11.3	64	1	LHA3_RHOPA	Q8thp2 methanosarc
888	24.5	11.6	73	1	YH12_ARCFU	P44120 haemophilus	961	24	11.3	65	1	RL35_THETH	P31503 rhodospseud
889	24.5	11.6	74	1	ABL_CALVI	P11681 calliphora	962	24	11.3	65	1	Y319_ARCFU	P12141 oryza sativ
890	24.5	11.6	76	1	RS18_XYLFA	O9paf8 xylella fas	963	24	11.3	65	1	Y319_ARCFU	P80341 thermus the
891	24.5	11.6	77	1	RS20_STRPY	O992h0 streptococc	964	24	11.3	65	1	Y319_ARCFU	O29926 archaeoglob
892	24.5	11.6	78	1	DLTC_BACSU	P39579 bacillus su	965	24	11.3	65	1	ATP8_CEREH	O78517 guillardia
893	24.5	11.6	78	1	RV1E_SULTO	O975v4 sulfolobus	966	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
894	24.5	11.6	79	1	ACP2_PSEAE	O52658 pseudomonas	967	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
895	24.5	11.6	79	1	Y607_METJA	O58024 treponema p	968	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
896	24.5	11.6	80	1	Y607_METJA	O83876 treponema p	969	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
897	24.5	11.6	81	1	RS16_GLOPE	O8xjp4 clostridium	970	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
898	24.5	11.6	82	1	APVL_MELGA	P02860 meleagris g	971	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
899	24.5	11.6	82	1	GATC_METJA	Q57654 methanococc	972	24	11.3	66	1	ATP8_CEREH	O9a143 aquilex pyr
900	24.5	11.6	83	1	RS21_HUMAN	P35265 homo sapien	973	24	11.3	67	1	HARA_PYRAB	Q9vlt0 pyrococcus
901	24.5	11.6	83	1	RS21_HUMAN	P55833 homarus ame	974	24	11.3	67	1	HARA_PYRAB	O74098 pyrococcus
902	24.5	11.6	83	1	RS21_HUMAN	P20330 bacteriophia	975	24	11.3	67	1	HARB_PYRPU	O59627 pyrococcus
903	24.5	11.6	84	1	Y607_BP73	O44156 actinobacil	976	24	11.3	69	1	Y3BJ_ECOLI	P32691 escherichia
904	24.5	11.6	84	1	Y607_BP73	O9wx15 buchnera ap	977	24	11.3	70	1	YOG6_CAEEL	P34615 caenorhabdi
905	24.5	11.6	85	1	PTHP_BUCAL	O9pr18 gallus gall	978	24	11.3	71	1	Y416_UREPA	Q9pqr73 ureaplasma
906	24.5	11.6	86	1	ACBP_CHICK	O9pr18 gallus gall	979	24	11.3	71	1	EX7S_STRPY	Q95yx4 streptococc
907	24.5	11.6	86	1	PTHP_STRMU	P45596 streptococc	980	24	11.3	71	1	VTB2_XENLA	P19011 xenopus lae
908	24.5	11.6	86	1	Y425_TREPA	O83440 treponema p	981	24	11.3	71	1	YE35_METJA	Q58830 methanococc
909	24.5	11.6	87	1	PTHP_STRBO	O9wxk8 streptococc	982	24	11.3	71	1	YHRI_VACCV	P17359 vaccinia vi

SEQUENCE FROM N.A.  
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

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18 KVAERFLKDLSSQGMWKETREARAKKOLEEGLEWAKK 59

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DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein MJ0567.  
 GN MJ0567.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8680807;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 RT Science 273:1058-1073(1996).  
 RL [1]  
 CC -----  
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 CC -----  
 DR EMBL; U67505; AAB98558.1; -  
 DR TIGR; MJ0567; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 82 AA; 8766 MW; 3F3810EEFC9F81CE CRC64;  
 Query Match 19.8%; Score 42; DB 1; Length 82;  
 Best Local Similarity 32.5%; Pred. No. 77;  
 Matches 13; Conservative 8; Mismatches 11; Indels 8; Gaps 2;  
 QY 10 LVAMDFSGKSLVIRNQNGPVIIITKGSNIATIGRLAK 41  
 DB 28 LVSMGINIGSLKLVIRNQNGPVIIITKGSNIATIGRLAK 67  
 RESULT 4  
 RACD\_STAAU STANDARD; PRT; 82 AA.  
 AC P31337;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA repair protein radc homolog (25 kda protein) (Fragment).  
 DE RACD.  
 GN Staphylococcus aureus.  
 OS Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RN450;  
 RA Murphy E.;  
 RL Submitted (JAN-1986) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RC STRAIN=RN450;  
 RX MEDLINE=84117462; PubMed=6320000;  
 RA Murphy E.; Loerdahl S.;  
 RT "Transposition of Tn554 does not generate a target duplication.";  
 RL Nature 307:292-294(1984).  
 CC -!- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE RACD FAMILY.

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 CC -----  
 DR EMBL; K02985; AAA26680.1; -  
 DR InterPro; IPR001405; RACD.  
 DR ProDom; PD007415; RACD; 1.  
 DR PROSITE; PS01302; RACD; 1.  
 KW DNA repair.  
 FT NON\_TER  
 SQ SEQUENCE 82 AA; 8920 MW; 65E8BF06E3DEC3A4 CRC64;  
 Query Match 18.9%; Score 40; DB 1; Length 82;  
 Best Local Similarity 40.9%; Pred. No. 1.4e+02;  
 Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
 QY 15 FSGKSRVIEPTALSVAAVEE 36  
 DB 1 FKGTUNSSIVHPREIFSIAVRE 22  
 RESULT 5  
 RS22\_ECOLI STANDARD; PRT; 45 AA.  
 AC P28690;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30S ribosomal protein S22 (Stationary-phase-induced ribosome-  
 DE associated protein) (SRA) (Protein D).  
 GN RPSV OR SRA OR B1480 OR Z2230 OR ECS2084.  
 OS Escherichia coli, and  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia  
 OX NCBI\_TaxID=562, 83334;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-37.  
 RC STRAIN=K12 / W3110;  
 RX MEDLINE=21189300; PubMed=11292794;  
 RA Izutsu K., Wada C., Komine Y., Sako T., Ueguchi C., Nakura S.,  
 RA Wada A.;  
 RT "Escherichia coli ribosome-associated protein SRA, whose copy number  
 RT increases during stationary phase.";  
 RL J. Bacteriol. 183:2765-2773(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=90337272; PubMed=2199308;  
 RA Mahajan S.K., Chu C.C., Willis D.K., Templin A., Clark A.J.;  
 RT "Physical analysis of spontaneous and mutagen-induced mutants of  
 RT Escherichia coli K-12 expressing DNA exonuclease VIII activity.";  
 RL Genetics 125:261-273(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

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CC -----
CC EMBL: AF158101; AAD42616.1; -
CC DR Hypothetical protein.
CC KW
CC SQ
CC
CC Query Match 18.4%; Score 39; DB 1; Length 71;
CC Best Local Similarity 32.4%; Pred. No. 1.6e+02;
CC Matches 11; Conservative 5; Mismatches 16; Indels 2; Gaps 1;
CC
CC Qy 1 PMSISENSLVAMDFSGQKSR--VIENTPEALSV 32
CC Db 26 PLKSTSEKTVNATLANNSERFCIENDTETV 59
CC
CC
CC RESULT 7
CC CSPE CSPE
CC ID ID CSPE STRCO STANDARD; PRT; 67 RA.
CC P48859;
CC DC 01-FEB-1996 (Rel. 33, Created)
CC DPT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DPT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Cold shock protein SCF
CC GN SCOF OR SCO0527 OR SCF1_07C.
CC OS Streptomyces coelicolor.
CC OS Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
CC OC Neimycetales; Streptomycetaceae; Streptomycetaceae; Streptomycetes.
CC [1]_Taxid=1902;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=A3(2);
CC AV-gay Y., Ravin S., Aharonowitz Y., Cohen G.;
CC Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=A3(2)/MI45;
CC MEDLINE=21996410; PubMed=12000953;
CC Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
CC Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
CC Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
CC Cronin A., Fraser A., Goble A., Hidalgo J., Hensby T., Howarth S.,
CC Huang C.H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
CC Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
CC Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
CC Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
CC Hopwood D.A.;
CC "Complete genome sequence of the model actinomycete Streptomyces
CC coelicolor A3(2).";
CC Nature 417:141-147(2002).
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
CC -----
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CC -----
CC EMBL: X92686; CAA63367.1; -
CC DR EMBL: AL132662; CAB59584.1; -
CC KW HSPSP; P32081; ICSP.
CC SQ
CC InterPro: IPR002059; Cold_shock.
CC Pfam: PF00313; CSD; 1.
CC

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DR PRINTS: PRO0050; COLD SHOCK.  
 DR PRODOM; PRO0062; Cold\_shock; 1.  
 DR SHARI; SH00357; CSP; 1.  
 DR PROSITE; PS00352; COLD\_SHOCK; 1.  
 KW TRANSCRIPTION REGULATION; DNA-BINDING; Activator; Complete proteome.  
 FT DOMAIN 4 64 CSD.  
 SQ SEQUENCE 67 AA; 7179 MW; E4FDAD9BB1D92B34 CRC64;  
 Query Match 18.2%; Score 38.5; DB 1; Length 67;  
 Best Local Similarity 39.3%; Pred. No. 1.8e+02;  
 Matches 11; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
 OY 3 RSTSENSVAMDFFS-GQKSRVIENTTETA 29  
 DB 40 RELQEGQAVTDTQGGKGPQANITPA 67  
 RESULT 8  
 NIFH\_NOSSN STANDARD; PRT; 74 AA.  
 AC P42336  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Nitrogenase iron protein (EC 1.18.6.1) (Nitrogenase component II)  
 DE (Nitrogenase Fe protein) (Nitrogenase reductase) (Fragment).  
 GN NIFH.  
 OS Nostoc sp. (strain MUN 8820).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 ON NCBI\_TaxID=55397;  
 RX SEQUENCE FROM N.A.  
 RP MEDLINE=97086627; PubMed=8932316;  
 RA Hill D.R., Belbin T.J., Thorsteinsson M.V., Bassam D., Brass S.,  
 RA Ernst A., Beger P., Paerl H., Mulligan M.E., Potts M.;  
 RT "Gln (cyanoglobin) is a peripheral membrane protein that is  
 RT restricted to certain Nostoc spp.";  
 RL J. Bacteriol. 178:6587-6598(1996).  
 CC CATALYZED BY THE KEY ENZYMIC REACTIONS IN NITROGEN FIXATION ARE  
 CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.  
 CC -!- FUNCTION: THE KEY ENZYMIC REACTIONS IN NITROGEN FIXATION ARE  
 CC -!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP  
 CC -!- COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE NIFH / BCLH / CHLL FAMILY.  
 CC  
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 CC  
 CC EMBL; L47979; AAB41123.1; -  
 DR HSP6; P00459; ITP6.  
 DR InterPro; IPR000392; NitrogenaseII.  
 DR Pfam; PF00142; fer4\_NifH; 1.  
 DR PROSITE; PS00692; NIFH\_FRAC\_2; PARTIAL.  
 DR PROSITE; PS00746; NIFH\_FRAC\_1; PARTIAL.  
 KW Oxidoreductase; Nitrogen fixation; Iron-sulfur; 4Fe-4S; ATP-binding.  
 FT NE\_BIND 13 20 ATP (POTENTIAL).  
 FT NON\_TER 74 74  
 SQ SEQUENCE 74 AA; 7919 MW; 14B88F560242DCDE CRC64;  
 Query Match 18.2%; Score 38.5; DB 1; Length 74;  
 Best Local Similarity 25.5%; Pred. No. 2e+02;  
 Matches 12; Conservative 7; Mismatches 13; Indels 15; Gaps 1;  
 OY 6 SENSVAMDFFSQKSRV1-----ENPTALSVAVEEG 37  
 DB 23 SONTLAAMGSRILLVGCDDPKADSTRMLHLSKATQTVLHLAERG 69

RESULT 9  
 CINA\_STRGV STANDARD; PRT; 78 AA.  
 AC P29827;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lantibiotic cinnamycin precursor (Lanthiopeptin) (Lantibiotic RO  
 DE 09-0198).  
 GN CINA OR ROCA.  
 OS Streptovorticillum griseovorticillatum.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Streptomycetaceae; Streptomyces.  
 OC Actinomycetales; Streptomycetaceae; Streptomyces.  
 ON NCBI\_TaxID=68215;  
 RX SEQUENCE FROM N.A.  
 RP STRAIN=MAR\_164C-M16;  
 RC MEDLINE=91301152; PubMed=2070795;  
 RA Kaletta C., Entian K.-D., Jung G.;  
 RA "Peptide sequence of cinnamycin (RO 09-0198): the first structural  
 RT gene of a duramycin-type lantibiotic.";  
 RL Eur. J. Biochem. 199:411-415(1991).  
 RN [2]  
 RP SEQUENCE OF 60-78.  
 RX MEDLINE=91107436; PubMed=2125590;  
 RA Fredenhagen A., Fendrich G., Markl F., Gruner J.,  
 RA Raschdorf F., Peter H.H.;  
 RT "Duramycins B and C, two new lanthionine containing antibiotics as  
 RT inhibitors of phospholipase A2. Structural revision of duramycin and  
 RT cinnamycin.";  
 RL J. Antibiot. 43:1403-1412(1990).  
 RN [3]  
 RP SEQUENCE OF 60-78.  
 RX MEDLINE=89291558; PubMed=2544544;  
 RA Naruse N., Tennyson O., Tomita K., Konishi M., Miyaki T., Kawaguchi H.,  
 RA Fukase K., Wakamiya T., Shiba T.;  
 RT Lanthiopeptin, a new peptide antibiotic. Production, isolation and  
 RT properties of lanthiopeptin.";  
 RL J. Antibiot. 42:837-845(1989).  
 CC -!- FUNCTION: CAN ACT AS INHIBITOR OF THE ENZYME PHOSPHOLIPASE A2, AND  
 CC OF THE ANGIOTENSIN-CONVERTING ENZYME. SHOWS INHIBITORY ACTIVITIES  
 CC AGAINST HERPES SIMPLEX VIRUS AND IMMUNOPOTENTIATING ACTIVITIES.  
 CC ITS ANTIMICROBIAL ACTIVITIES ARE NOT VERY PRONOUNCED.  
 CC -!- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF  
 CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE  
 CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND  
 CC CLEAVAGE OF THE MODIFIED PRECURSOR.  
 CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.  
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 CC  
 CC EMBL; X58545; CA941436.1; -  
 DR PIR; S17181; EWSMIG.  
 DR PIR; A45767; EWSMCN.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT PROPEP 1 59 POTENTIAL.  
 FT CHAIN 60 78 LANTIBIOTIC CINNAMYCIN.  
 FT MOD\_RES 63 63 D-ALANINE.  
 FT MOD\_RES 65 65 D-ALANINE (BONDED TO 78).  
 FT MOD\_RES 70 70 D-ABU (AMINOBTYRIC ACID).  
 FT MOD\_RES 77 77 D-ABU (AMINOBTYRIC ACID).  
 FT MOD\_RES 78 78 LYSINOALANINE (BONDED TO 65).  
 FT THIOETH 63 73 ALA-S-CYS (LANTHIONINE).  
 FT THIOETH 64 70 ABU-S-CYS (BETA-METHYLLANTHIONINE).  
 FT THIOETH 65 78 ALA-S-CYS (BETA-METHYLLANTHIONINE).



FT THIOETH 60 77 ABU-S-CYS (BETA-METHYLLANTHIONINE).  
 SQ SEQUENCE 78 AA; 8205 MW; OACDAE5BA54E5E7A CRC64;  
 Query Match 18.2%; Score 38.5; DB 1; Length 78;  
 Best Local Similarity 34.2%; Pred. No. 2.1e+02;  
 Matches 13; Conservative 6; Mismatches 10; Indels 2;  
 Gaps 2;  
 QY 4 SISENSLVAMDFGSKSRVIENTP-----TEALSVAVE 35  
 ||:||:| || :||:| ||  
 Db 4 SILEQSVVDADF---RAALENPAAGASAAALPTPVE 38  
 ||:||:| || :||:| ||

RESULT 10  
 FER\_METHA STANDARD; PRT; 59 AA.  
 AC P00202;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ferredoxin.  
 OS Methanosarcina barkeri.  
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2208;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=MS / DSM 800;  
 RX MEDLINE=83056954; PubMed=6754724;  
 RA LaSinger R.P., Moura I., Moura J.J.G., Xavier A.V., Santos M.H.,  
 RA Regall J., Howard J.B.;  
 RT "Amino acid sequence of a 3Fe:3S ferredoxin from the  
 RT 'archaeobacterium' Methanosarcina barkeri (DSM 800).";  
 RL J. Biol. Chem. 257:14192-14197(1982).  
 CC -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER  
 CC ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.  
 CC -!- COFACTOR: BINDS ONE OR MORE 3FE-4S CLUSTERS.  
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.  
 DR PIR; A00204; FEMZB.  
 DR HSSP; P00214; 2FDZ.  
 DR InterPro; IPR001450; 4Fe4S\_ferredoxin.  
 DR Pfam; PF00037; fer4; 2.  
 DR PRINTS; PR00353; 4FE4SFRDOXIN.  
 DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; 2;  
 KW Electron transport; Iron-sulfur; 3Fe-4S.  
 SQ SEQUENCE 59 AA; 6121 MW; 22D1EB8E443422CA CRC64;

Query Match 17.9%; Score 38; DB 1; Length 59;  
 Best Local Similarity 35.7%; Pred. No. 1.8e+02;  
 Matches 10; Conservative 8; Mismatches 10; Indels 0;  
 Gaps 0;  
 QY 12 AMDFSGGSKSRVIENTPTEALSVAVEGLA 39  
 ||:||:| || :||:| ||  
 Db 6 ADECSGGCTVDECPNDAILDEEGIA 33  
 ||:||:| || :||:| ||

RESULT 11  
 FER2\_DESMV STANDARD; PRT; 63 AA.  
 AC P10624;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Ferredoxin II (Fd II).  
 OS Desulfovibrio vulgaris (strain Miyazaki).  
 OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrionaceae;  
 OC Desulfovibrio.  
 OX NCBI\_TaxID=883;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kitamura M., Konishi T., Kawanishi K., Ohashi K., Kishida M.,  
 RA Kohno K., Akutsu H., Kumagai I., Nakaya T.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE.  
 RX MEDLINE=89274328; PubMed=2855025;  
 RA Okawara N., Ogata M., Yagi T., Wakabayashi S., Matsubara H.;  
 RT "Characterization and complete amino acid sequence of ferredoxin II  
 RT from Desulfovibrio vulgaris Miyazaki.";  
 RL Biochimie 70:1815-1820(1988).  
 CC -!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER  
 CC ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.  
 CC -!- COFACTOR: BINDS 1 4FE-4S CLUSTER.  
 CC -!- SUBUNIT: HOMODIMER.  
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.  
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DR EMBL; AB005550; RA21477.1;  
 DR DLR; S07154; FBDV2V.  
 DR HSSP; P00210; IPRX.  
 DR InterPro; IPR001080; 3Fe4S\_ferredoxin.  
 DR InterPro; IPR001450; 4Fe4S\_ferredoxin.  
 DR Pfam; PF00037; fer4; 1.  
 DR PRINTS; PR00352; 3FE4SFRDOXIN.  
 DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; 1.  
 KW Electron transport; Iron-sulfur; Repeat; 4Fe-4S.  
 FT INIT\_MET 0  
 FT METAL 11 11 IRON-SULFUR (4FE-4S).  
 FT METAL 14 14 IRON-SULFUR (4FE-4S).  
 FT METAL 17 17 IRON-SULFUR (4FE-4S).  
 FT METAL 53 53 IRON-SULFUR (4FE-4S).  
 SQ SEQUENCE 63 AA; 7091 MW; 82232C1244A5C84B CRC64;

Query Match 17.9%; Score 38; DB 1; Length 63;  
 Best Local Similarity 27.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 9; Mismatches 12; Indels 1;  
 Gaps 1;  
 QY 13 MDFSOGSKSRVIENTP-----EALSVAVEGLAWKK 43  
 ||:||:| || :||:| ||  
 Db 27 MSSAGEAIEVDITTAECVEDAISTCPVECIEMREE 63  
 ||:||:| || :||:| ||

RESULT 12  
 RPON\_THEAC STANDARD; PRT; 72 AA.  
 AC Q9HL09;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA-directed RNA polymerase subunit N (EC 2.7.7.6).  
 GN RPON OR TA0431.  
 OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
 OC Thermoplasmataceae; Thermoplasma.  
 OX NCBI\_TaxID=2303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 1728;  
 RX MEDLINE=20479972; PubMed=11029001;  
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma  
 RT acidophilum";  
 RL Nature 407:508-513(2000).  
 CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
 CC of DNA into RNA using the four ribonucleoside triphosphates as  
 CC substrates.  
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +  
 CC [RNA](N).  
 CC -!- SIMILARITY: BELONGS TO THE ARCHAEABACTERIA RPON / EUKARYOTIC RPB10



ID V085\_BPML5 STANDARD; PRT; 88 AA.  
 AC Q05302;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Gene 85 protein (GP85)...  
 GN 85.  
 OS Mycobacteriophage L5.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC L5-like viruses  
 OX NCBI\_TaxID=31757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93211282; PubMed=8459766;  
 RA Hatfull G.F., Sarkis G.J.;  
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
 a phage system for mycobacterial genetics.";  
 RL Mol. Microbiol. 7:395-403(1993).  
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 CC -----  
 DR EMBL; Z18946; CAA79461.1;  
 DR PIR; S31030; S31030.  
 SQ SEQUENCE 88 AA; 10159 MW; 2927841F7D6D4BC CRC64;  
 Query Match 17.5%; Score 37; DB 1; Length 88;  
 Best Local Similarity 50.0%; Pred. No. 3.8e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 28 EALSVAVEEGLAWKK 43  
 DB 61 EALFDITWDGVAAWAKK 76  
 RESULT 16  
 RS19\_CHLPN STANDARD; PRT; 88 AA.  
 ID RS19\_CHLPN  
 AC Q27R1; Q9JRT8;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S19  
 GN RPSS OR RS19 OR CPN0643 OR CP0104.  
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=CW1029;  
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
 RL Nat. Genet. 21:385-389(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=AR39;  
 RA MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=J138;  
 RX MEDLINE=20330349; PubMed=10871362;  
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 RT from Japan and CW1029 from USA.";  
 RL Nucleic Acids Res. 28:2311-2314(2000).  
 CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL; A001647; AAD18782.1;  
 DR EMBL; A002173; AAF73629.1;  
 DR EMBL; AP002547; BAA98850.1;  
 DR HSSP; P80381; 1QKF.  
 DR TIGR; CP0104;  
 DR InterPro; IPR002222; Ribosomal\_S19.  
 DR Pfam; PF00203; Ribosomal\_S19; 1.  
 DR ProDom; PD001012; Ribosomal\_S19; 1.  
 DR TIGRFAMs; TIGR01050; rpss\_bact; 1.  
 DR PROSITE; PS00323; RIBOSOMAL\_S19; 1.  
 KW Ribosomal protein; rRNA-binding; Complete proteome.  
 FT CONFLICT 2 2 S-> G (IN REF. 1).  
 SQ SEQUENCE 88 AA; 10201 MW; EB1E98E3B4BC2588 CRC64;  
 Query Match 17.2%; Score 36.5; DB 1; Length 88;  
 Best Local Similarity 26.2%; Pred. No. 4.5e+02;  
 Matches 11; Conservative 9; Mismatches 21; Indels 1; Gaps 1;  
 QY 1 PMRSISENSLVAMDFSGKSRVIENPTEALSVAVEEGLAWRK 42  
 DB 30 PIKTSRSRSMITPMIGHTFEV-HNGKKELTVFVSETVGHK 70  
 RESULT 17  
 RS19\_CHLTP STANDARD; PRT; 88 AA.  
 ID RS19\_CHLTP  
 AC Q84329; Q9PJL8;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30S ribosomal protein S19  
 GN RPSS OR RS19 OR CT524 OR TC0811.  
 OS Chlamydia trachomatis, and  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813, 83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=C.trachomatis; STRAIN=D/UW-3/Cx;  
 RC MEDLINE=99000809; PubMed=9784136;  
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
 RA Davis R.W.;  
 RT "Genome sequence of an obligate intracellular pathogen of humans:  
 RT Chlamydia trachomatis.";  
 RL Science 282:754-759(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C.muridarum; STRAIN=MoPn / N19g;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,



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RESULT 20
ID  IPKG HUMAN STANDARD; PRT; 76 AA.
AC  O9Y2B9.
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  CAMP-dependent protein kinase inhibitor, gamma form (PKI-gamma).
GN  PKIG.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RA  Saito T., Miyajima N.;
RA  Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Parathyroid;
RX  MEDLINE=97364742; PubMed=9218452;
RA  Collins S.P., Uhler M.D.;
RT  "Characterization of PKI-gamma, a novel isoform of the protein kinase
RT  inhibitor of CAMP-dependent protein kinase.";
RL  J. Biol. Chem. 272:18169-18178(1997).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21060778; PubMed=10880337;
RA  Zheng L., Yu L., Tu Q., Zhang M., He H., Chen W., Gao J., Yu J.,
RA  Wu Q., Zhao S.;
RT  "Cloning and mapping of human PKI8 and PKIG, and comparison of tissue
RT  expression patterns of three members of the protein kinase inhibitor
RT  family, including PKIA.";
RL  Biochem. J. 349:403-407(2000).
RN  [4]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21638749; PubMed=11780052;
RA  Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA  Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA  Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA  Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA  Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA  Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clegg S.,
RA  Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA  Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA  Ellington A.G., Frankland J.A., Fraser A.D., French L., Garner P.,
RA  Grafham D.V., Griffiths C., Griffiths M.N.D., Griffin R., Hall R.E.,
RA  Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA  Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA  Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA  Lehtsalaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA  Marsh V.L., Martin S.L., McConnell L.J., McLay K., McMurray A.A.,
RA  Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA  Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA  Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA  Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA  Skuce C.D., Smith M.I., Soderlund C., Steward C.A., Sulston J.E.,
RA  Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA  Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA  Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA  Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA  Rogers J.;
RT  "The DNA sequence and comparative analysis of human chromosome 20.";
RL  Nature 414:865-871(2001).
CC  -!- FUNCTION: EXTREMELY POTENT COMPETITIVE INHIBITOR OF CAMP-DEPENDENT
CC  PROTEIN KINASE ACTIVITY. THIS PROTEIN INTERACTS WITH THE
CC  CATALYTIC SUBUNIT OF THE ENZYME AFTER THE CAMP-INDUCED
CC  DISSOCIATION OF ITS REGULATORY CHAINS (BY SIMILARITY).
CC  -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC  -!- SIMILARITY: BELONGS TO THE PKI FAMILY.
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CC  EMBL; U9170; AAC09065.1;
CC  MGO; MGI:1343086; PKig.
CC  InterPro: IPR004171; CAMP_dep_PKI.
CC  Pfam; PF02827; PKI; 1.
CC  Protein kinase inhibitor.
CC  SEQUENCE 76 AA; 7943 MW; 965F577D80C8DE59 CRC64;
SQ
Query Match 17.0%; Score 36; DB 1; Length 76;
Best Local Similarity 31.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 10; Mismatches 8; Indels 2; Gaps 1;
QY 6 SENSLVAMDFSGQKSRV--IENPTALSV 32
DB 7 SYSDFISCDRTGRNAVPIQDSEAVSV 35
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RESULT 21
ID  IPKG MOUSE STANDARD; PRT; 76 AA.
AC  O70139.
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  CAMP-dependent protein kinase inhibitor, gamma form (PKI-gamma).
GN  PKIG.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RA  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J;
RX  MEDLINE=97364742; PubMed=9218452;
RA  Collins S.P., Uhler M.D.;
RT  "Characterization of PKI-gamma, a novel isoform of the protein kinase
RT  inhibitor of CAMP-dependent protein kinase.";
RL  J. Biol. Chem. 272:18169-18178(1997).
CC  -!- FUNCTION: EXTREMELY POTENT COMPETITIVE INHIBITOR OF CAMP-DEPENDENT
CC  PROTEIN KINASE ACTIVITY. THIS PROTEIN INTERACTS WITH THE
CC  CATALYTIC SUBUNIT OF THE ENZYME AFTER THE CAMP-INDUCED
CC  DISSOCIATION OF ITS REGULATORY CHAINS (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE PKI FAMILY.
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CC  EMBL; U9170; AAC09065.1;
CC  MGO; MGI:1343086; PKig.
CC  InterPro: IPR004171; CAMP_dep_PKI.
CC  Pfam; PF02827; PKI; 1.
CC  Protein kinase inhibitor.
CC  SEQUENCE 76 AA; 7943 MW; 965F577D80C8DE59 CRC64;
SQ
Query Match 17.0%; Score 36; DB 1; Length 76;
Best Local Similarity 31.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 10; Mismatches 8; Indels 2; Gaps 1;
QY 6 SENSLVAMDFSGQKSRV--IENPTALSV 32

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Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	46.5	21.9	62	2	E64510		hypothetical prote
2	46	21.7	76	2	E64324		DNA-directed RNA p
3	45.5	21.5	73	2	T25763		hypothetical prote
4	45	21.2	60	2	A43960		ferredoxin 2[4fe-4
5	45	21.2	77	2	H63420		hydrogenase expres
6	45	21.2	82	2	D63087		hydrogenase prote
7	42	19.8	53	2	C82776		hypothetical prote
8	42	19.8	79	2	A8517		hypothetical prote
9	42	19.8	79	2	B72106		hypothetical prote
10	42	19.8	81	2	D81565		hypothetical prote
11	42	19.8	82	1	G64370		conserved hypothet
12	41.5	19.6	87	2	S60284		B12D protein - bar
13	40.5	19.1	73	2	A60172		proteoglycan core
14	40	18.9	66	2	A43602		T-cell-stimulating
15	40	18.9	67	2	G97092		endoglucanase (tru
16	40	18.9	70	2	E70985		hypothetical prote
17	39.5	18.6	61	2	F86996		4-oxalocrotonate t
18	39.5	18.6	67	2	AF1487		probable transcrip
19	39.5	18.6	77	2	AD1945		hypothetical prote
20	39	18.4	45	1	C64901		ribosomal protein
21	39	18.4	45	2	D90889		30S ribosomal subu
22	39	18.4	45	2	E85728		30S ribosomal subu
23	39	18.4	62	2	T06654		hypothetical prote
24	39	18.4	72	2	A03532		hypothetical prote
25	39	18.4	77	2	B03269		hypothetical prote
26	39	18.4	87	2	D32861		hypothetical prote
27	39	18.4	90	2	H72072		conserved hypothet
28	39	18.4	90	2	E86552		CT388 hypothetical
29	38.5	18.2	48	2	T35253		small hypothetical



103	34	16.0	69	2	AB1333	hypothenical prote	176	32.5	15.3	90	2	176722	phosphocarrier pro
104	34	16.0	69	2	AB1704	hypothenical prote	177	32.5	15.3	90	2	F91119	phosphocarrier pro
105	34	16.0	71	2	AF2303	hypothenical prote	178	32.5	15.3	90	2	F84289	probable membrane
106	34	16.0	72	2	S54448	hypothenical prote	179	32.5	15.3	90	2	H59581	phosphocarrier pro
107	34	16.0	74	2	F96670	hypothenical prote	180	32.5	15.3	90	2	H59584	hypothenical prote
108	34	16.0	78	2	S03233	hypothenical prote	181	32	15.1	41	2	H40459	bcl-2-associated p
109	34	16.0	79	2	S03448	T-cell receptor al	182	32	15.1	41	2	C47538	hypothenical prote
110	34	16.0	82	2	G81247	Bola/VRBA family p	183	32	15.1	52	2	S00580	1-(5-phosphoribos
111	34	16.0	82	2	D82020	hypothenical prote	184	32	15.1	54	2	B90538	hypothenical prote
112	34	16.0	84	1	WAWL	E4 protein - human	185	32	15.1	54	2	B36943	chemoreceptor prote
113	34	16.0	84	2	S74779	conserved hypothe	186	32	15.1	54	2	AH1885	hypothenical prote
114	34	16.0	84	2	E75545	hypothenical prote	187	32	15.1	55	1	FEPE	ferredoxin 2[4Fe-4
115	34	16.0	88	2	D69190	hypothenical prote	188	32	15.1	56	2	G72355	hypothenical prote
116	34	16.0	90	2	G84257	hypothenical prote	189	32	15.1	57	2	S35727	protein-tyrosine k
117	33.5	15.8	63	2	T31143	hypothenical prote	190	32	15.1	58	2	G95036	hypothenical prote
118	33.5	15.8	65	2	S74783	hypothenical prote	191	32	15.1	58	2	C97907	hypothenical prote
119	33.5	15.8	76	2	AF1997	hypothenical prote	192	32	15.1	60	1	NLEPIV	short neurotoxin 1
120	33.5	15.8	81	2	D95065	conserved domain p	193	32	15.1	60	1	NLEPIV	short neurotoxin 1
121	33.5	15.8	81	2	E97932	hypothenical prote	194	32	15.1	60	1	NLEPIV	short neurotoxin 1
122	33.5	15.8	84	2	S58483	hypothenical prote	195	32	15.1	60	2	B82795	hypothenical prote
123	33.5	15.8	84	2	F84388	hypothenical prote	196	32	15.1	60	2	H89944	hypothenical prote
124	33.5	15.8	84	2	T51257	hypothenical prote	197	32	15.1	61	2	B84589	hypothenical prote
125	33.5	15.8	88	2	T29024	hypothenical prote	198	32	15.1	61	2	AG1770	4-oxalocrotonate i
126	33	15.6	44	2	A95166	hypothenical prote	199	32	15.1	62	1	S63968	ribosomal protein
127	33	15.6	47	2	AB0673	30S ribosomal prot	200	32	15.1	63	2	G90979	hypothenical prote
128	33	15.6	54	2	B56657	ferredoxin 2[4Fe-4	201	32	15.1	63	2	B46245	androgen-induced g
129	33	15.6	55	2	JU0126	PFEMP2/MESA (clone	202	32	15.1	64	2	A82608	hypothenical prote
130	33	15.6	56	2	F70183	protein-tyrosine k	203	32	15.1	64	2	D85825	hypothenical prote
131	33	15.6	56	2	F95077	hypothenical prote	204	32	15.1	64	2	D88044	hypothenical prote
132	33	15.6	56	2	B97945	hypothenical prote	205	32	15.1	64	2	B64955	hypothenical prote
133	33	15.6	58	2	C84389	hypothenical prote	206	32	15.1	65	2	C93178	hypothenical prote
134	33	15.6	59	2	AG2271	CAB/ELIP/HLIP supe	207	32	15.1	66	2	F90146	DNA-directed RNA p
135	33	15.6	60	2	J50583	hypothenical 7K pr	208	32	15.1	66	2	F97733	hypothenical prote
136	33	15.6	64	2	B48411	herculin homolog -	209	32	15.1	67	2	F90897	hypothenical prote
137	33	15.6	67	2	AF2590	hypothenical prote	210	32	15.1	67	2	H85720	hypothenical prote
138	33	15.6	71	2	G84810	probable proteinase	211	32	15.1	67	2	H64908	hypothenical prote
139	33	15.6	71	2	T03353	gene e44 protein -	212	32	15.1	69	2	AD1147	hypothenical prote
140	33	15.6	72	2	S49415	major carboxysome	213	32	15.1	69	2	AD1506	hypothenical prote
141	33	15.6	72	2	S48011	tpo protein - phag	214	32	15.1	71	2	H91105	hypothenical prote
142	33	15.6	79	2	G75347	hypothenical prote	215	32	15.1	71	2	T31215	hypothenical prote
143	33	15.6	79	2	B95367	conserved hypothe	216	32	15.1	71	2	C85951	hypothenical prote
144	33	15.6	80	2	D90965	hypothenical prote	217	32	15.1	71	2	C65079	hypothenical prote
145	33	15.6	80	2	D72808	gp68.1 protein - M	218	32	15.1	72	2	G64024	hypothenical prote
146	33	15.6	80	2	D85813	hypothenical prote	219	32	15.1	72	2	A86664	hypothenical prote
147	33	15.6	84	2	F64959	hypothenical prote	220	32	15.1	72	2	A69292	archaeal histone A
148	33	15.6	84	2	D70611	ribosomal protein	221	32	15.1	72	2	AH3473	lactoylglutathione
149	33	15.6	87	2	S41863	hypothenical prote	222	32	15.1	73	2	T36840	C18L protein var
150	33	15.6	87	2	R5H523	gene NS-3 protein	223	32	15.1	73	2	T03199	hypothenical prote
151	33	15.6	88	2	S41863	major carboxysome	224	32	15.1	73	2	T07244	hypothenical prote
152	33	15.6	88	2	S49416	hypothenical prote	225	32	15.1	73	2	AF0258	hypothenical prote
153	33	15.6	88	2	AF2243	hypothenical prote	226	32	15.1	73	2	S61501	flagellar biosynth
154	32.5	15.3	46	2	G86705	hypothenical prote	227	32	15.1	74	2	B69391	DNA-directed RNA p
155	32.5	15.3	63	2	A81872	hypothenical prote	228	32	15.1	75	2	S73297	hypothenical prote
156	32.5	15.3	64	2	T12921	hypothenical prote	229	32	15.1	75	2	S73297	hypothenical prote
157	32.5	15.3	64	2	AB2271	periplasmic mercur	230	32	15.1	76	2	A72218	hypothenical prote
158	32.5	15.3	64	2	AC2544	hypothenical prote	231	32	15.1	76	2	B64660	hypothenical prote
159	32.5	15.3	65	2	A49529	3C-like serine pro	232	32	15.1	76	2	S75641	hypothenical prote
160	32.5	15.3	65	2	S32904	hypothenical prote	233	32	15.1	78	2	B81883	hypothenical prote
161	32.5	15.3	67	2	A97725	hypothenical prote	234	32	15.1	78	2	A75411	hypothenical prote
162	32.5	15.3	69	2	F72354	hypothenical prote	235	32	15.1	79	2	AG0340	hypothenical prote
163	32.5	15.3	71	2	S51665	ribosomal protein	236	32	15.1	80	2	A69816	thiol-specific ant
164	32.5	15.3	73	2	A83935	hypothenical prote	237	32	15.1	81	2	F75409	hypothenical prote
165	32.5	15.3	75	2	A12832	kappa-casein - wat	238	32	15.1	81	2	JC5345	cd11 protein - clo
166	32.5	15.3	75	2	C81952	hypothenical prote	239	32	15.1	82	2	D81056	hypothenical prote
167	32.5	15.3	75	2	T45183	hypothenical prote	240	32	15.1	82	2	S07766	hypothenical prote
168	32.5	15.3	77	2	G90429	hypothenical prote	241	32	15.1	82	2	F89987	hypothenical prote
169	32.5	15.3	82	2	C64623	ss-DNA binding pro	242	32	15.1	83	2	S29325	hypothenical prote
170	32.5	15.3	84	2	C97925	degenerate transpo	243	32	15.1	83	2	H85523	hypothenical prote
171	32.5	15.3	85	2	S17463	glutathione transf	244	32	15.1	84	2	T03163	hypothenical prote
172	32.5	15.3	85	2	B24886	P(-)rp(-) fibrilal	245	32	15.1	85	2	C75523	hypothenical prote
173	32.5	15.3	87	2	S75480	hypothenical prote	246	32	15.1	85	2	T40431	hypothenical prote
174	32.5	15.3	89	2	D83372	hypothenical prote	247	32	15.1	86	2	E86703	hypothenical prote
175	32.5	15.3	89	2	F70953	hypothenical prote	248	32	15.1	87	2	S08401	neurotoxin homolog

249	32	15.1	87	2	B90161	small nuclear ribo	322	31	14.6	69	2	S66650	proteinase inhibit
250	32	15.1	89	2	H36943	chemoreceptor prot	323	31	14.6	70	2	T12849	hypothetical prote
251	32	15.1	90	2	A50443	hypothetical 10.3k	324	31	14.6	71	2	I49244	Mi protein - mouse
252	32	15.1	90	2	E60464	probable membrane	325	31	14.6	72	2	F95136	NrdH-redoxin [Impo
253	31.5	14.9	48	2	C60008	hypothetical 5.3k	326	31	14.6	72	2	D70167	hypothetical prote
254	31.5	14.9	49	2	B97874	degenerate transpo	327	31	14.6	73	2	A84271	hypothetical prote
255	31.5	14.9	50	2	I52702	estrogen receptor	328	31	14.6	73	2	E84286	hypothetical prote
256	31.5	14.9	53	1	LNLDAF	lectin alpha chain	329	31	14.6	73	2	D72155	E14L protein - var
257	31.5	14.9	56	2	G64912	ydfB protein - Esc	330	31	14.6	73	2	E84048	hypothetical prote
258	31.5	14.9	59	2	T06016	hypothetical prote	331	31	14.6	74	2	I45714	Dpp receptor TKV,
259	31.5	14.9	62	2	A11734	hypothetical prote	332	31	14.6	74	2	E97870	hypothetical prote
260	31.5	14.9	62	2	A11364	hypothetical prote	333	31	14.6	75	2	S30358	T-cell receptor be
261	31.5	14.9	65	2	D86788	hypothetical prote	334	31	14.6	75	2	T01621	hypothetical prote
262	31.5	14.9	65	2	A95330	hypothetical prote	335	31	14.6	75	2	A10753	conserved hypotet
263	31.5	14.9	66	2	G72804	gp41.1 protein - M	336	31	14.6	76	2	A93391	DNA-directed RNA p
264	31.5	14.9	67	2	C71854	hypothetical prote	337	31	14.6	76	2	T30403	late expression fa
265	31.5	14.9	68	2	I49136	dopamine transport	338	31	14.6	76	2	D94332	hypothetical prote
266	31.5	14.9	71	2	AG1893	hypothetical prote	339	31	14.6	76	2	E84104	iron-sulfur cluste
267	31.5	14.9	74	2	C83393	hypothetical prote	340	31	14.6	77	2	B90959	ribosomal protein
268	31.5	14.9	74	2	AH1649	hypothetical prote	341	31	14.6	78	2	E64472	probable phage tai
269	31.5	14.9	74	2	AH1590	hypothetical prote	342	31	14.6	78	2	B90959	hypothetical prote
270	31.5	14.9	75	2	S23602	hypothetical prote	343	31	14.6	78	2	C64472	hypothetical prote
271	31.5	14.9	75	2	E82761	conserved hypotet	344	31	14.6	78	2	H98004	hypothetical prote
272	31.5	14.9	79	1	A70312	conserved hypotet	345	31	14.6	79	2	G69294	hypothetical prote
273	31.5	14.9	81	2	A97803	hypothetical prote	346	31	14.6	80	2	T26398	hypothetical prote
274	31.5	14.9	82	2	F17890	hypothetical prote	347	31	14.6	80	2	A62207	cell growth regula
275	31.5	14.9	82	2	F82644	hypothetical prote	348	31	14.6	82	2	F90468	copper binding pro
276	31.5	14.9	83	2	G90914	excisionase [Impr	349	31	14.6	82	2	A97820	hypothetical prote
277	31.5	14.9	83	2	AB2319	hypothetical prote	350	31	14.6	83	2	JW0086	trichothecene 3-O-
278	31.5	14.9	86	2	F64527	hypothetical prote	351	31	14.6	83	2	C90283	hypothetical prote
279	31.5	14.9	86	2	F71978	hypothetical prote	352	31	14.6	85	2	S29576	Ig light chain - r
280	31.5	14.9	86	2	AD1384	hypothetical prote	353	31	14.6	85	2	E97648	thioradon/gutar
281	31.5	14.9	86	2	AD1230	hypothetical prote	354	31	14.6	85	2	E97648	hypothetical 8.9k
282	31	14.6	43	2	H82712	cysteine proteinase	355	31	14.6	86	2	A28282	conserved hypotet
283	31	14.6	43	2	H82712	hypothetical prote	356	31	14.6	86	2	A28186	nitrogenase (EC 1.
284	31	14.6	44	2	S09548	nitrogenase (EC 1.	357	31	14.6	86	2	F97124	phosphocarrier pro
285	31	14.6	46	2	S09537	gene i-1 protein -	358	31	14.6	86	2	A20133	probable bacteriop
286	31	14.6	49	2	S62326	cystatin C, parori	359	31	14.6	86	2	A65181	hypothetical prote
287	31	14.6	50	2	H82007	hypothetical prote	360	31	14.6	87	2	E84990	Napo protein - Esc
288	31	14.6	51	2	H85807	hypothetical prote	361	31	14.6	87	2	B58860	Napo protein - Esc
289	31	14.6	53	2	D85807	hypothetical prote	362	31	14.6	87	2	C75458	M-related protein
290	31	14.6	53	2	S24404	NADH2 dehydrogenas	363	31	14.6	87	2	H70079	hypothetical prote
291	31	14.6	53	2	F82856	hypothetical prote	364	31	14.6	87	2	T48942	hypothetical prote
292	31	14.6	53	2	A96216	hypothetical prote	365	31	14.6	87	2	H91015	Napo protein - Esc
293	31	14.6	55	2	F70186	protein-tyrosine k	366	31	14.6	88	2	F71305	probable phosphoca
294	31	14.6	55	2	A69152	hypothetical prote	367	31	14.6	88	2	E83219	conserved hypotet
295	31	14.6	56	2	JW0095	DNA-dependent RNA	368	31	14.6	88	2	F83979	hypothetical prote
296	31	14.6	57	2	A61479	P5 protein - human	369	31	14.6	89	1	W4BP57	gene 4.5 protein -
297	31	14.6	59	2	G91095	cytochrome c - try	370	31	14.6	89	1	D69782	hypothetical prote
298	31	14.6	59	2	G91095	hypothetical prote	371	31	14.6	90	1	D69782	hypothetical prote
299	31	14.6	60	2	C85941	hypothetical prote	372	31	14.6	90	2	A82044	conserved hypotet
300	31	14.6	60	2	A81904	hypothetical prote	373	31	14.6	90	2	AB1207	DNA-directed RNA p
301	31	14.6	61	2	C75321	preprotein translo	374	31	14.6	90	2	A11563	B. subtilis ykta p
302	31	14.6	62	1	CCB017	ubiquinol-cytochro	375	30.5	14.4	40	2	A12387	B. subtilis ykta p
303	31	14.6	62	2	T00057	4-oxalocrotonate t	376	30.5	14.4	53	2	S73028	photosystem I Psam
304	31	14.6	62	2	S78537	tnpW protein - Clo	377	30.5	14.4	54	2	H90803	dehydrogenase d030
305	31	14.6	62	2	G83944	hypothetical prote	378	30.5	14.4	54	2	B69176	hypothetical prote
306	31	14.6	63	1	QOECLM	vaIA protein - Esc	379	30.5	14.4	54	2	B69176	hypothetical prote
307	31	14.6	63	2	AD0550	conserved hypotet	380	30.5	14.4	57	1	WMIH81	3a protein - avian
308	31	14.6	63	2	C85534	hypothetical prote	381	30.5	14.4	57	1	WMIH87	3a protein - avian
309	31	14.6	63	2	G90683	hypothetical prote	382	30.5	14.4	58	2	G90306	hypothetical prote
310	31	14.6	63	2	A64929	ydIE protein - Esc	383	30.5	14.4	61	2	C69280	carbon storage reg
311	31	14.6	63	2	D90830	hypothetical prote	384	30.5	14.4	63	1	H64095	hypothetical prote
312	31	14.6	63	2	TC4002	carboxymycin resista	385	30.5	14.4	64	2	AF3568	hypothetical prote
313	31	14.6	63	2	D86673	hypothetical prote	386	30.5	14.4	65	2	AC2923	hypothetical prote
314	31	14.6	63	2	S29654	juvenile-hormone e	387	30.5	14.4	66	2	A10046	probable membrane
315	31	14.6	63	2	D84219	hypothetical prote	388	30.5	14.4	67	2	T34593	1-aminocyclopropan
316	31	14.6	64	2	AH1024	hypothetical prote	389	30.5	14.4	68	2	S20921	cold-shock domain
317	31	14.6	65	2	AH1024	hypothetical prote	390	30.5	14.4	68	2	AD1306	probable mercuric
318	31	14.6	66	2	H71940	copper-associated	391	30.5	14.4	70	2	PC2063	neurite outgrowth
319	31	14.6	67	2	C81174	hypothetical prote	392	30.5	14.4	70	2	A12632	conserved hypotet
320	31	14.6	68	2	AD1678	probable mercuric	393	30.5	14.4	71	2	E87617	4-oxalocrotonate t
321	31	14.6	69	2	FN0453	adenylate cyclase	394	30.5	14.4	73	2	C97786	hypothetical prote

395	30.5	14.4	76	2	T40983	hypothetical prote	468	30	14.2	68	2	E81445	probable isomerase
396	30.5	14.4	76	2	I53107	CD24 precursor - r	469	30	14.2	69	2	A12422	hypothetical prote
397	30.5	14.4	77	2	T17720	hypothetical prote	470	30	14.2	72	2	JC1474	alpha-neurotoxin -
398	30.5	14.4	77	2	G70227	feon-like protein,	471	30	14.2	72	2	F91230	hypothetical prote
399	30.5	14.4	77	2	AH1279	hypothetical prote	472	30	14.2	72	2	B70517	hypothetical prote
400	30.5	14.4	77	2	AH1642	hypothetical prote	473	30	14.2	73	2	AF2114	ferredoxin-thiore
401	30.5	14.4	78	2	AG0927	conserved hypotet	474	30	14.2	73	2	T36355	probable ribosomal
402	30.5	14.4	79	2	G82863	hypothetical prote	475	30	14.2	73	2	A98919	hypothetical prote
403	30.5	14.4	80	2	T38250	hypothetical prote	476	30	14.2	73	2	S72849	hypothetical prote
404	30.5	14.4	80	2	T32868	hypothetical prote	477	30	14.2	73	2	B84020	hypothetical prote
405	30.5	14.4	81	2	T12015	vpu protein - huma	478	30	14.2	74	2	F85767	hypothetical prote
406	30.5	14.4	81	2	T09386	hypothetical prote	479	30	14.2	74	2	S48592	translation initia
407	30.5	14.4	81	2	T44031	hypothetical prote	480	30	14.2	74	2	E69871	hypothetical prote
408	30.5	14.4	81	2	A11230	hypothetical prote	481	30	14.2	74	2	A41711	hypothetical prote
409	30.5	14.4	82	2	A98165	insertion element	482	30	14.2	74	2	I60294	coileptericin - be
410	30.5	14.4	82	2	G98128	hypothetical prote	483	30	14.2	74	2	T60294	protein-tyrosine k
411	30.5	14.4	83	2	T17809	hypothetical prote	484	30	14.2	74	2	A96967	uncharacterized sm
412	30.5	14.4	83	2	H75612	hypothetical prote	485	30	14.2	75	2	H86756	prophage p12 prote
413	30.5	14.4	83	2	AD2896	hypothetical prote	486	30	14.2	75	2	T44139	hypothetical prote
414	30.5	14.4	84	2	S76443	hypothetical prote	487	30	14.2	75	2	B89582	protein C18A11.2 [
415	30.5	14.4	85	2	T32439	hypothetical prote	488	30	14.2	76	2	PC4256	protein-tyrosine k
416	30.5	14.4	86	2	H95239	conserved hypotet	489	30	14.2	76	2	A81858	hypothetical prote
417	30.5	14.4	87	2	S73988	ribosomal protein	490	30	14.2	77	1	WZVZA5	8.8K HindIII-C pro
418	30.5	14.4	87	2	B69932	hypothetical prote	491	30	14.2	77	2	S24471	gag polyprotein -
419	30.5	14.4	87	2	D56273	probable transposa	492	30	14.2	78	2	F64429	DNA-directed RNA p
420	30.5	14.4	88	1	Q8P777	gene 6.7 protein -	493	30	14.2	78	2	S07572	T-cell receptor de
421	30.5	14.4	88	2	B97373	hypothetical prote	494	30	14.2	78	2	JQ1781	Salp6R 8.8K protei
422	30.5	14.4	88	2	AD2591	conserved hypotet	495	30	14.2	78	2	C71978	hypothetical prote
423	30.5	14.4	89	2	D82717	30S ribosomal prot	496	30	14.2	78	2	T30726	hypothetical prote
424	30.5	14.4	89	2	T50245	hypothetical prote	497	30	14.2	80	2	G86417	unknown protein, 6
425	30.5	14.4	90	2	T57732	hypothetical prote	498	30	14.2	80	2	B83097	hypothetical prote
426	30.5	14.4	90	2	F97577	hypothetical prote	499	30	14.2	80	2	A81361	hypothetical prote
427	30.5	14.4	90	2	A82798	hypothetical prote	500	30	14.2	81	1	FEBSFF	ferredoxin [4Fe-4S
428	30	14.2	41	2	T03647	probable ribosomal	501	30	14.2	81	1	C70910	hypothetical prote
429	30	14.2	43	2	T36044	probable thiamin b	502	30	14.2	81	1	B90109	40S ribosomal prot
430	30	14.2	45	2	T11980	ribosomal protein	503	30	14.2	81	2	H85691	unknown protein en
431	30	14.2	47	2	D87675	hypothetical prote	504	30	14.2	82	2	S8562	SBI1 protein - yea
432	30	14.2	49	2	S33347	complement C4 prot	505	30	14.2	82	2	F5326	conserved hypotet
433	30	14.2	52	2	T15384	hypothetical prote	506	30	14.2	83	2	B90338	hypothetical prote
434	30	14.2	54	2	H31442	ovomucoid, third d	507	30	14.2	83	2	B97880	bone protein II -
435	30	14.2	54	2	A31440	ovomucoid, third d	508	30	14.2	84	2	T33867	hypothetical prote
436	30	14.2	54	2	I31444	ovomucoid, third d	509	30	14.2	84	2	AB2513	hypothetical prote
437	30	14.2	54	2	F82568	hypothetical prote	510	30	14.2	85	2	AH1010	conserved hypotet
438	30	14.2	54	2	AC0896	gene 36 protein	511	30	14.2	86	2	AD0356	probable [4Fe-4S]
439	30	14.2	56	2	S30981	hypothetical prote	512	30	14.2	86	2	AD0356	30S ribosomal prot
440	30	14.2	56	2	H82647	hypothetical prote	513	30	14.2	86	2	C81310	protein kinase 3 (
441	30	14.2	57	2	D69120	hypothetical prote	514	30	14.2	86	2	C41139	variant shiga-like
442	30	14.2	57	2	AD3483	heme exporter prot	515	30	14.2	87	2	I76712	phosphoribosyl-ATP
443	30	14.2	58	2	S77421	glycoprotein 64 -	516	30	14.2	87	2	S72856	hypothetical prote
444	30	14.2	58	2	E87008	hypothetical prote	517	30	14.2	87	2	F87163	hypothetical prote
445	30	14.2	59	2	T03588	pyrophosphate-fruc	518	30	14.2	87	2	T05905	hypothetical prote
446	30	14.2	59	2	G84395	probable retroelem	519	30	14.2	87	2	B97814	hypothetical prote
447	30	14.2	59	2	F82004	m protein curso	520	30	14.2	88	2	AF3030	hypothetical prote
448	30	14.2	60	2	S60851	hypothetical prote	521	30	14.2	88	2	S77431	hypothetical prote
449	30	14.2	60	2	B90729	hypothetical prote	522	30	14.2	88	2	S72265	hypothetical prote
450	30	14.2	60	2	B90775	hypothetical prote	523	30	14.2	88	2	A97425	translation initia
451	30	14.2	60	2	SI8017	flocculant active	524	30	14.2	89	1	S42609	hypothetical prote
452	30	14.2	60	2	AD1832	hypothetical prote	525	30	14.2	89	2	S77787	shiga-like toxin -
453	30	14.2	61	2	G69333	hypothetical prote	526	30	14.2	89	2	A60279	probable glycerol
454	30	14.2	61	2	C91004	hypothetical prote	527	30	14.2	89	2	A82718	shiga-like toxin I
455	30	14.2	62	2	D59103	hypothetical prote	528	30	14.2	89	2	A84189	30S ribosomal prot
456	30	14.2	62	2	AF2059	hypothetical prote	529	30	14.2	89	2	S72538	hypothetical prote
457	30	14.2	63	2	A43397	hypothetical prote	530	30	14.2	89	2	B84143	hypothetical prote
458	30	14.2	63	2	JE0393	4-oxalocrotonate t	531	30	14.2	89	2	AG3246	conserved hypotet
459	30	14.2	63	2	F89385	marinostat - Alt	532	30	14.2	90	2	B24556	hypothetical prote
460	30	14.2	65	2	F69385	hypothetical prote	533	30	14.2	90	2	F90555	conserved hypotet
461	30	14.2	65	2	H84400	conserved hypotet	534	30	14.2	90	2	B24556	hypothetical prote
462	30	14.2	65	2	A82657	hypothetical prote	535	29.5	13.9	41	2	B47752	hypothetical prote
463	30	14.2	65	2	B82547	hypothetical prote	536	29.5	13.9	46	2	PT0034	baseplate protein
464	30	14.2	65	2	B82371	hypothetical prote	537	29.5	13.9	52	2	D82682	hypothetical prote
465	30	14.2	65	4	S60192	probable glutamate	538	29.5	13.9	53	2	D86058	probable fimbrial
466	30	14.2	67	2	A84376	hypothetical prote	539	29.5	13.9	53	2	D91212	hypothetical prote
467	30	14.2	67	2	AE0441	probable DNA-damag	540	29.5	13.9	54	2	AD2296	hypothetical prote
												B48834	basic fibroblast 9

541	29.5	13.9	55	2	G87704	hypothetical prote	614	29	13.7	61	2	AD0401	carbon storage reg
542	29.5	13.9	55	2	JG6188	csaB protein - Ba	615	29	13.7	61	2	AE0843	carbon storage reg
543	29.5	13.9	56	2	B95096	hypothetical prote	616	29	13.7	61	2	D85917	glycogen biosynthe
544	29.5	13.9	57	2	E82787	hypothetical prote	617	29	13.7	62	2	S59004	lipase, pregastric
545	29.5	13.9	57	2	C35058	MHC class II histo	618	29	13.7	62	2	A38891	subtilisin inhibit
546	29.5	13.9	63	2	D86688	prophage p42 prote	619	29	13.7	62	2	A24463	transfer complex P
547	29.5	13.9	64	2	T15163	hypothetical prote	620	29	13.7	62	2	A38891	hypothetical prote
548	29.5	13.9	67	2	E81042	hypothetical prote	621	29	13.7	63	2	G96517	protein T2E6.24 [1
549	29.5	13.9	71	2	T17598	hypothetical prote	622	29	13.7	63	2	T33630	hypothetical prote
550	29.5	13.9	71	2	H97137	hypothetical prote	623	29	13.7	63	2	T30614	hypothetical prote
551	29.5	13.9	71	2	A81355	gp44 [Bacteriophag	624	29	13.7	64	2	S41059	probable aspartate
552	29.5	13.9	72	1	D93550	hypothetical prote	625	29	13.7	64	2	A36689	50K integrin-assoc
553	29.5	13.9	72	2	A81875	hypothetical prote	626	29	13.7	64	2	H75204	ferredoxin PAB3048
554	29.5	13.9	73	2	A20755	hypothetical prote	627	29	13.7	64	2	B26722	hypothetical prote
555	29.5	13.9	74	2	H70944	hypothetical 10.1	628	29	13.7	64	2	A12881	hypothetical prote
556	29.5	13.9	74	2	H70944	hypothetical prote	629	29	13.7	65	2	E82308	carbon storage reg
557	29.5	13.9	74	2	T47434	hypothetical prote	630	29	13.7	65	2	AE2575	hypothetical prote
558	29.5	13.9	74	2	T71080	hypothetical prote	631	29	13.7	66	2	S47027	DNA-directed RNA p
559	29.5	13.9	76	2	T29085	hypothetical prote	632	29	13.7	66	2	A99455	histone H1 I-1 (cl
560	29.5	13.9	79	2	B81014	hypothetical prote	633	29	13.7	67	2	I47395	histone-like prote
561	29.5	13.9	81	1	G44001	vpu protein - huma	634	29	13.7	67	2	S71485	hypothetical prote
562	29.5	13.9	81	2	AG1584	hypothetical prote	635	29	13.7	68	2	F70706	hypothetical prote
563	29.5	13.9	82	2	H87010	conserved hypotet	636	29	13.7	68	2	E87471	hypothetical prote
564	29.5	13.9	82	2	E49890	fdxH 3'-region hyp	637	29	13.7	68	2	T00309	hypothetical prote
565	29.5	13.9	83	2	S62705	ribosomal protein	638	29	13.7	68	2	G64027	hypothetical prote
566	29.5	13.9	83	2	G88921	ribosomal protein	639	29	13.7	68	2	D69093	histone HmtA2 - Me
567	29.5	13.9	83	2	TN0400	hypothetical 8.8K	640	29	13.7	69	2	D69302	conserved hypotet
568	29.5	13.9	86	2	T11989	acyl carrier prote	641	29	13.7	69	2	E86945	hypothetical prote
569	29.5	13.9	86	2	C95304	hypothetical trans	642	29	13.7	69	2	E97745	hypothetical prote
570	29.5	13.9	87	2	B64217	ribosomal protein	643	29	13.7	69	2	AF3505	hypothetical prote
571	29.5	13.9	87	2	AG2076	phage hypothetical	644	29	13.7	69	2	AG1818	hypothetical prote
572	29.5	13.9	87	2	AG4786	hypothetical prote	645	29	13.7	70	2	S24171	cytochrome-c oxida
573	29.5	13.9	88	1	R37M19	ribosomal protein	646	29	13.7	70	2	A47395	histone H1 I-1 (N-
574	29.5	13.9	88	2	D82195	ribosomal protein	647	29	13.7	71	2	A23876	vitellogenin Al -
575	29.5	13.9	88	2	AB1200	PTS phosphocarrier	648	29	13.7	71	2	F83214	probable molybdopt
576	29.5	13.9	88	2	AH1557	PTS phosphocarrier	649	29	13.7	71	2	AC3531	hypothetical prote
577	29.5	13.9	88	2	PC4238	heat shock protein	650	29	13.7	71	2	AB2179	hypothetical prote
578	29.5	13.9	88	2	G81178	conserved hypotet	651	29	13.7	72	2	C82681	translation initia
579	29.5	13.9	88	2	B81926	hypothetical prote	652	29	13.7	72	2	B97112	RNA polymerase-ass
580	29.5	13.9	90	2	I46472	alpha-actin - rabb	653	29	13.7	73	2	F69062	molybdenum transp
581	29.5	13.9	90	2	D38179	hypothetical prote	654	29	13.7	73	2	T07335	hypothetical prote
582	29	13.7	40	2	S16170	osteonection - rabb	655	29	13.7	74	2	S04144	ribosomal protein
583	29	13.7	43	2	T13194	hypothetical prote	656	29	13.7	74	2	AH2642	hypothetical prote
584	29	13.7	44	2	S34838	tyrosine-rich acid	657	29	13.7	75	2	E86891	hypothetical prote
585	29	13.7	45	2	S48787	sucrose transport	658	29	13.7	75	2	T04547	hypothetical prote
586	29	13.7	45	2	E83757	hypothetical prote	659	29	13.7	75	2	A97745	hypothetical prote
587	29	13.7	46	2	E90676	hypothetical prote	660	29	13.7	76	2	T37389	probable 8.9K prot
588	29	13.7	46	2	H85526	hypothetical prote	661	29	13.7	76	2	E59944	hypothetical prote
589	29	13.7	48	2	AH2633	hypothetical prote	662	29	13.7	76	2	H90883	hypothetical prote
590	29	13.7	49	2	T01800	recP protein - Cl	663	29	13.7	76	2	S38554	tec protein - phag
591	29	13.7	51	2	B32040	dihydrolipoamide S	664	29	13.7	76	2	H72412	hypothetical prote
592	29	13.7	51	2	S23291	light-harvesting p	665	29	13.7	76	2	G85734	hypothetical prote
593	29	13.7	53	2	F97231	hypothetical prote	666	29	13.7	76	2	G64895	hypothetical prote
594	29	13.7	54	2	S34728	ribose-phosphate d	667	29	13.7	77	2	AD1599	host factor-1 prot
595	29	13.7	54	2	C31436	ovomucoid, third d	668	29	13.7	77	2	AG1236	host factor-1 prot
596	29	13.7	54	2	A61587	ovomucoid (PSTI-ty	669	29	13.7	77	2	C90475	hypothetical prote
597	29	13.7	54	2	T30410	FP-protein ORF63b	670	29	13.7	77	2	S33665	hypothetical prote
598	29	13.7	56	2	A85956	hypothetical prote	671	29	13.7	77	2	H69451	hypothetical prote
599	29	13.7	56	2	C41476	ribonucleoside-dip	672	29	13.7	77	2	T06954	hypothetical prote
600	29	13.7	57	2	C53260	hypothetical prote	673	29	13.7	77	2	T41731	probable proteinas
601	29	13.7	57	2	C84977	carbon storage reg	674	29	13.7	78	2	T21427	hypothetical prote
602	29	13.7	57	2	C72857	AcOrf-58 protein -	675	29	13.7	78	2	T21427	hypothetical prote
603	29	13.7	57	2	AF1381	hypothetical prote	676	29	13.7	78	2	AH1969	hypothetical prote
604	29	13.7	57	2	AG1750	hypothetical prote	677	29	13.7	79	2	A94660	hypothetical prote
605	29	13.7	58	2	E96595	unknown protein, 2	678	29	13.7	79	2	F97704	hypothetical prote
606	29	13.7	58	2	D81150	hypothetical prote	679	29	13.7	79	2	AH0810	hypothetical prote
607	29	13.7	58	2	B83527	lactaldehyde dehyd	680	29	13.7	80	2	T12947	conserved hypotet
608	29	13.7	59	1	FEDVEG	ferredoxin [4Fe-4S	681	29	13.7	80	2	S88775	SSS1 protein - yea
609	29	13.7	60	2	D81898	hypothetical prote	682	29	13.7	80	2	E90686	hypothetical prote
610	29	13.7	60	2	A69464	hypothetical prote	683	29	13.7	80	2	T31032	hypothetical prote
611	29	13.7	60	2	AH2737	hypothetical prote	684	29	13.7	80	2	A85537	unknown [imported]
612	29	13.7	61	2	B40608	hypothetical prote	685	29	13.7	80	2	AF0738	probable cro repre
613	29	13.7	61	2	A91073	glycogen biosynthe	686	29	13.7	81	2	F90496	conserved hypotet

687	29	13.7	81	2	B70966	hypothenical prote	160	28.5	13.4	71	2	AC1734	gp44 (Bacteriophag
688	29	13.7	81	2	AF2570	hypothenical prote	761	28.5	13.4	72	2	G97751	hypothenical prote
689	29	13.7	82	2	S58349	H+-transporting tw	762	28.5	13.4	73	2	T42113	transposase homolo
690	29	13.7	82	2	C81329	hypothenical prote	763	28.5	13.4	74	2	C81197	hypothenical prote
691	29	13.7	83	2	I49494	B-1 alpha-amyase	764	28.5	13.4	75	2	T12210	endopeptidase Clp
692	29	13.7	83	2	S73226	ribosomal protein	765	28.5	13.4	76	2	A84068	hypothenical prote
693	29	13.7	83	2	G90167	regulatory protein	766	28.5	13.4	77	2	AF0231	hypothenical prote
694	29	13.7	83	2	G87309	conserved hypotet	767	28.5	13.4	78	2	AB1193	hypothenical prote
695	29	13.7	84	1	S43422	ribosomal protein	768	28.5	13.4	79	2	I59567	histone H2A - rat
696	29	13.7	84	2	B53372	dihydroxy-acid deh	769	28.5	13.4	80	2	S29082	SRY protein homolo
697	29	13.7	84	2	F43321	50S ribosomal prot	770	28.5	13.4	81	1	B84252	hypothetical prote
698	29	13.7	84	2	S72700	probable ketoacyl	771	28.5	13.4	82	2	S75193	hypothetical prote
699	29	13.7	84	2	T07444	hypothetical prote	772	28.5	13.4	83	2	F83880	hypothetical prote
700	29	13.7	85	2	S27217	chymotrypsin inhib	773	28.5	13.4	84	2	A91099	acyl-carrier prote
701	29	13.7	85	2	S27218	chymotrypsin inhib	774	28.5	13.4	85	2	T27603	pancreatic ribonuc
702	29	13.7	85	2	S08109	carcinoembryonic a	775	28.5	13.4	86	2	C97759	hypothetical prote
703	29	13.7	85	2	G84217	ribosomal protein	776	28.5	13.4	87	1	ASLJNK	hypothetical prote
704	29	13.7	85	2	F95171	conserved hypotet	777	28.5	13.4	88	1	S06409	vpu protein - huma
705	29	13.7	85	2	E94211	hypothetical prote	778	28.5	13.4	89	2	S54383	vpu protein - huma
706	29	13.7	85	2	C25974	39K rod phycocyan	779	28.5	13.4	90	2	H86176	hypothetical prote
707	29	13.7	85	2	G70824	hypothetical prote	780	28.5	13.4	91	2	S46776	ribosomal protein
708	29	13.7	85	2	C97880	conserved hypotet	781	28.5	13.4	92	2	E84301	hypothetical prote
709	29	13.7	85	2	F98037	conserved hypotet	782	28.5	13.4	93	2	S23703	capsid gene 5'-reg
710	29	13.7	85	2	A13150	hypothetical prote	783	28.5	13.4	94	2	T15818	hypothetical prote
711	29	13.7	86	2	E64074	ferredoxin 2[4Fe-4	784	28.5	13.4	95	2	A81063	hypothetical prote
712	29	13.7	86	2	JC1214	polyketide synthas	785	28.5	13.4	96	2	D83947	hypothetical prote
713	29	13.7	86	2	E81144	hypothetical prote	786	28.5	13.4	97	2	AC3327	hypothetical prote
714	29	13.7	86	2	A08050	doubtful COS found	787	28.5	13.4	98	2	PS0142	hypothetical prote
715	29	13.7	87	2	S75281	hypothetical prote	788	28.5	13.4	99	2	E84345	replication-associ
716	29	13.7	87	2	T08641	hypothetical prote	789	28.5	13.4	100	2	S03239	hypothetical prote
717	29	13.7	88	2	C90178	hypothetical prote	790	28.5	13.4	101	2	D64033	hypothetical prote
718	29	13.7	88	2	D50957	15S ribosomal prot	791	28.5	13.4	102	2	T16045	hypothetical prote
719	29	13.7	88	2	H72221	hypothetical prote	792	28.5	13.4	103	2	AD2048	hypothetical prote
720	29	13.7	88	2	D82570	hypothetical prote	793	28.5	13.4	104	2	I56980	hypothetical prote
721	29	13.7	88	2	F97888	degenerative trans	794	28.5	13.4	105	2	S78142	arginine decarboxy
722	29	13.7	89	2	T46384	hypothetical prote	795	28.5	13.4	106	2	F87057	ribosomal protein
723	29	13.7	89	2	B43312	hypothetical prote	796	28.5	13.4	107	2	A38725	hypothetical prote
724	29	13.7	89	2	D71940	hypothetical prote	797	28.5	13.4	108	2	T00775	transferrin - shee
725	29	13.7	90	2	T46007	hypothetical prote	798	28.5	13.4	109	2	WCAD9	early ELB 9K prote
726	29	13.7	90	2	AC2024	penicillin-binding	799	28.5	13.4	110	1	JC5816	cytochrome c6 [val
727	28.5	13.4	90	2	S06495	lectin alpha chain	800	28.5	13.4	111	2	C64249	ribosomal protein
728	28.5	13.4	91	1	LNDDAA	mannose/glucose-sp	801	28.5	13.4	112	2	A69423	protein [imported
729	28.5	13.4	93	2	B25989	sex-determining pr	802	28.5	13.4	113	2	D95347	hypothetical prote
730	28.5	13.4	95	2	T46158	hypothetical prote	803	28.5	13.4	114	2	E95305	hypothetical prote
731	28.5	13.4	95	2	AC2366	hypothetical prote	804	28.5	13.4	115	2	S77531	hypothetical prote
732	28.5	13.4	95	2	E86930	hypothetical prote	805	28.5	13.4	116	2	A69163	hypothetical prote
733	28.5	13.4	97	2	P00021	aadA protein - Pse	806	28.5	13.4	117	2	D82760	hypothetical prote
734	28.5	13.4	98	2	E86517	hypothetical prote	807	28.5	13.4	118	2	B82864	hypothetical prote
735	28.5	13.4	59	2	S13128	probable homeotic	808	28.5	13.4	119	2	AC3430	hypothetical prote
736	28.5	13.4	60	2	A69321	DR-beta chain MHC	809	28.5	13.2	120	2	S73115	photosystem I chal
737	28.5	13.4	61	2	F77824	probable cell divi	810	28.5	13.2	121	2	A25520	hypothetical prote
738	28.5	13.4	61	2	F82736	hypothetical prote	811	28.5	13.2	122	2	I36602	ADP/ATP transport
739	28.5	13.4	62	2	T23216	hypothetical prote	812	28.5	13.2	123	2	C84020	hypothetical prote
740	28.5	13.4	62	2	AD3240	hypothetical prote	813	28.5	13.2	124	2	PN0589	tyrosine 3-monooxy
741	28.5	13.4	63	2	T16021	hypothetical prote	814	28.5	13.2	125	2	PN0591	tyrosine 3-monooxy
742	28.5	13.4	63	2	H89761	hypothetical prote	815	28.5	13.2	126	2	PN0592	tyrosine 3-monooxy
743	28.5	13.4	64	2	H95275	hypothetical prote	816	28.5	13.2	127	2	PN0593	tyrosine 3-monooxy
744	28.5	13.4	65	2	T31044	hypothetical prote	817	28.5	13.2	128	2	T01784	spectrin beta tand
745	28.5	13.4	66	2	S09146	insulin II precurs	818	28.5	13.2	129	2	G82580	hypothetical prote
746	28.5	13.4	66	2	T47270	hypothetical prote	819	28.5	13.2	130	2	AH3067	hypothetical prote
747	28.5	13.4	66	2	A86729	mercuric reductase	820	28.5	13.2	131	2	E85572	hypothetical prote
748	28.5	13.4	66	2	F79592	conserved hypotet	821	28.5	13.2	132	2	I57670	folliotropin recept
749	28.5	13.4	66	2	F69161	homeobox protein c	822	28.5	13.2	133	2	S31007	gene 62 protein -
750	28.5	13.4	67	2	T37298	hypothetical prote	823	28.5	13.2	134	2	T09185	outer membrane pro
751	28.5	13.4	67	2	D84870	hypothetical prote	824	28.5	13.2	135	2	AP2492	hypothetical prote
752	28.5	13.4	67	2	G69817	hypothetical prote	825	28.5	13.2	136	2	A38942	chemoreceptor prot
753	28.5	13.4	67	2	G17126	hypothetical prote	826	28.5	13.2	137	2	AD0076	hypothetical prote
754	28.5	13.4	68	2	A81968	hypothetical prote	827	28.5	13.2	138	2	C84067	hypothetical prote
755	28.5	13.4	68	2	A81168	hypothetical prote	828	28.5	13.2	139	2	131446	ovomucoid, third d
756	28.5	13.4	68	2	A81168	hypothetical prote	829	28.5	13.2	140	2	F31439	
757	28.5	13.4	69	2	G70839	hypothetical prote	830	28.5	13.2	141	2		
758	28.5	13.4	69	2	C96021	hypothetical prote	831	28.5	13.2	142	2		
759	28.5	13.4	70	2	E83791	hypothetical prote	832	28.5	13.2	143	2		

833	28	13.2	54	2	C31447	ovomucoid, third d	906	28	13.2	73	2	T10809	leghemoglobin 1 -
834	28	13.2	54	2	I61588	ovomucoid (PSTI-ty	907	28	13.2	73	2	D71834	ribosomal protein
835	28	13.2	54	2	A61589	ovomucoid (PSTI-ty	908	28	13.2	73	2	D64683	ribosomal protein
836	28	13.2	54	2	H82718	hypothetical prote	909	28	13.2	73	2	T13134	protein gp47 - pha
837	28	13.2	55	2	E90618	ATP synthase F0 ch	910	28	13.2	74	1	N3KFU	long neurotoxin 1
838	28	13.2	55	2	A90882	hypothetical prote	911	28	13.2	74	2	F17109	Arp synthase C cha
839	28	13.2	55	2	H69811	hypothetical prote	912	28	13.2	74	2	S37768	metallothionein-11
840	28	13.2	55	2	H64836	hypothetical prote	913	28	13.2	74	2	S60839	W protein precurs
841	28	13.2	55	2	G64893	hypothetical prote	914	28	13.2	74	2	C70501	hypothetical prote
842	28	13.2	56	2	A45028	sox2 protein her	915	28	13.2	74	2	B75199	hypothetical prote
843	28	13.2	56	2	B68066	hypothetical prote	916	28	13.2	74	2	D65183	hypothetical prote
844	28	13.2	56	2	G72804	gp6 protein - Myc	917	28	13.2	75	2	B42534	A-ORF-F protein -
845	28	13.2	57	1	OXB96L	ribosomal protein	918	28	13.2	75	2	F83630	hypothetical prote
846	28	13.2	57	2	C97383	hypothetical prote	919	28	13.2	75	2	S69085	ribonuclease p3 (E
847	28	13.2	57	2	B69787	conserved domain p	920	28	13.2	75	2	H83840	hypothetical prote
848	28	13.2	59	2	F93204	conserved hypotet	921	28	13.2	75	2	D84003	hypothetical prote
849	28	13.2	60	2	A97781	hypothetical prote	922	28	13.2	75	2	H90059	hypothetical prote
850	28	13.2	61	2	T12578	thioredoxin h - co	923	28	13.2	75	2	AG1917	hypothetical prote
851	28	13.2	61	2	AD1395	4-oxalocrotonate i	924	28	13.2	76	2	S17560	metallothionein-11
852	28	13.2	61	2	F87653	hypothetical prote	925	28	13.2	76	2	S55054	transcription regu
853	28	13.2	61	2	F83624	conserved hypotet	926	28	13.2	76	2	B87584	hypothetical prote
854	28	13.2	61	2	F83624	hypothetical prote	927	28	13.2	76	2	C83583	hypothetical prote
855	28	13.2	61	2	E82602	hypothetical prote	928	28	13.2	76	2	H81214	hypothetical prote
856	28	13.2	61	2	H97887	hypothetical prote	929	28	13.2	76	2	F97947	hypothetical prote
857	28	13.2	62	1	F1P840	photosystem I chai	930	28	13.2	77	2	D81267	50S ribosomal prot
858	28	13.2	62	2	S21301	Ig heavy chain v r	931	28	13.2	77	2	D06833	hypothetical prote
859	28	13.2	62	2	S73247	photosystem I chai	932	28	13.2	77	2	D64382	hypothetical prote
860	28	13.2	62	2	C69940	hypothetical prote	933	28	13.2	77	2	E97137	hypothetical prote
861	28	13.2	62	2	T36447	hypothetical prote	934	28	13.2	78	1	R5EC28	ribosomal protein
862	28	13.2	63	2	S10303	cytochrome-c oxida	935	28	13.2	78	2	A86040	50S ribosomal subu
863	28	13.2	63	2	G70250	hypothetical prote	936	28	13.2	78	2	C43859	hypothetical prote
864	28	13.2	63	2	T34759	probable transcrip	937	28	13.2	78	2	D91160	hypothetical prote
865	28	13.2	63	2	H82160	hypothetical prote	938	28	13.2	78	2	H91192	50S ribosomal subu
866	28	13.2	64	2	T12869	hypothetical prote	939	28	13.2	78	2	H90405	hypothetical prote
867	28	13.2	64	2	H95284	hypothetical prote	940	28	13.2	78	2	F81093	hypothetical prote
868	28	13.2	65	2	F72738	hypothetical prote	941	28	13.2	78	2	C86006	hypothetical prote
869	28	13.2	65	2	D84156	hypothetical prote	942	28	13.2	78	2	A13302	hypothetical prote
870	28	13.2	65	2	A44859	ribosomal protein	943	28	13.2	78	2	B65136	hypothetical prote
871	28	13.2	66	2	E69464	hypothetical prote	944	28	13.2	79	2	F91093	hypothetical 8.7 k
872	28	13.2	66	2	T18859	hypothetical prote	945	28	13.2	79	2	G86722	type III secretion
873	28	13.2	66	2	D83695	hypothetical prote	946	28	13.2	79	2	T04983	hypothetical prote
874	28	13.2	66	2	AF1869	transcription regu	947	28	13.2	79	2	F84076	hypothetical prote
875	28	13.2	67	2	S76270	ribosomal protein	948	28	13.2	80	2	S34540	photosystem I iron
876	28	13.2	67	2	T27279	hypothetical prote	949	28	13.2	80	2	X32364	photosystem I iron
877	28	13.2	67	2	G97307	hypothetical prote	950	28	13.2	80	2	S00858	t-cell receptor al
878	28	13.2	67	2	A64321	hypothetical prote	951	28	13.2	80	2	C81003	hypothetical prote
879	28	13.2	67	2	D64416	archaeal histone -	952	28	13.2	80	2	P00016	hypothetical 9k pr
880	28	13.2	67	2	AC1954	archaeal histone -	953	28	13.2	80	2	A48996	B cell surface ant
881	28	13.2	68	2	G69969	hypothetical prote	954	28	13.2	80	2	AH2563	hypothetical prote
882	28	13.2	68	2	T37135	hypothetical prote	955	28	13.2	81	1	FELVA	photosystem I iron
883	28	13.2	68	2	H95674	hypothetical prote	956	28	13.2	81	1	FEW1	photosystem I iron
884	28	13.2	68	2	G95264	hypothetical prote	957	28	13.2	81	1	FEZM1C	photosystem I iron
885	28	13.2	68	2	C69294	hypothetical prote	958	28	13.2	81	2	S39511	photosystem I iron
886	28	13.2	69	2	S47574	ferredoxin (fdx-3)	959	28	13.2	81	2	S16351	photosystem I iron
887	28	13.2	69	2	C84275	H+-transporting tw	960	28	13.2	81	2	S73295	photosystem I iron
888	28	13.2	69	2	F81278	hypothetical prote	961	28	13.2	81	2	T07571	photosystem I iron
889	28	13.2	69	2	C81788	conserved hypotet	962	28	13.2	81	2	T07199	photosystem I iron
890	28	13.2	69	2	S72828	hypothetical prote	963	28	13.2	81	2	S14638	translation elonga
891	28	13.2	69	2	S58539	hypothetical prote	964	28	13.2	81	2	F90454	hypothetical prote
892	28	13.2	69	2	T34236	hypothetical prote	965	28	13.2	81	2	G64699	hypothetical prote
893	28	13.2	69	2	G97804	phosphotransferase	966	28	13.2	81	2	G64699	probable acyl carr
894	28	13.2	70	1	WPSAHP	A-ORF-K protein -	967	28	13.2	81	2	T36197	hypothetical prote
895	28	13.2	70	2	G42524	hypothetical prote	968	28	13.2	81	2	T31199	hypothetical prote
896	28	13.2	70	2	S76589	hypothetical prote	969	28	13.2	81	2	H97567	hypothetical prote
897	28	13.2	70	2	T50844	hypothetical prote	970	28	13.2	82	2	S78241	photosystem I iron
898	28	13.2	70	2	F51705	stathmin - African	971	28	13.2	82	2	S37118	class II histocomp
899	28	13.2	71	2	F87539	translation initia	972	28	13.2	82	2	A82307	ribosomal protein
900	28	13.2	72	2	D86751	prophage p12 prote	973	28	13.2	82	2	AE0272	hypothetical prote
901	28	13.2	72	2	E53306	Kiebel protein - pla	974	28	13.2	82	2	AE0850	probable acyl carr
902	28	13.2	72	2	US0654	hypothetical 8.2k	975	28	13.2	82	2	AG3594	hypothetical prote
903	28	13.2	72	2	T28324	ORF MSV163 hypothe	976	28	13.2	83	2	C83156	molybdopterin bios
904	28	13.2	72	2	S56770	RNA-directed RNA p	977	28	13.2	83	2	B90342	hypothetical prote
905	28	13.2	72	2	S56770		978	28	13.2	83	2	G81806	hypothetical prote

979 28 13.2 83 2 A71710  
 980 28 13.2 83 2 I48263  
 981 28 13.2 84 1 WBPWB  
 982 28 13.2 84 2 G3202  
 983 28 13.2 84 2 G37294  
 984 28 13.2 84 2 G8069  
 985 28 13.2 84 2 A3321  
 986 28 13.2 85 1 IWBV  
 987 28 13.2 85 2 S2832  
 988 28 13.2 85 2 B2695  
 989 28 13.2 85 2 B7422  
 990 28 13.2 85 2 H8399  
 991 28 13.2 85 2 C8392  
 992 28 13.2 85 2 B9048  
 993 28 13.2 85 2 A2412  
 994 28 13.2 86 1 Q1BP67  
 995 28 13.2 86 2 B37402  
 996 28 13.2 86 2 S21595  
 997 28 13.2 86 2 S74367  
 998 28 13.2 86 2 T17806  
 999 28 13.2 86 2 H75509  
 1000 28 13.2 86 2 T05982

## ALIGNMENTS

RESULT 1  
 E64324  
 A:Accession: E64324  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-62 <BUL>  
 A:Cross-references: GB:L77118; NID:gl500644; TIGR:MJECLO5; PIDN:AC37071.1; PID:gl500644  
 A:Map position: ECLFOR3265-3453  
 A:Genome: plasmid  
 A:Start codon: GTG  
 A:Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromosomal)

Query Match 21.9%; Score 46.5; DB 2; Length 62;  
 Best Local Similarity 28.6%; Pred. No. 28;  
 Matches 12; Conservative 8; Mismatches 21; Indels 1; Gaps 1;  
 Oy 3 RSTSENSLVAMDFS-GOKSRVIENTPEALSVAVEGLAWRK 43  
 Db 18 KKAERFLKLESSQGMKEIRERAKKQLESGIEWAK 59

RESULT 2  
 E64324  
 A:Accession: E64324  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-62 <BUL>  
 A:Cross-references: GB:L77118; NID:gl500644; TIGR:MJECLO5; PIDN:AC37071.1; PID:gl500644  
 A:Map position: ECLFOR3265-3453  
 A:Genome: plasmid  
 A:Start codon: GTG  
 A:Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromosomal)

A:Accession: E64324  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-76 <BUL>  
 A:Cross-references: GB:U67475; GB:L77117; NID:gl590930; PID:gl590941; TIGR:MJ0196; PI  
 A:Map position: FOR190573-190803  
 A:Start codon: GTG  
 A:Superfamily: DNA-directed RNA polymerase II chain RPB10  
 C:Keywords: nucleotidyltransferase; transcription

Query Match 21.7%; Score 46; DB 2; Length 76;  
 Best Local Similarity 34.4%; Pred. No. 41;  
 Matches 11; Conservative 7; Mismatches 12; Indels 2; Gaps 1;  
 Oy 1 PMSISENSLVAMDFS-GOKSRVIENTPEAL 30  
 Db 7 PIRCFSCGNVIAEVEFYKERILKGENPKDVL 38

RESULT 3  
 T25763  
 A:Accession: T25763  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-73 <PAU>  
 A:Cross-references: EMBL:U88173; PIDN:AB42266.1; GSPDB:GN00019; CESP:F46F11.4  
 A:Experimental source: strain Bristol N2; clone F46F11  
 A:Map position: 1  
 A:Introns: 38/2

Query Match 21.5%; Score 45.5; DB 2; Length 73;  
 Best Local Similarity 29.4%; Pred. No. 46;  
 Matches 10; Conservative 7; Mismatches 12; Indels 5; Gaps 1;  
 Oy 14 DFSGOKSRVIENTPEALS-----VAVEGLAWRK 42  
 Db 8 DRLGKVKVKNCPNPSDTIGDLKKLIAAQTGTWEK 41

RESULT 4  
 A42960  
 A:Accession: A42960  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-60 <GLE>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:110322, NCBIP:110324)  
 C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein  
 F:3-59/Domain: ferredoxin 2[4Fe-4S] homology <FER>  
 F:10,13,16,51/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
 F:20,41,44,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 21.5%; Score 45.5; DB 2; Length 73;  
 Best Local Similarity 29.4%; Pred. No. 46;  
 Matches 10; Conservative 7; Mismatches 12; Indels 5; Gaps 1;  
 Oy 14 DFSGOKSRVIENTPEALS-----VAVEGLAWRK 42  
 Db 8 DRLGKVKVKNCPNPSDTIGDLKKLIAAQTGTWEK 41





C:Accession: B72106  
 R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nare Genet. 21, 385-389, 1999  
 A:Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.  
 A:Reference number: A72000; MUID:99205606; PMID:10192388  
 A:Accession: B72106  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-79 <ARN>  
 A:Cross-references: GB:AE001607; GB:AE001363; NID:q4376474; PIDN:AAD18362.1; PID:9437648  
 A:Experimental source: strain CWL029  
 C:Genetics:  
 A:Gene: CPn0209

Query Match 19.8%; Score 42; DB 2; Length 79;  
 Best Local Similarity 33.3%; Pred. No. 1.5e+02;  
 Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 15 FSGOKSRVIENTEALVAEGL 38  
 I:::|||||  
 Db 28 FOGKTRVIAITPAGLAIAEQNI 51  
 I:::|||||

RESULT 10  
 D81565  
 Hypothetical protein CP0557 [imported] - *Chlamydia pneumoniae* (strain AR39)  
 C:Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000  
 C:Accession: D81565  
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
 A:Title: Genome sequences of *Chlamydia trachomatis* MoPo and *Chlamydia pneumoniae* AR39.  
 A:Reference number: A81500; MUID:20150255; PMID:10684935  
 A:Accession: D81565  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-81 <REA>  
 A:Cross-references: GB:AE002214; GB:AE002161; NID:g7189460; PIDN:AAF38377.1; PID:g718946  
 A:Experimental source: Strain AR39, HL cells  
 C:Genetics:  
 A:Gene: CP0557

Query Match 19.8%; Score 42; DB 2; Length 81;  
 Best Local Similarity 33.3%; Pred. No. 1.6e+02;  
 Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 15 FSGOKSRVIENTEALVAEGL 38  
 I:::|||||  
 Db 30 FOGKTRVIAITPAGLAIAEQNI 53  
 I:::|||||

RESULT 11  
 G64370  
 conserved hypothetical protein MJ0567 - *Methanococcus jannaschii*  
 C:Species: *Methanococcus jannaschii*  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: G64370  
 R:Reich, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996  
 A:Authors: Kainer, B.F.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*.  
 A:Reference number: A64300; MUID:196337999; PMID:868087  
 A:Accession: G64370  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-82 <BBU>  
 A:Cross-references: GB:U67505; GB:L77117; NID:g2826297; PIDN:AAB98558.1; PID:g1591273; T  
 C:Genetics:  
 A:Map position: REV504744-504496  
 C:Superfamily: *Methanococcus jannaschii* conserved hypothetical protein MJ0567

Query Match 19.8%; Score 42; DB 1; Length 82;  
 Best Local Similarity 32.5%; Pred. No. 1.6e+02;  
 Matches 13; Conservative 8; Mismatches 11; Indels 8; Gaps 2;

Oy 10 LVAMDFSGOKSRVIENTEALVAEGLAWR 41  
 I:::|||||  
 Db 28 LVSMGINIGSKLVIRNONGPVITSTKGSNIAIGRLAMK 67  
 I:::|||||

RESULT 12  
 S60284  
 B12D protein - barley  
 C:Species: *Hordeum vulgare* (barley)  
 C:Date: 20-Jul-1996 #sequence\_revision 27-Feb-1997 #text\_change 21-Jul-2000  
 C:Accession: S60284  
 R:Aalen, R.B.; Opsahl-Ferstad, H.G.; Lindestad, C.; Olsen, O.A. Plant J. 5, 385-396, 1994  
 A:Title: Transcripts encoding an oleosin and a dormancy-related protein are present i  
 A:Reference number: S60284; MUID:94236153; PMID:8180622  
 A:Accession: S60284  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-87 <AAI>  
 A:Cross-references: EMBL:X76604; NID:q471318; PIDN:CAA54065.1; PID:g471319

Query Match 19.6%; Score 41.5; DB 2; Length 87;  
 Best Local Similarity 35.1%; Pred. No. 2e+02;  
 Matches 13; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

Oy 2 MRSISESLVAMDFSGOKSRVIENTEALVAEGL 38  
 I:::|||||  
 Db 29 LRNTGNPEVRVSKMGRAAGVLENHEGRRYA-EHGL 64  
 I:::|||||

RESULT 13  
 A60172  
 Proteoglycan core protein, laryngeal cartilage - pig (fragments)  
 C:Species: *Sus scrofa domestica* (domestic pig)  
 C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 13-Aug-1999  
 C:Accession: A60172  
 R:Harris, M.; Kenneally, B.; Barry, F. Biochem. Soc. Trans. 18, 299, 1990  
 A:Title: Primary structure of the hyaluronic acid-binding region of porcine laryngeal  
 A:Reference number: A60172; MUID:90337042; PMID:1696222  
 A:Accession: A60172  
 A:Molecule type: protein  
 A:Residues: 1-73 <HAR>  
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology;  
 C:Keywords: cartilage  
 F:41-73/Domain: link protein repeat homology (fragment) <LNK1>

Query Match 19.1%; Score 40.5; DB 2; Length 73;  
 Best Local Similarity 38.7%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 3; Mismatches 7; Indels 9; Gaps 2;

Oy 18 QKSRVIENTEALVAEGL 40  
 I:::|||||  
 Db 44 QNSAIIATP-ENLNAATEDGPHQCAGLAW 73  
 I:::|||||

RESULT 14  
 A43602  
 T-cell-stimulating antigen - *Coccidioides immitis* (fragment)  
 C:Species: *Coccidioides immitis*  
 C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 11-Jan-2000  
 C:Accession: A43602; S18767  
 R:Kirkland, T.N.; Zhu, S.; Kruse, D.; Hsu, L.; Seshan, K.R.; Cole, G.T. Infect. Immun. 59, 3952-3961, 1991  
 A:Title: *Coccidioides immitis* fractions which are antigenic for immune T lymphocytes.  
 A:Reference number: A43602; MUID:92040063; PMID:1840578  
 A:Accession: A43602  
 A:Molecule type: mRNA



A:Reference number: ABL807; MUID:21595285; PMID:11759840  
 A:Accession: AD1945  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-77 <KUR>  
 A:Cross-references: GB:BA0000019; PIDN:BAB73068.1; PID:g17130457; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: asl1111

Query Match 18.6%; Score 39.5; DB 2; Length 77;  
 Best Local Similarity 22.2%; Pred. No. 3.2e+02;  
 Matches 8; Conservative 10; Mismatches 13; Indels 5; Gaps 1;

OY 2 MRSISESLVAMDFSGOKSRVIENTEALSVAVEEG 37  
 Db 10 LKAVKQALR-----ERLQNTNPEAFIKQAEQ 40

RESULT 20  
 C64901  
 ribosomal protein S22 [validated] - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Date: 24-Sep-1999 #sequence\_revision 24-Sep-1999 #text\_change 01-Mar-2002  
 C:Accession: C64901  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: C64901  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-45 <BLAT>  
 A:Cross-references: GB:AE000245; GB:U00096; NID:g1787752; PIDN:AACT4553.1; PID:g1787755;  
 A:Experimental source: strain K-12, substrain MG1655  
 R:Arnold, R.J.; Reilly, J.P.  
 Anal. Biochem. 269, 106-112, 1999  
 A:Title: Observation of Escherichia coli ribosomal proteins and their posttranslational  
 A:Reference number: A59071; MUID:99196679; PMID:10094780  
 A:Contents: annotation; mass spectrographic analysis  
 A:Note: a ribosomal protein with these mass spectrographic characteristics was found; no  
 may have been missed  
 C:Genetics:  
 A:Gene: rpsv  
 C:Complex: the ribosome is composed of the large (50S) and small (30S) subunit; the large  
 S rRNA and 22 distinct proteins  
 C:Complex: small subunit ribosomal proteins: S1 (PIR:R3EC1), S2 (PIR:R3EC2), S3 (PIR:R3EC10), S11 (PIR:R3EC11), S12 (PIR:R3EC12), S13 (PIR:R3EC13), S14 (PIR:R3EC14), S15 (PIR:R3EC21), S22 (PIR:C64901) [validated, MUID:99196679]  
 C:Function:  
 A:Pathway: protein biosynthesis  
 C:Superfamily: Escherichia coli ribosomal protein S22  
 C:Keywords: protein biosynthesis; ribosome  
 F:1-45/Product: ribosomal protein S22 #status experimental <MAT>

Query Match 18.4%; Score 39; DB 1; Length 45;  
 Best Local Similarity 63.6%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 17 GOKSRVIENTPT 27  
 Db 27 GOKSSVVNNPT 37

RESULT 21  
 D90889  
 30S ribosomal subunit protein S22 [imported] - Escherichia coli (strain O157:H7, substrain  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 17-May-2002  
 C:Accession: D90889  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.;  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 9  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: D90889  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-45 <HAY>  
 A:Cross-references: PIDN:BA000007; PIDN:BA035507.1; PID:g13361550; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RMD 0509952  
 C:Genetics:  
 A:Gene: ECs2084  
 C:Superfamily: Escherichia coli ribosomal protein S22

Query Match 18.4%; Score 39; DB 2; Length 45;  
 Best Local Similarity 63.6%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 17 GOKSRVIENTPT 27  
 Db 27 GOKSSVVNNPT 37

RESULT 22  
 E85728

30S ribosomal subunit protein S22 [imported] - Escherichia coli (strain O157:H7, subs  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 17-May-2002  
 C:Accession: E85728  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: E85728  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-45 <STO>  
 A:Cross-references: GB:AE005174; NID:g12515201; PIDN:AAG56289.1; GSPDB:GN00145; UMGP:  
 A:Experimental source: strain O157:H7, substrain EBL933  
 C:Genetics:  
 A:Gene: rpsv  
 C:Superfamily: Escherichia coli ribosomal protein S22

Query Match 18.4%; Score 39; DB 2; Length 45;  
 Best Local Similarity 63.6%; Pred. No. 2e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 17 GOKSRVIENTPT 27  
 Db 27 GOKSSVVNNPT 37

RESULT 23  
 T06654

hypothetical protein T6G15.70 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 22-Oct-1999  
 C:Accession: T06654  
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.  
 submitted to the Protein Sequence Database, April 1999  
 A:Reference number: Z15791  
 A:Accession: T06654  
 A:Molecule type: DNA  
 A:Residues: 1-62 <BEV>  
 A:Cross-references: EMBL:AL049656; GSPDB:GN00062; ATSP:T6G15.70  
 A:Experimental source: cultivar Columbia; BAC clone T6G15  
 C:Genetics:  
 A:Gene: ATSP:T6G15.70  
 A:Map position: 4

Query Match 18.4%; Score 39; DB 2; Length 62;  
 Best Local Similarity 29.7%; Pred. No. 2.9e+02;  
 Matches 11; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 2 MRSISESLVAMDFSGOKSRVIENTEALSVAVEEGL 38  
 || : : | || : : : : || : : ||  
 Db 1 MRPMOLDMLSEMDDAGSSMAMVDVDDLEAMEILNEGGL 37

RESULT 24

AD3532  
 Hypothetical protein BMEI10182 [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: AD3532  
 R:DelVecchio, V.G.; Kaprat, R.J.; Redkar, G.; Patra, C.; Los, T.; Ivanova,  
 ; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A:Reference number: AD3532; PMID:11756688  
 A:Accession: AD3532  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-72 <KUR>  
 A:Cross-references: GB:AE008918; PIDN:AAL53423.1; PID:g17984319; GSPDB:GN00191  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI10182  
 A:Map position: II

Query Match 18.4%; Score 39; DB 2; Length 72;  
 Best Local Similarity 41.7%; Pred. No. 3.5e+02;  
 Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 17 GQSRVIENTEALSVAVEEGLAW 40  
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RESULT 25

B83269  
 Hypothetical protein PA3009 [imported] - Pseudomonas aeruginosa (strain PA01)  
 C:Species: Pseudomonas aeruginosa  
 C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: B83269  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 ; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A:Reference number: B83269; MUID:20437337; PMID:10984043  
 A:Accession: B83269  
 A:Status: preliminary  
 A:Molecule type: DNA  
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 A:Cross-references: GB:AE004726; GB:AE004091; NID:g9949108; PIDN:AAG06397.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA3009

Query Match 18.4%; Score 39; DB 2; Length 77;  
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QY 3 RSISESLVAMDFSGOKSRVIE 24  
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 Db 20 RADDEALVTLFSGDAKNFLQ 41

Search completed: March 28, 2003, 09:08:54  
 Job time : 42.2677 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 09:08:20 ; Search time 13.8819 Seconds  
(without alignments)  
181.900 Million cell updates/sec

File: US09-936-697-5

Sequence: 1 PMRSISNSLVAMDFSGQKS.....ENPTALSVAEGLAWRK 43

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 29382

Minimum DB seq length: 40

Maximum DB seq length: 90

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications: AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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8	40	18.9	71	9	US-09-864-761-41352
9	39.5	18.6	68	10	US-09-864-761-47104
10	39.5	18.6	78	10	US-09-864-761-47104
11	39.5	18.6	89	10	US-09-815-242-4918
12	39	18.4	47	10	US-09-864-761-43815
13	38.5	18.2	66	10	US-09-864-761-45291
14	38.5	18.2	66	10	US-09-864-761-36073
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16	38	17.9	62	10	US-09-939-980-301
17	38	17.9	68	10	US-09-925-300-1560
18	37.5	17.7	51	10	US-09-864-761-43411
19	37.5	17.7	64	10	US-09-925-300-1765

## SUMMARIES

20	37.5	17.7	65	9	US-10-092-154-735	Sequence 735, App
21	37.5	17.7	65	10	US-09-764-847-735	Sequence 735, App
22	37.5	17.7	89	10	US-09-925-297-543	Sequence 543, App
23	37	17.5	57	10	US-09-071-838-294	Sequence 294, App
24	37	17.5	57	10	US-09-764-877-1480	Sequence 1480, App
25	36.5	17.2	59	10	US-09-867-550-980	Sequence 980, App
26	36.5	17.2	61	10	US-09-879-957-208	Sequence 208, App
27	36.5	17.2	71	9	US-10-001-876-151	Sequence 151, App
28	36.5	17.2	79	10	US-09-864-761-38542	Sequence 38542, A
29	36.5	17.2	83	9	US-09-908-931B-50	Sequence 50, Appl
30	36.5	17.2	90	9	US-09-764-872-374	Sequence 374, App
31	36	17.0	46	10	US-09-864-761-33369	Sequence 33369, A
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34	36	17.0	63	9	US-10-083-357-900	Sequence 900, App
35	36	17.0	64	10	US-09-764-869-864	Sequence 864, App
36	36	17.0	74	9	US-09-738-626-4797	Sequence 4797, App
37	36	17.0	78	10	US-09-864-761-33623	Sequence 33623, A
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46	35	16.5	58	10	US-09-925-302-651	Sequence 651, App
47	35	16.5	59	10	US-09-864-761-39483	Sequence 39483, A
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49	35	16.5	64	10	US-09-864-761-48795	Sequence 48795, A
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52	35	16.5	76	9	US-10-092-154-881	Sequence 881, App
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75	33.5	15.8	67	10	US-09-864-761-43927	Sequence 43927, A
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77	33.5	15.8	74	9	US-09-796-692-1911	Sequence 1911, App
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84	33	15.6	56	10	US-09-864-761-40879	Sequence 40879, A
85	33	15.6	62	10	US-09-864-761-48027	Sequence 48027, A
86	33	15.6	64	10	US-09-864-761-34561	Sequence 34561, A
87	33	15.6	64	10	US-09-864-761-34993	Sequence 34993, A
88	33	15.6	69	9	US-09-925-299-1037	Sequence 1037, App
89	33	15.6	65	10	US-09-864-761-39839	Sequence 39839, App
90	33	15.6	65	10	US-09-925-299-1037	Sequence 1037, App
91	33	15.6	67	10	US-09-864-761-38332	Sequence 38332, A
92	33	15.6	67	10	US-09-820-893-109	Sequence 109, App

93	33	15.6	67	10	US-09-873-880-20	Sequence 20, Appl	166	32	89	10	US-09-867-550-212	Sequence 212, App	
94	33	15.6	68	10	US-09-795-501-8	Sequence 8, Appl	167	32	90	10	US-09-864-761-40114	Sequence 40114, A	
95	33	15.6	69	9	US-10-083-357-694	Sequence 694, App	168	31.5	54	10	US-09-864-761-46492	Sequence 46492, A	
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99	33	15.6	73	10	US-09-864-761-44101	Sequence 44101, A	172	31.5	65	10	US-09-864-761-39828	Sequence 39828, A	
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104	33	15.6	84	9	US-10-013-379-18	Sequence 18, Appl	177	31	44	12	US-10-042-417-72	Sequence 417, Appl	
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113	32.5	15.3	63	10	US-09-925-300-1332	Sequence 1332, App	186	31	57	10	US-09-864-761-35718	Sequence 35718, App	
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117	32.5	15.3	72	10	US-09-929-924-17	Sequence 17, Appl	190	31	62	10	US-09-864-761-45366	Sequence 45366, A	
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124	32.5	15.3	86	12	US-10-153-064-69	Sequence 69, Appl	197	31	77	10	US-10-112-793-26	Sequence 26, Appl	
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126	32	15.1	41	10	US-09-864-761-45355	Sequence 45355, A	199	31	77	10	US-10-072-783-5	Sequence 5, Appl	
127	32	15.1	51	10	US-09-864-761-47302	Sequence 47302, A	200	31	86	9	US-10-156-273-34	Sequence 34, Appl	
128	32	15.1	52	9	US-09-764-847-806	Sequence 1779, App	201	31	86	9	US-09-751-100B-48	Sequence 48, Appl	
129	32	15.1	53	9	US-10-001-883-126	Sequence 126, App	202	31	90	10	US-09-922-261-304	Sequence 304, App	
130	32	15.1	54	9	US-09-920-280	Sequence 280, App	203	31	45	10	US-09-205-658-69	Sequence 69, Appl	
131	32	15.1	54	9	US-10-092-154-862	Sequence 862, App	204	31	48	10	US-09-844-353A-69	Sequence 69, Appl	
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133	32	15.1	54	10	US-09-864-761-46759	Sequence 46759, A	206	31	50	9	US-10-083-357-921	Sequence 921, App	
134	32	15.1	55	10	US-09-864-761-46169	Sequence 46169, A	207	31	57	9	US-10-012-896-561	Sequence 561, App	
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138	32	15.1	58	10	US-09-879-957-131	Sequence 131, App	211	30.5	57	10	US-09-864-761-37466	Sequence 37466, A	
139	32	15.1	60	10	US-09-815-242-5488	Sequence 5488, App	212	30.5	60	10	US-09-864-761-42598	Sequence 42598, A	
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143	32	15.1	62	10	US-09-864-761-38019	Sequence 38019, A	216	30.5	64	10	US-09-867-550-1098	Sequence 1098, App	
144	32	15.1	62	10	US-09-820-893-91	Sequence 91, Appl	217	30.5	65	10	US-09-785-272-146	Sequence 272, App	
145	32	15.1	63	10	US-09-820-893-91	Sequence 91, Appl	218	30.5	68	10	US-09-864-761-43485	Sequence 43485, A	
146	32	15.1	65	12	US-10-078-929-24	Sequence 24, Appl	219	30.5	70	10	US-09-881-752A-332	Sequence 332, App	
147	32	15.1	68	9	US-09-925-299-1186	Sequence 1186, App	220	30.5	72	10	US-10-062-023-3	Sequence 3, Appl	
148	32	15.1	68	10	US-09-925-299-1186	Sequence 1186, App	221	30.5	72	10	US-09-783-320-10	Sequence 10, Appl	
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151	32	15.1	70	10	US-09-820-893-52	Sequence 52, Appl	224	30.5	77	9	US-10-072-349-141	Sequence 141, App	
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162	32	15.1	81	10	US-09-410-194-10	Sequence 10, Appl	235	30.5					
163	32	15.1	83	10	US-09-867-550-1736	Sequence 1736, App	236	30.5					
164	32	15.1	83	10	US-09-764-877-1070	Sequence 1070, App	237	30.5					
165	32	15.1	84	10	US-09-764-877-1985	Sequence 1985, App	238	30.5					

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242	30	14.2	42	10	US-09-843-845-30	Sequence 30, Appl	315	29.5	13.9	55	10	US-09-864-761-45582	Sequence 45582, A
243	30	14.2	42	10	US-09-864-761-35922	Sequence 35922, A	316	29.5	13.9	60	10	US-09-864-761-45942	Sequence 45942, A
244	30	14.2	44	10	US-10-133-159-10	Sequence 10, Appl	317	29.5	13.9	61	10	US-09-521-397-33	Sequence 33, Appl
245	30	14.2	44	9	US-09-821-176-10	Sequence 10, Appl	318	29.5	13.9	66	9	US-09-738-626-3628	Sequence 3628, Ap
246	30	14.2	44	9	US-09-821-176-10	Sequence 10, Appl	319	29.5	13.9	66	9	US-09-796-692-2165	Sequence 2165, Ap
247	30	14.2	46	9	US-09-869-919-115	Sequence 115, App	320	29.5	13.9	66	9	US-10-091-483-224	Sequence 224, App
248	30	14.2	46	9	US-10-091-572-327	Sequence 327, App	321	29.5	13.9	66	12	US-09-764-846-224	Sequence 224, App
249	30	14.2	47	10	US-09-779-451-42	Sequence 42, Appl	322	29.5	13.9	66	12	US-10-028-415-39	Sequence 224, App
250	30	14.2	47	10	US-10-000-256A-167	Sequence 167, App	323	29.5	13.9	68	10	US-09-864-761-48084	Sequence 48084, A
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267	30	14.2	63	10	US-09-864-761-48895	Sequence 48895, A	340	29.5	13.9	89	10	US-09-867-550-136	Sequence 126, App
268	30	14.2	64	9	US-09-864-761-46549	Sequence 46549, A	341	29.5	13.9	90	10	US-09-870-963-4	Sequence 4, Appl
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289	30	14.2	75	9	US-09-925-299-788	Sequence 788, App	362	29	13.7	45	10	US-09-736-960-44	Sequence 44, Appl
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310	29.5	13.9	49	9	US-10-178-213-93	Sequence 93, Appl	383	29	13.7	53	10	US-09-864-761-41458	Sequence 41458, A
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390	29	13.7	55	9	US-09-925-299-1150	Sequence 1150, App	463	28.5	13.4	52	9	US-09-864-761-34294	Sequence 34294, A
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394	29	13.7	59	9	US-09-796-692-2400	Sequence 2400, App	467	28.5	13.4	57	10	US-09-205-558-245	Sequence 245, App
395	29	13.7	59	9	US-10-083-357-1209	Sequence 1209, App	468	28.5	13.4	61	10	US-09-841-132-6	Sequence 6, Appl
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398	29	13.7	59	10	US-09-864-761-44773	Sequence 44773, A	471	28.5	13.4	62	9	US-09-796-692-2316	Sequence 2316, App
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403	29	13.7	61	10	US-09-864-761-36999	Sequence 36999, A	476	28.5	13.4	67	9	US-09-738-626-3758	Sequence 3758, App
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405	29	13.7	65	10	US-09-731-872-355	Sequence 355, App	478	28.5	13.4	67	10	US-09-864-761-41235	Sequence 41235, A
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408	29	13.7	67	10	US-09-871-874-18	Sequence 18, Appl	481	28.5	13.4	72	10	US-09-925-297-569	Sequence 569, App
409	29	13.7	68	9	US-09-983-802-277	Sequence 277, App	482	28.5	13.4	73	10	US-09-864-761-48180	Sequence 48180, A
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411	29	13.7	68	10	US-09-864-761-36677	Sequence 36677, A	484	28.5	13.4	77	10	US-09-864-761-35099	Sequence 35099, App
412	29	13.7	68	10	US-09-864-761-40058	Sequence 40058, A	485	28.5	13.4	77	10	US-09-864-761-41250	Sequence 41250, A
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414	29	13.7	69	10	US-09-864-761-48665	Sequence 48665, A	487	28.5	13.4	81	10	US-09-864-761-32550	Sequence 32550, A
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417	29	13.7	70	10	US-09-726-643-88	Sequence 88, Appl	490	28.5	13.4	86	10	US-09-864-761-503	Sequence 503, App
418	29	13.7	71	10	US-09-864-761-46777	Sequence 46777, A	491	28.5	13.4	88	9	US-09-841-132-5	Sequence 5, Appl
419	29	13.7	71	9	US-10-077-111-9	Sequence 9, Appl	492	28.5	13.4	88	9	US-09-796-692-2288	Sequence 2288, App
420	29	13.7	72	10	US-09-867-550-968	Sequence 968, App	493	28.5	13.4	89	9	US-10-043-487-521	Sequence 521, App
421	29	13.7	73	10	US-09-864-761-42518	Sequence 385, App	494	28.5	13.4	90	9	US-09-922-199A-22	Sequence 22, App
422	29	13.7	73	10	US-09-864-761-33523	Sequence 42518, A	495	28.5	13.4	90	9	US-09-738-626-3796	Sequence 3796, App
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425	29	13.7	76	9	US-09-864-921-170	Sequence 170, App	498	28	13.2	41	8	US-08-732-630-76	Sequence 76, Appl
426	29	13.7	76	10	US-09-815-242-4896	Sequence 4896, App	499	28	13.2	41	9	US-10-080-375-24	Sequence 24, Appl
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437	29	13.7	82	9	US-09-796-692-1135	Sequence 1135, App	510	28	13.2	44	9	US-09-996-140-166	Sequence 166, App
438	29	13.7	82	9	US-09-796-692-1585	Sequence 1585, App	511	28	13.2	44	9	US-09-996-140-167	Sequence 167, App
439	29	13.7	82	9	US-09-796-692-2202	Sequence 2202, App	512	28	13.2	44	9	US-09-996-140-237	Sequence 237, App
440	29	13.7	82	10	US-09-864-761-35480	Sequence 35480, A	513	28	13.2	44	9	US-09-996-140-238	Sequence 238, App
441	29	13.7	83	10	US-09-864-761-44293	Sequence 44293, A	514	28	13.2	44	9	US-09-996-140-239	Sequence 239, App
442	29	13.7	83	10	US-09-754-997A-16	Sequence 16, Appl	515	28	13.2	44	9	US-09-774-638-218	Sequence 218, App
443	29	13.7	84	9	US-09-808-387-34	Sequence 34, Appl	516	28	13.2	44	9	US-09-369-730-371	Sequence 371, App
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450	29	13.7	87	9	US-09-852-797-98	Sequence 98, App	523	28	13.2	46	10	US-09-864-761-37981	Sequence 37981, A
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597	28	13.2	74	9	US-09-796-692-2489	Sequence 2489, App	670	27.5	13.0	54	10	US-09-864-761-40033	Sequence 40033, A
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706	27.5	13.0	86	10	US-09-925-300-1139	Sequence 1139, App	779	27	12.7	55	9	US-09-908-711-80	Sequence 80, Appl
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720	27.5	13.0	41	10	US-09-864-761-42451	Sequence 42451, A	793	27	12.7	57	9	US-09-895-814-565	Sequence 565, App
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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864,761
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2000-09-21
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; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; Sequence 111, Application US/09879957
; Patent No. US20020034755A1
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; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. US20020034755a1h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
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; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872

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; TELEPHONE: (212) 790-9080
; TELEFAX: (212) 869-8664/9741
; TELEX: 86141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-879-957-111
Query Match 20.5% Score 43.5; DB 10; Length 55;
Best Local Similarity 41.4%; Pred. No. 23;
Matches 12; Conservative 8; Mismatches 4; Indels 5; Gaps 2;
Qy 4 SISENSLVAMDFS-COKSRVTENTALS 31
Db 23 TVNKGSLVAGFSGQGEAR-----PEEILN 47

RESULT 3
US-09-864-761-34262
; Sequence 34262, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmiga-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

```

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; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34262
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031734.9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.87
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 74
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
; OTHER INFORMATION: EST_HUMAN HIT: A1075970.1, EVALU 7.00e-03
US-09-864-761-34262
Query Match 19.8% Score 42; DB 10; Length 63;
Best Local Similarity 31.8%; Pred. No. 44;
Matches 14; Conservative 7; Mismatches 11; Indels 12; Gaps 2;
Qy 6 SENSELVAMDFSQKSRVI-----ENPTEALSVAVEEGLAWRK 42
Db 13 SOVGLPILYFSGRRRLRLRPEVLAEIPREAFIVE-----AWVK 51

RESULT 4
US-09-738-626-6764
; Sequence 6764, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6764
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6764
Query Match 19.8% Score 42; DB 9; Length 72;
Best Local Similarity 22.0%; Pred. No. 53;
Matches 11; Conservative 12; Mismatches 19; Indels 8; Gaps 1;
Qy 2 MRSISENSLVAMDFSQKSRVI-----ENPTEALSVAVEEGLAWRK 43
Db 1 MHFIKENLITSAESNALRAQLMLSLGSAEFERSIIREROAEGIAWKR 50

```

RESULT 5  
 US-09-864-761-41352  
 ; Sequence 41352, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Acomica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263,6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/774,203  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 49117  
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 41352  
 ; LENGTH 49  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO AL158049.2  
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5  
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1  
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3  
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
 ; OTHER INFORMATION: EST HUMAN HIT: R15413.1, EVALUATE 2.00e-22  
 ; OTHER INFORMATION: SWISSPROT HIT: Q03712, EVALUATE 4.80e-02  
 US-09-864-761-41352

Query Match 18.9%; Score 40; DB 10; Length 49;  
 Best Local Similarity 38.7%; Pred. No. 63;  
 Matches 12; Conservative 7; Mismatches 8; Indels 4; Gaps 2;

QY 12 AMDF-SGOKSRVIENTPTALSVAVEGLAMR 41  
 Db 10 AVEFLASNESRI--QTESHVRVAGEDMLVWR 37  
 RESULT 6  
 US-09-983-802-611  
 ; Sequence 611, Application US/09983802  
 ; Publication No. US20030022185A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer et al.  
 ; TITLE OF INVENTION: 123 Human Secreted Proteins  
 ; FILE REFERENCE: P2010P1  
 ; CURRENT APPLICATION NUMBER: US/09/983,802  
 ; PRIOR FILING DATE: 2001-10-25  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984

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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 611
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-611

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Query Match          18.9%; Score 40; DB 9; Length 63;
Best Local Similarity 47.18; Pred. No. 86;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 5 ISNSLVAMDFSGQKSR 21
DB 20 VSSNLFSPFFGQKAR 36

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RESULT 7
US-09-895-913A-280
; Sequence 280, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Comen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in the
; FILE OF INVENTION: Genome
; FILE OF INVENTION: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/861,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-280

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Query Match          18.9%; Score 40; DB 9; Length 70;
Best Local Similarity 25.08; Pred. No. 99;
Matches 8; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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QY 1 PMRISISLVAMDFSGQKSRVIENTPEALSV 32
DB 19 PMFLYKNEWLVKFSNSDALPINKSTLSI 50

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RESULT 8
US-09-764-872-351
; Sequence 351, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper

```

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; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 351
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-872-351

```

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Query Match          18.9%; Score 40; DB 9; Length 71;
Best Local Similarity 44.08; Pred. No. 1e+02;
Matches 11; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

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QY 19 KSRVIENTPEALSVAVEEGLAWRKK 43
DB 20 KVRVKNPREAVN-----FHWRRK 38

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```

RESULT 9
US-09-864-761-47104
; Sequence 47104, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL I
; FILE OF INVENTION: X-1
; FILE REFERENCE: X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21

```

```

; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47104
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005083.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
; OTHER INFORMATION: SWISSPROT HIT: P43802, EVALU8 8.80e-01
US-09-864-761-47104

Query Match
Best Local Similarity 18.6%; Score 39.5; DB 10; Length 68;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 9 SLVAMDFSGQKSRVIENTPALSVAEEGLWRK 42
Db 1 ALIKMDQELVARLQIE-AAVLTSVAVLKCKGWRE 33

RESULT 10
US-09-764-887-218
; Sequence 218, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 218
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-887-218

Query Match
Best Local Similarity 18.6%; Score 39.5; DB 10; Length 78;
Matches 12; Conservative 7; Mismatches 9; Indels 5; Gaps 1;

QY 3 RSISENSLVAMDFSGQKSRVIENTPALSVAEEGLWRK 35
Db 8 RSDSDSSTLA-----KKSIFVNRSTERRSLRVK 35

RESULT 11
US-09-815-242-4918
; Sequence 4918, Application US/09815242
; Patent No. US20020081509A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: PROKAYOTES
; CURRENT APPLICATION NUMBER: US/09/815,242

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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4918
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4918

Query Match
Best Local Similarity 18.6%; Score 39.5; DB 10; Length 89;
Matches 11; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 5 ISENSLVAMDFSGQKSRVIENTPALSVAEEGL 38
Db 8 ITEKSLAND---EKKYTFEVDTRANKTLVKQAV 38

RESULT 12
US-09-864-761-43815
; Sequence 43815, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661

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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 43815  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC005881.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.73  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.6  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76  
; OTHER INFORMATION: SWISSPROT HIT: Q60349, EVALUATE 4.70e+00  
US-09-864-761-43815

Query Match 18.4%; Score 39; DB 10; Length 47;  
Best Local Similarity 34.8%; Pred. No. 83;  
Matches 8; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 10 LVAMDFSGQKSRVIENTEALVS 32  
I: | | | | | | | | | |  
Db 3 LLMFSPHGDVSVKTEKPTVKLMI 25

## RESULT 13

US-09-864-761-45291  
; Sequence 45291, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 45291  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC009079.4  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48  
; OTHER INFORMATION: EST\_HUMAN HIT: AV756022.1, EVALUATE 6.00e-28  
; OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUATE 2.00e+00  
US-09-864-761-45291

Query Match 18.4%; Score 39; DB 10; Length 60;  
Best Local Similarity 33.3%; Pred. No. 11e+02;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 5 ISESLVAMDFSGQKSRVIE 25  
: | | | | | | | | | |  
Db 34 LSENLQTYNFRQKESVVQH 54

## RESULT 14

US-09-864-761-36073  
; Sequence 36073, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30

## POLYPEPTIDES and Their Uses

NUMBER OF SEQUENCES: 534  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,980  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/936.165  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gimmi, Edward R  
 REGISTRATION NUMBER: 38,891  
 REFERENCE/DOCKET NUMBER: P50549  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-4478  
 TELEFAX: 610-270-5090  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 301:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 62 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 301:  
 980-301

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Query Match      17.9%;   Score 38;   DB 10;   Length 62;
Best Local Similarity 31.0%;   Pred. No. 1.6e+02;
Matches 9;   Conservative 6;   Mismatches 14;   Indels 0;   Gaps 0;

OY 10 LVAMDFSGQKSRVIENTPEALSVAVEGL 38
Db 7 MMALNTAGXTQRTVETLAEYSGVPVNNGL 35

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; Sequence: 1560, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: US/09/925,300  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1560  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-1560

Query Match 17.9%; Score 38; DB 10; Length 68;  
Best Local Similarity 34.6%; Pred. No. 1.9e+02;  
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 18 OKSRVIENTEALSVAVEEGLAWRK 43  
DB 31 KKNSSVKNLCCGLSIFAAFGURWRIK 56

RESULT 18  
US-09-864-761-43411  
; Sequence 43411, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 43411  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; OTHER INFORMATION: MAP TO AC006257.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.76  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.85  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71  
; OTHER INFORMATION: SWISSPROT HIT: P49643, EVALUE 1.00e-21  
US-09-864-761-43411

Query Match 17.7%; Score 37.5; DB 10; Length 51;  
Best Local Similarity 26.1%; Pred. No. 1.5e+02;  
Matches 12; Conservative 7; Mismatches 8; Indels 19; Gaps 1;

QY 13 MDSGQKSR-----VIENTEALSVAVEEGLA 39  
DB 3 MEFSGRKWRKRLAGDQRNASYPHCLQFYLPSPSENISLIEFENLA 48

RESULT 19  
US-09-925-300-1765  
; Sequence 1765, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1765  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (26)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1765

Query Match 17.7%; Score 37.5; DB 10; Length 64;  
Best Local Similarity 60.0%; Pred. No. 2e+02;  
Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 29 ALSV-AVEEGLAWRK 42  
DB 11 ALSDSVEDHLAWSK 25

RESULT 20  
US-10-092-154-735  
; Sequence 735, Application US/10092154  
; Publication No. US20030054375A1

RESULT 24

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; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1480
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1480

Query Match      17.5%; Score 37; DB 10; Length 86;
Best Local Similarity 32.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

Qy 16 SGOKSRVIENPTEALSVAVEEGLAW 40
   ||| : | : : : ||||
Db 18 SQO-----VFGPRRSQTLLFQSGLAW 38

RESULT 25
US-09-867-550-980
; Sequence 980, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 980
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-980

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Best Local Similarity 27.6%; Pred. No. 2.6e+02;
Matches 8; Conservative 6; Mismatches 4; Indels 11; Gaps 1;

Qy 15 FSGOKSRVIENPTEALSVAVEEGLAWKK 43
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Db 32 YSGKKPR-----PIAAGLSWQOK 49

Search completed: March 28, 2003, 09:19:16
Job time : 22.8619 secs
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GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 28, 2003, 09:03:25 ; Search time 12.5276 Seconds  
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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 20297

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	44	20.8	80	4	US-09-574-141A-20
5	44	20.8	80	4	US-09-707-780-20
6	43.5	20.5	55	4	US-08-630-915A-111
7	42	19.8	47	4	US-08-776-059-16
8	41	19.3	40	1	US-07-641-971B-5
9	41	19.3	40	1	US-07-781-248A-5
10	40.5	19.1	66	2	US-08-459-568-52
11	40.5	19.1	66	2	US-08-516-859A-52
12	40.5	19.1	66	3	US-09-586-472-52
13	40.5	19.1	66	4	US-09-528-706-52
14	40.5	19.1	66	4	US-09-006-428A-14
15	40.5	19.1	79	4	US-08-905-223-420
16	40.5	19.1	86	4	US-09-227-357-611
17	40	18.9	63	4	US-09-331-930A-2
18	39.5	18.6	73	4	US-09-331-930A-19
19	39.5	18.6	73	4	US-09-331-930A-20
20	39.5	18.6	73	4	US-09-331-930A-21
21	39.5	18.6	73	4	US-09-331-930A-24
22	39.5	18.6	73	4	US-09-331-930A-25
23	39.5	18.6	73	4	US-09-100-804-30
24	39	18.4	68	3	US-09-081-320-9
25	39	18.4	80	3	US-09-574-141A-9
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28	39	18.4	80	4	US-09-707-780-9
29	38.5	18.2	59	1	US-08-524-677-16
30	38	17.9	62	4	US-08-167-035A-301
31	38	17.9	70	1	US-08-167-035-26
32	38	17.9	70	1	US-08-208-887A-26
33	38	17.9	70	2	US-08-539-005-26
34	38	17.9	70	4	US-09-280-598-28
35	38	17.9	80	3	US-09-081-320-31
36	38	17.9	80	4	US-09-574-141A-31
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42	37	17.5	73	2	US-08-891-837B-2
43	36.5	17.2	89	2	US-08-461-990B-16
44	36.5	17.2	43	4	US-09-131-750-25
45	36	17.0	61	4	US-08-630-915A-208
46	36	17.0	47	4	US-08-776-059-17
47	36	17.0	58	1	US-08-446-646-13
48	36	17.0	66	1	US-08-203-808B-11
49	36	17.0	66	2	US-08-414-657D-54
50	36	17.0	66	2	US-08-414-657D-55
51	36	17.0	66	4	US-03-017-754A-11
52	36	17.0	76	2	US-08-667-679-2
53	36	17.0	76	2	US-08-892-150-2
54	36	17.0	89	2	US-08-461-990B-17
55	35.5	16.7	56	4	US-08-461-990B-18
56	35.5	16.7	56	4	US-08-973-462-21
57	35.5	16.7	78	4	US-08-973-462-24
58	35.5	16.7	88	4	US-09-254-352B-23
59	35.5	16.7	88	4	US-08-818-113-87
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61	35.5	16.7	88	4	US-09-056-556-87
62	34.5	16.3	88	4	US-09-072-596-88
63	34.5	16.3	58	1	US-08-222-616-30
64	34.5	16.3	58	4	US-08-446-648-30
65	34.5	16.3	58	5	PCT-US95-04228-30
66	34	16.0	83	3	US-09-100-804-24
67	34	16.0	43	2	US-08-531-927B-5
68	34	16.0	50	3	US-08-938-830-4
69	34	16.0	50	3	US-09-020-222-4
70	34	16.0	53	4	US-08-274-366-2
71	34	16.0	58	1	US-08-905-223-326
72	34	16.0	58	2	US-08-572-951-37
73	34	16.0	58	3	US-08-735-491-5
74	34	16.0	58	3	US-08-941-445A-34
75	34	16.0	64	3	PCT-US95-07828-2
76	34	16.0	77	1	US-08-759-463-4
77	34	16.0	77	1	US-08-182-175A-57
78	34	16.0	77	1	US-08-474-633A-75
79	34	16.0	77	4	US-08-823-771-75
80	34	16.0	77	5	PCT-US92-06412-57
81	33.5	15.8	68	6	5196523-11
82	33.5	15.8	68	4	US-08-905-223-369
83	33.5	15.8	72	1	US-08-280-443-14
84	33.5	15.8	72	1	US-08-457-459-14
85	33.5	15.8	72	1	US-08-555-678-14
86	33.5	15.8	72	5	PCT-US95-02275-14
87	33.5	15.8	73	4	US-09-254-352B-25
88	33.5	15.8	73	4	US-09-254-352B-26
89	33.5	15.8	73	4	US-09-254-352B-27
90	33.5	15.8	78	4	US-08-354-352B-21
91	33.5	15.8	78	4	US-09-254-352B-22
92	33.5	15.8	81	4	US-08-458-207A-537
93	33	15.6	40	1	US-08-781-020-7
94	33	15.6	40	1	US-09-038-935-7
95	33	15.6	42	1	US-07-641-971B-4
96	33	15.6	42	1	US-07-781-248A-4
97	33	15.6	50	2	US-08-459-568-56
98	33	15.6	50	2	US-08-399-411-56
99	33	15.6	50	3	US-08-516-859A-56
100	33	15.6	50	4	US-09-586-472-56

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Sequence 208, Appl  
Sequence 17, Appl  
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Sequence 56, Appl

101	33	15.6	50	4	US-08-528-706-56	Sequence 56, Appl	174	31.5	14.9	46	1	US-08-339-152A-25	Sequence 25, Appl
102	33	15.6	54	1	US-08-167-033-29	Sequence 29, Appl	175	31.5	14.9	46	2	US-08-007-999B-8	Sequence 8, Appl
103	33	15.6	54	1	US-08-080-887A-29	Sequence 29, Appl	176	31.5	14.9	46	2	US-08-689-276A-8	Sequence 8, Appl
104	33	15.6	54	2	US-08-469-537A-9	Sequence 9, Appl	177	31.5	14.9	69	4	US-08-905-223-419	Sequence 419, Appl
105	33	15.6	54	2	US-08-469-537A-33	Sequence 33, Appl	178	31.5	14.9	80	4	US-08-737-226-5	Sequence 5, Appl
106	33	15.6	54	4	US-08-539-005-29	Sequence 29, Appl	179	31.5	14.9	81	2	US-08-245-511-14	Sequence 14, Appl
107	33	15.6	54	4	US-08-510B-18	Sequence 18, Appl	180	31.5	14.9	81	2	US-08-600-993A-14	Sequence 14, Appl
108	33	15.6	54	4	US-08-280-598-31	Sequence 31, Appl	181	31.5	14.9	85	4	US-09-134-001C-3387	Sequence 3387, Ap
109	33	15.6	55	2	US-08-456-647B-2	Sequence 2, Appl	182	31.5	14.9	87	3	US-09-023-083A-76	Sequence 76, Appl
110	33	15.6	55	2	US-08-237-401A-2	Sequence 2, Appl	183	31.5	14.9	89	4	US-09-134-001C-4563	Sequence 4563, Ap
111	33	15.6	59	2	US-08-393-816-18	Sequence 18, Appl	184	31	14.6	41	1	US-08-179-634-8	Sequence 8, Appl
112	33	15.6	69	1	US-08-410-804-5	Sequence 5, Appl	185	31	14.6	41	1	US-08-440-174A-8	Sequence 8, Appl
113	33	15.6	69	1	US-08-259-514-5	Sequence 5, Appl	186	31	14.6	41	5	PCT-US95-00052-8	Sequence 8, Appl
114	33	15.6	69	2	US-08-858-311-5	Sequence 13, Appl	187	31	14.6	49	4	US-09-323-872A-27	Sequence 27, Appl
115	32.5	15.3	47	1	US-08-262-037-13	Sequence 13, Appl	188	31	14.6	54	2	US-08-456-647B-51	Sequence 51, Appl
116	32.5	15.3	50	4	US-09-177-249-167	Sequence 167, App	189	31	14.6	54	2	US-08-237-401A-51	Sequence 51, Appl
117	32.5	15.3	51	1	US-08-026-145-6	Sequence 6, Appl	190	31	14.6	54	2	US-08-456-647B-8	Sequence 8, Appl
118	32.5	15.3	53	1	US-07-985-692-4	Sequence 4, Appl	191	31	14.6	55	2	US-08-266-311-3	Sequence 3, Appl
119	32.5	15.3	53	1	US-08-153-371-8	Sequence 8, Appl	192	31	14.6	61	2	US-08-467-528A-3	Sequence 3, Appl
120	32.5	15.3	53	1	US-08-147-710-8	Sequence 10, Appl	193	31	14.6	61	2	US-08-467-528B-3	Sequence 3, Appl
121	32.5	15.3	53	1	US-08-321-658B-10	Sequence 10, Appl	194	31	14.6	61	6	5320958-19	Patent No. 5320958
122	32.5	15.3	53	1	US-08-384-489-7	Sequence 7, Appl	195	31	14.6	66	4	US-09-007-905-41	Sequence 41, Appl
123	32.5	15.3	53	1	US-08-334-773A-4	Sequence 4, Appl	196	31	14.6	66	4	US-09-233-074-41	Sequence 41, Appl
124	32.5	15.3	53	1	US-08-424-022-4	Sequence 11, Appl	197	31	14.6	66	4	US-08-961-083-142	Sequence 142, App
125	32.5	15.3	53	1	US-08-446-846-11	Sequence 8, Appl	198	31	14.6	70	4	US-09-056-556-233	Sequence 233, App
126	32.5	15.3	53	1	US-08-458-090-8	Sequence 8, Appl	199	31	14.6	71	4	US-09-073-596-228	Sequence 228, App
127	32.5	15.3	53	2	US-08-457-887-8	Sequence 8, Appl	200	31	14.6	71	4	US-07-955-700B-32	Sequence 32, Appl
128	32.5	15.3	53	2	US-08-424-017B-4	Sequence 4, Appl	201	31	14.6	71	4	US-08-475-537-32	Sequence 32, Appl
129	32.5	15.3	53	5	PCT-US93-11696-4	Sequence 4, Appl	202	31	14.6	74	1	US-08-475-537-32	Sequence 32, Appl
130	32.5	15.3	61	4	US-09-134-001C-5046	Sequence 5046, Ap	203	31	14.6	74	1	US-08-475-537-32	Sequence 32, Appl
131	32.5	15.3	65	2	US-08-633-879C-16	Sequence 16, Appl	204	31	14.6	74	1	US-08-475-537-32	Sequence 32, Appl
132	32.5	15.3	71	4	US-09-073-297-10	Sequence 10, Appl	205	31	14.6	74	2	US-08-475-537-32	Sequence 32, Appl
133	32.5	15.3	73	4	US-09-254-352B-29	Sequence 29, Appl	206	31	14.6	74	2	US-08-475-537-32	Sequence 32, Appl
134	32.5	15.3	90	1	US-07-618-312A-11	Sequence 11, Appl	207	31	14.6	75	4	US-08-475-537-32	Sequence 32, Appl
135	32.5	15.3	90	1	US-08-280-228-11	Sequence 11, Appl	208	31	14.6	75	4	US-08-475-537-32	Sequence 32, Appl
136	32	15.1	41	1	US-08-347-808C-7	Sequence 7, Appl	209	31	14.6	76	4	US-08-828-683A-26	Sequence 26, Appl
137	32	15.1	41	1	US-08-347-808C-7	Sequence 7, Appl	210	31	14.6	76	4	US-08-828-683A-26	Sequence 26, Appl
138	32	15.1	41	2	US-08-337-646A-7	Sequence 7, Appl	211	31	14.6	86	1	US-08-602-010A-34	Sequence 34, Appl
139	32	15.1	41	2	US-08-337-646A-7	Sequence 7, Appl	212	31	14.6	86	1	US-08-680-726A-34	Sequence 34, Appl
140	32	15.1	41	2	US-08-337-646A-7	Sequence 7, Appl	213	31	14.6	86	1	US-09-092-409-34	Sequence 48, Appl
141	32	15.1	41	2	US-08-337-646A-7	Sequence 7, Appl	214	31	14.6	90	3	US-08-894-173-48	Sequence 48, Appl
142	32	15.1	41	4	US-08-856-034-7	Sequence 10, Appl	215	31	14.6	90	4	US-09-398-193-48	Sequence 304, App
143	32	15.1	42	3	US-08-504-538A-10	Sequence 10, Appl	216	30.5	14.4	43	4	US-09-461-697-304	Sequence 604, App
144	32	15.1	42	5	PCT-US95-09307-10	Sequence 10, Appl	217	30.5	14.4	43	4	US-09-461-697-304	Sequence 604, App
145	32	15.1	47	4	US-08-776-059-19	Sequence 19, Appl	218	30.5	14.4	53	3	US-09-605-785-561	Sequence 80, Appl
146	32	15.1	51	1	US-08-188-228-34	Sequence 34, Appl	219	30.5	14.4	53	3	US-09-605-785-561	Sequence 80, Appl
147	32	15.1	51	1	US-08-332-643-34	Sequence 34, Appl	220	30.5	14.4	65	4	US-08-961-083-146	Sequence 146, App
148	32	15.1	51	1	US-08-332-643-34	Sequence 34, Appl	221	30.5	14.4	74	1	US-09-017-754A-13	Sequence 13, Appl
149	32	15.1	54	2	US-08-469-537A-10	Sequence 10, Appl	222	30.5	14.4	74	1	US-09-017-754A-13	Sequence 13, Appl
150	32	15.1	58	4	US-08-630-915A-131	Sequence 31, Appl	223	30.5	14.4	74	1	US-09-017-754A-13	Sequence 13, Appl
151	32	15.1	58	4	US-09-227-357-549	Sequence 549, App	224	30.5	14.4	76	3	US-09-083-524-5	Sequence 5, Appl
152	32	15.1	62	1	US-08-464-531-117	Sequence 117, App	225	30.5	14.4	77	3	US-08-475-668A-211	Sequence 211, App
153	32	15.1	62	1	US-08-464-531-117	Sequence 117, App	226	30.5	14.4	77	3	US-08-475-668A-211	Sequence 211, App
154	32	15.1	62	3	US-08-322-137-117	Sequence 117, App	227	30.5	14.4	77	3	US-08-475-668A-211	Sequence 211, App
155	32	15.1	70	1	US-08-193-863-2	Sequence 2, Appl	228	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
156	32	15.1	70	1	US-08-377-833-2	Sequence 2, Appl	229	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
157	32	15.1	70	1	US-08-324-502-2	Sequence 2, Appl	230	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
158	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	231	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
159	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	232	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
160	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	233	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
161	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	234	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
162	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	235	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
163	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	236	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
164	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	237	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
165	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	238	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
166	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	239	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
167	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	240	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
168	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	241	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
169	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	242	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
170	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	243	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
171	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	244	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
172	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	245	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl
173	32	15.1	70	1	US-08-413-939-2	Sequence 2, Appl	246	30.5	14.4	81	1	US-08-239-992A-24	Sequence 24, Appl

247	30	14.2	51	1	US-08-208-108-11	Sequence 11, Appl	320	29	13.7	48	4	US-09-082-279B-970	Sequence 970, App
248	30	14.2	52	2	US-08-809-860-3	Sequence 3, Appl	321	29	13.7	48	4	US-09-315-304B-970	Sequence 970, App
249	30	14.2	53	2	US-08-856-444-3	Sequence 3, Appl	322	29	13.7	48	4	US-08-117-083-16	Sequence 16, Appl
250	30	14.2	54	2	US-08-469-537A-29	Sequence 29, Appl	323	29	13.7	53	4	US-09-271-608-12	Sequence 12, Appl
251	30	14.2	55	2	US-08-592-646A-15	Sequence 15, Appl	324	29	13.7	53	4	US-09-695-950-12	Sequence 12, Appl
252	30	14.2	56	2	US-09-165-422-15	Sequence 15, Appl	325	29	13.7	53	4	US-09-696-147-12	Sequence 12, Appl
253	30	14.2	57	2	US-08-456-647B-42	Sequence 42, Appl	326	29	13.7	53	4	US-09-696-364-12	Sequence 12, Appl
254	30	14.2	58	2	US-08-237-401A-42	Sequence 42, Appl	327	29	13.7	53	4	US-09-586-563C-6	Sequence 6, Appl
255	30	14.2	59	2	US-09-058-459-48	Sequence 48, Appl	328	29	13.7	53	4	US-09-586-562C-6	Sequence 6, Appl
256	30	14.2	60	2	US-09-058-459-48	Sequence 48, Appl	329	29	13.7	54	1	US-08-446-692-34	Sequence 34, Appl
257	30	14.2	61	2	US-09-127-926-86	Sequence 86, Appl	330	29	13.7	54	2	US-08-488-351A-34	Sequence 34, Appl
258	30	14.2	62	2	US-09-127-926-86	Sequence 86, Appl	331	29	13.7	56	4	US-09-020-880-96	Sequence 96, Appl
259	30	14.2	63	2	US-08-446-692-107	Sequence 107, Appl	332	29	13.7	56	4	US-09-101-544-96	Sequence 96, Appl
260	30	14.2	64	2	US-08-488-351A-107	Sequence 107, Appl	333	29	13.7	59	1	US-07-938-782A-5	Sequence 5, Appl
261	30	14.2	65	2	US-08-488-351A-94	Sequence 94, Appl	334	29	13.7	59	1	US-08-630-524-5	Sequence 5, Appl
262	30	14.2	66	2	US-08-887-534A-94	Sequence 94, Appl	335	29	13.7	59	1	US-08-194-211A-3	Sequence 3, Appl
263	30	14.2	67	2	US-08-209-521-19	Sequence 19, Appl	336	29	13.7	61	1	US-08-456-748B-3	Sequence 3, Appl
264	30	14.2	68	2	US-08-209-521-20	Sequence 20, Appl	337	29	13.7	61	2	US-08-209-521-14	Sequence 14, Appl
265	30	14.2	69	2	US-08-209-521-20	Sequence 20, Appl	338	29	13.7	64	2	US-08-209-521-15	Sequence 15, Appl
266	30	14.2	70	2	US-08-961-810-129	Sequence 129, Appl	339	29	13.7	64	2	US-08-961-810-124	Sequence 124, Appl
267	30	14.2	71	2	US-08-961-810-129	Sequence 129, Appl	340	29	13.7	64	4	US-08-961-810-125	Sequence 125, Appl
268	30	14.2	72	2	US-08-352-902D-129	Sequence 129, Appl	341	29	13.7	64	4	US-08-352-902D-124	Sequence 124, Appl
269	30	14.2	73	2	US-08-352-902D-130	Sequence 130, Appl	342	29	13.7	64	4	US-08-352-902D-125	Sequence 125, Appl
270	30	14.2	74	2	US-09-188-930-297	Sequence 297, Appl	343	29	13.7	64	4	US-09-134-001C-5429	Sequence 5429, Ap
271	30	14.2	75	2	US-08-643C-11	Sequence 11, Appl	344	29	13.7	65	2	US-08-867-087B-33	Sequence 33, Appl
272	30	14.2	76	2	US-08-905-223-435	Sequence 435, Appl	345	29	13.7	65	2	US-08-867-087B-34	Sequence 34, Appl
273	30	14.2	77	2	US-09-134-001C-5238	Sequence 5238, Ap	346	29	13.7	65	4	US-09-134-001C-4870	Sequence 4870, Ap
274	30	14.2	78	2	US-08-858-207A-540	Sequence 540, Ap	347	29	13.7	67	3	US-09-227-357-277	Sequence 277, App
275	30	14.2	79	2	US-08-858-207A-540	Sequence 540, Ap	348	29	13.7	68	4	US-09-911-927-33	Sequence 33, Appl
276	30	14.2	80	2	US-08-134-001C-3435	Sequence 3435, Ap	349	29	13.7	68	4	US-09-911-927-33	Sequence 33, Appl
277	30	14.2	81	2	US-08-134-001C-4092	Sequence 4092, Ap	350	29	13.7	68	4	US-08-965-762-33	Sequence 33, Appl
278	30	14.2	82	2	US-08-308-643C-9	Sequence 9, Appl	351	29	13.7	69	4	US-08-884-569A-7	Sequence 7, Appl
279	30	14.2	83	2	US-09-025-151-20	Sequence 20, Appl	352	29	13.7	70	4	US-08-884-569A-7	Sequence 7, Appl
280	30	14.2	84	2	US-08-995-159-6	Sequence 6, Appl	353	29	13.7	72	1	US-08-468-674B-61	Sequence 61, Appl
281	30	14.2	85	2	US-09-446-920-2	Sequence 2, Appl	354	29	13.7	72	1	US-08-760-371-61	Sequence 61, Appl
282	30	14.2	86	2	US-08-461-990B-24	Sequence 24, Appl	355	29	13.7	76	2	US-08-468-674B-67	Sequence 67, Appl
283	30	14.2	87	2	US-08-353-476-80	Sequence 80, Appl	356	29	13.7	76	2	US-08-468-674B-73	Sequence 73, Appl
284	30	14.2	88	2	US-08-679-493A-99	Sequence 99, Appl	357	29	13.7	78	1	US-08-780-371-73	Sequence 73, Appl
285	30	14.2	89	2	US-08-461-990B-19	Sequence 19, Appl	358	29	13.7	81	4	US-08-134-001C-3196	Sequence 3196, Ap
286	29.5	13.9	90	2	519523-15	Patent No. 519523	359	29	13.7	83	1	US-07-662-193-7	Sequence 7, Appl
287	29.5	13.9	91	2	US-08-208-108-12	Sequence 12, Appl	360	29	13.7	83	1	US-08-370-225-23	Sequence 23, Appl
288	29.5	13.9	92	2	US-08-459-568-53	Sequence 53, Appl	361	29	13.7	83	1	US-08-461-859-23	Sequence 23, Appl
289	29.5	13.9	93	2	US-08-399-411-53	Sequence 53, Appl	362	29	13.7	83	5	PCT-US93-10069-23	Sequence 23, Appl
290	29.5	13.9	94	2	US-08-516-859A-53	Sequence 53, Appl	363	29	13.7	84	4	US-09-134-001C-2919	Sequence 2919, Ap
291	29.5	13.9	95	2	US-09-586-472-53	Sequence 53, Appl	364	29	13.7	85	2	US-08-480-229C-2	Sequence 2, Appl
292	29.5	13.9	96	2	US-09-528-706-53	Sequence 53, Appl	365	29	13.7	85	2	US-08-659-235C-2	Sequence 2, Appl
293	29.5	13.9	97	2	US-09-134-001C-4792	Sequence 4792, Ap	366	29	13.7	86	4	US-08-858-207A-361	Sequence 361, App
294	29.5	13.9	98	2	US-08-475-668A-210	Sequence 210, Ap	367	29	13.7	87	4	US-09-152-060-98	Sequence 98, Appl
295	29.5	13.9	99	2	US-09-065-474-162	Sequence 162, Ap	368	29	13.7	88	1	US-08-468-674B-75	Sequence 75, Appl
296	29.5	13.9	100	2	US-08-485-551A-210	Sequence 210, Ap	369	29	13.7	88	1	US-08-780-371-75	Sequence 75, Appl
297	29.5	13.9	101	2	US-08-557-034-182	Sequence 182, Ap	370	29	13.7	90	3	US-08-894-173-49	Sequence 49, Appl
298	29.5	13.9	102	2	US-08-312-272-19	Sequence 19, Appl	371	29	13.7	90	3	US-09-398-193-49	Sequence 49, Appl
299	29.5	13.9	103	2	US-09-026-039-19	Sequence 19, Appl	372	28.5	13.4	47	1	US-08-339-152A-28	Sequence 28, Appl
300	29.5	13.9	104	2	US-09-109-266-16	Sequence 16, Appl	373	28.5	13.4	47	2	US-08-007-592B-15	Sequence 15, Appl
301	29.5	13.9	105	2	US-08-464-164-4	Sequence 4, Appl	374	28.5	13.4	47	2	US-08-669-276A-15	Sequence 15, Appl
302	29.5	13.9	106	2	US-08-338-057-4	Sequence 4, Appl	375	28.5	13.4	53	4	US-08-936-165A-460	Sequence 460, App
303	29.5	13.9	107	2	US-08-464-164-4	Sequence 4, Appl	376	28.5	13.4	56	1	US-08-182-175A-112	Sequence 112, App
304	29.5	13.9	108	2	US-09-173-581-4	Sequence 4, Appl	377	28.5	13.4	56	5	PCT-US92-06412-112	Sequence 112, App
305	29.5	13.9	109	2	US-09-420-915-4	Sequence 4, Appl	378	28.5	13.4	59	1	US-08-287-959-17	Sequence 17, Appl
306	29	13.7	110	2	US-08-272-882D-4	Sequence 4, Appl	379	28.5	13.4	61	4	US-09-208-277-6	Sequence 6, Appl
307	29	13.7	111	2	PCT-US92-05532-4	Sequence 4, Appl	380	28.5	13.4	61	4	US-09-556-877-6	Sequence 6, Appl
308	29	13.7	112	2	US-09-562-773-199	Sequence 199, Ap	381	28.5	13.4	61	4	US-09-288-594A-6	Sequence 6, Appl
309	29	13.7	113	2	US-08-772-440-12	Sequence 12, Appl	382	28.5	13.4	61	4	US-09-620-412C-6	Sequence 6, Appl
310	29	13.7	114	2	US-08-446-692-56	Sequence 56, Appl	383	28.5	13.4	64	4	US-09-134-001C-5298	Sequence 5298, Ap
311	29	13.7	115	2	US-08-488-351A-56	Sequence 56, Appl	384	28.5	13.4	72	1	US-08-182-175A-87	Sequence 87, Appl
312	29	13.7	116	2	US-08-312-202B-1	Sequence 274, Ap	385	28.5	13.4	72	1	US-08-469-260A-233	Sequence 233, App
313	29	13.7	117	2	US-09-079-347-1	Sequence 1, Appl	386	28.5	13.4	72	5	PCT-US92-06412-87	Sequence 87, Appl
314	29	13.7	118	2	US-09-075-725-1	Sequence 1, Appl	387	28.5	13.4	80	3	US-08-461-607-5	Sequence 5, Appl
315	29	13.7	119	2	US-08-905-223-467	Sequence 1, Appl	388	28.5	13.4	80	4	US-09-363-600-5	Sequence 5, Appl
316	29	13.7	120	2	US-08-809-646-1	Sequence 467, App	389	28.5	13.4	82	2	US-08-117-952-756	Sequence 756, App
317	29	13.7	121	2	PCT-US95-12433-1	Sequence 1, Appl	390	28.5	13.4	84	1	US-08-798-897-16	Sequence 16, Appl
318	29	13.7	122	2	US-08-936-165A-365	Sequence 365, App	391	28.5	13.4	84	1	US-08-978-523-16	Sequence 16, Appl
319	29	13.7	123	2			392	28.5	13.4	86	4	US-09-208-277-5	Sequence 5, Appl



393	28.5	13.4	86	4	US-09-556-877-5	Sequence 5, Appl	466	28	13.2	52	2	US-08-209-521-16	Sequence 16, Appl
394	28.5	13.4	86	4	US-09-288-594A-5	Sequence 5, Appl	467	28	13.2	52	3	US-08-917-299-10	Sequence 10, Appl
395	28.5	13.4	86	4	US-08-620-412C-5	Sequence 5, Appl	468	28	13.2	52	4	US-09-188-930-167	Sequence 167, Appl
396	28.5	13.4	87	2	US-08-465-721-11	Sequence 11, Appl	469	28	13.2	52	4	US-08-961-810-126	Sequence 126, Appl
397	28.5	13.4	87	2	US-08-392-935-11	Sequence 11, Appl	470	28	13.2	52	4	US-08-352-9020-136	Sequence 136, Appl
398	28.5	13.4	87	2	US-09-134-001C-3693	Sequence 3693, Ap	471	28	13.2	52	4	US-09-422-662-1	Sequence 10, Appl
399	28.5	13.4	87	5	PCT-US93-08326-11	Sequence 26, Appl	472	28	13.2	52	4	US-08-630-916A-74	Sequence 74, Appl
400	28.5	13.4	90	4	US-09-103-478-26	Sequence 26, Appl	473	28	13.2	55	1	US-08-530-550-36	Sequence 36, Appl
401	28.5	13.4	90	4	US-09-193-931C-26	Sequence 92, Appl	474	28	13.2	55	1	US-08-262-037-12	Sequence 12, Appl
402	28.5	13.4	90	4	US-09-228-986-92	Sequence 20, Appl	475	28	13.2	55	4	US-08-336-165A-414	Sequence 414, Appl
403	28	13.2	40	3	US-09-035-619-20	Sequence 21, Appl	476	28	13.2	55	4	US-09-071-035-384	Sequence 384, Appl
404	28	13.2	40	3	US-09-035-619-21	Sequence 22, Appl	477	28	13.2	55	4	US-08-182-175A-91	Sequence 91, Appl
405	28	13.2	40	3	US-09-035-619-22	Sequence 23, Appl	478	28	13.2	56	1	US-08-474-633A-79	Sequence 79, Appl
406	28	13.2	40	3	US-09-035-619-23	Sequence 24, Appl	479	28	13.2	56	1	US-08-274-366-1	Sequence 36, Appl
407	28	13.2	40	3	US-09-035-619-24	Sequence 25, Appl	480	28	13.2	56	2	US-08-572-951-36	Sequence 4, Appl
408	28	13.2	40	3	US-09-082-2798-969	Sequence 969, App	481	28	13.2	56	3	US-08-735-491-4	Sequence 33, Appl
409	28	13.2	40	4	US-09-514-006-20	Sequence 20, Appl	482	28	13.2	56	3	US-08-941-445A-33	Sequence 79, Appl
410	28	13.2	40	4	US-09-514-006-21	Sequence 21, Appl	483	28	13.2	56	3	PCT-US92-06412-91	Sequence 91, Appl
411	28	13.2	40	4	US-09-514-006-22	Sequence 22, Appl	484	28	13.2	56	5	US-09-053-197A-17	Sequence 17, Appl
412	28	13.2	40	4	US-09-514-006-23	Sequence 23, Appl	485	28	13.2	56	5	US-09-085-761A-17	Sequence 15, Appl
413	28	13.2	40	4	US-09-514-006-24	Sequence 24, Appl	486	28	13.2	57	3	US-08-392-816-17	Sequence 15, Appl
414	28	13.2	40	4	US-09-514-006-25	Sequence 25, Appl	487	28	13.2	57	3	US-08-441-340-15	Sequence 2, Appl
415	28	13.2	40	4	US-08-315-304B-969	Sequence 969, App	488	28	13.2	58	3	US-08-484-223B-210	Sequence 210, Appl
416	28	13.2	40	4	US-08-783-333F-27	Sequence 27, Appl	489	28	13.2	58	3	US-09-425-061-15	Sequence 11, Appl
417	28	13.2	41	4	US-09-169-015-37	Sequence 37, Appl	490	28	13.2	58	4	US-08-825-886-15	Sequence 15, Appl
418	28	13.2	41	4	US-09-133-944-26	Sequence 26, Appl	491	28	13.2	58	4	US-09-326-039-2	Sequence 15, Appl
419	28	13.2	41	4	US-08-787-738B-27	Sequence 27, Appl	492	28	13.2	59	1	US-09-134-001C-4881	Sequence 4881, Ap
420	28	13.2	41	4	US-08-787-738B-27	Sequence 28, Appl	493	28	13.2	63	2	US-09-079-812E-31	Sequence 31, Appl
421	28	13.2	41	4	US-09-157-748-29	Sequence 29, Appl	494	28	13.2	63	2	US-09-025-151-24	Sequence 24, Appl
422	28	13.2	41	4	US-09-082-2798-747	Sequence 747, App	495	28	13.2	63	4	US-08-166-930-10	Sequence 10, Appl
423	28	13.2	42	4	US-09-315-304B-747	Sequence 6, Appl	496	28	13.2	64	4	US-08-727-045A-10	Sequence 10, Appl
424	28	13.2	43	1	US-08-179-632-6	Sequence 6, Appl	497	28	13.2	66	4	US-09-408-172-10	Sequence 10, Appl
425	28	13.2	43	2	US-08-440-174A-6	Sequence 3, Appl	498	28	13.2	66	6	US-08-847-065-16	Sequence 16, Appl
426	28	13.2	43	2	US-08-854-768-3	Sequence 3, Appl	499	28	13.2	68	6	US-08-847-065-17	Sequence 17, Appl
427	28	13.2	43	2	US-09-172-841-41	Sequence 41, Appl	500	28	13.2	69	1	US-08-338-579A-100	Sequence 100, App
428	28	13.2	43	4	US-08-988-856B-8	Sequence 8, Appl	501	28	13.2	69	2	US-08-176-427B-12	Sequence 12, Appl
429	28	13.2	43	4	US-08-988-856B-8	Sequence 8, Appl	502	28	13.2	69	2	US-08-356-060A-35	Sequence 35, Appl
430	28	13.2	43	4	US-09-186-276B-12	Sequence 12, Appl	503	28	13.2	69	4	US-08-460-900C-36	Sequence 36, Appl
431	28	13.2	43	4	US-08-842-445-12	Sequence 22, Appl	504	28	13.2	70	4	US-08-674-509B-35	Sequence 35, Appl
432	28	13.2	43	4	US-09-186-188B-12	Sequence 12, Appl	505	28	13.2	70	4	US-08-954-698-36	Sequence 36, Appl
433	28	13.2	43	4	PCT-US95-0062-12	Sequence 6, Appl	506	28	13.2	72	3	US-08-957-874-35	Sequence 35, Appl
434	28	13.2	43	5	US-08-110-788A-6	Sequence 5, Appl	507	28	13.2	72	3	US-08-336-165A-415	Sequence 415, App
435	28	13.2	44	1	US-08-362-037-5	Sequence 5, Appl	508	28	13.2	73	1	US-08-469-260A-407	Sequence 407, App
436	28	13.2	44	1	US-08-446-692-62	Sequence 62, Appl	509	28	13.2	73	1	US-08-117-952-754	Sequence 754, App
437	28	13.2	44	1	US-08-140-137A-48	Sequence 48, Appl	510	28	13.2	73	2	US-08-722-349-7	Sequence 7, Appl
438	28	13.2	44	2	US-08-488-351A-62	Sequence 62, Appl	511	28	13.2	73	2	US-09-204-328-7	Sequence 7, Appl
439	28	13.2	44	2	US-08-963-056-109	Sequence 109, App	512	28	13.2	73	2	US-09-196-048-2	Sequence 4603, Ap
440	28	13.2	44	2	US-09-202-712-12	Sequence 25, Appl	513	28	13.2	73	4	US-08-425-061-17	Sequence 17, Appl
441	28	13.2	44	4	US-08-715-034-2	Sequence 25, Appl	514	28	13.2	73	4	US-08-848-252-2	Sequence 2, Appl
442	28	13.2	44	4	US-09-082-279B-45	Sequence 45, Appl	515	28	13.2	73	4	US-08-825-886-17	Sequence 17, Appl
443	28	13.2	44	4	US-09-315-304B-45	Sequence 33, Appl	516	28	13.2	73	4	US-09-134-001C-4882	Sequence 4882, Ap
444	28	13.2	45	1	US-08-182-175A-33	Sequence 33, Appl	517	28	13.2	75	4	US-09-227-357-592	Sequence 592, App
445	28	13.2	45	1	US-08-182-175A-35	Sequence 35, Appl	518	28	13.2	75	4	US-09-376-330-32	Sequence 32, Appl
446	28	13.2	45	1	US-08-182-175A-45	Sequence 45, Appl	519	28	13.2	75	4	US-07-662-193-8	Sequence 8, Appl
447	28	13.2	45	1	US-08-478-633A-30	Sequence 30, Appl	520	28	13.2	75	4		
448	28	13.2	45	1	US-08-478-633A-32	Sequence 32, Appl	521	28	13.2	75	4		
449	28	13.2	45	1	US-09-037-900-6	Sequence 6, Appl	522	28	13.2	76	2		
450	28	13.2	45	4	US-08-833-771-30	Sequence 30, Appl	523	28	13.2	76	3		
451	28	13.2	45	4	US-08-833-771-32	Sequence 32, Appl	524	28	13.2	76	3		
452	28	13.2	45	5	PCT-US92-06412-33	Sequence 33, Appl	525	28	13.2	76	3		
453	28	13.2	45	5	PCT-US92-06412-35	Sequence 35, Appl	526	28	13.2	76	3		
454	28	13.2	45	5	US-08-262-037-104	Sequence 104, App	527	28	13.2	76	3		
455	28	13.2	50	1	US-08-715-034-1	Sequence 1, Appl	528	28	13.2	76	3		
456	28	13.2	50	4	US-09-082-279B-1513	Sequence 1513, Ap	529	28	13.2	76	3		
457	28	13.2	50	4			530	28	13.2	76	3		
458	28	13.2	50	4			531	28	13.2	76	3		
459	28	13.2	50	4			532	28	13.2	76	3		
460	28	13.2	50	4			533	28	13.2	76	3		
461	28	13.2	50	4			534	28	13.2	76	3		
462	28	13.2	50	4			535	28	13.2	76	3		
463	28	13.2	50	4			536	28	13.2	76	3		
464	28	13.2	50	4			537	28	13.2	76	3		
465	28	13.2	50	4			538	28	13.2	76	3		

539	28	13.2	88	4	US-09-222-938A-1	Sequence 1, Appl	612	27.5	13.0	90	4	US-09-199-534-11	Sequence 11, Appl
540	28	13.2	88	4	US-09-441-340-10	Sequence 10, Appl	613	27	12.7	40	1	US-08-386-729A-3	Sequence 3, Appl
541	28	13.2	89	1	US-08-090-523-6	Sequence 6, Appl	614	27	12.7	40	1	US-08-630-915A-86	Sequence 86, Appl
542	28	13.2	89	1	US-08-398-627-6	Sequence 6, Appl	615	27	12.7	41	1	US-08-056-200-108	Sequence 108, App
543	28	13.2	89	1	US-08-406-858-6	Sequence 6, Appl	616	27	12.7	41	2	US-08-800-644-108	Sequence 108, App
544	28	13.2	89	5	PCT-US91-04036-6	Sequence 6, Appl	617	27	12.7	42	4	US-03-262-773-200	Sequence 200, App
545	28	13.2	89	5	PCT-US91-05275-6	Sequence 6, Appl	618	27	12.7	42	4	US-08-988-856B-11	Sequence 11, Appl
546	28	13.2	90	4	US-09-522-433B-29	Sequence 29, Appl	619	27	12.7	42	4	US-08-988-856B-11	Sequence 11, Appl
547	28	13.2	90	4	US-08-397-787-17	Sequence 17, Appl	620	27	12.7	42	4	US-09-244-592-6	Sequence 6, Appl
548	27.5	13.0	42	2	US-08-766-858A-27	Sequence 27, Appl	621	27	12.7	42	4	US-09-284-819-1	Sequence 1, Appl
549	27.5	13.0	43	1	US-07-998-003A-85	Sequence 85, Appl	622	27	12.7	43	3	US-08-839-578-5	Sequence 5, Appl
550	27.5	13.0	43	1	US-08-453-274B-85	Sequence 85, Appl	623	27	12.7	44	1	US-08-208-008C-6	Sequence 6, Appl
551	27.5	13.0	43	1	US-08-453-695A-85	Sequence 85, Appl	624	27	12.7	44	2	US-08-248-839C-63	Sequence 63, Appl
552	27.5	13.0	43	1	US-08-468-161A-85	Sequence 85, Appl	625	27	12.7	45	1	US-03-209-525-53	Sequence 53, Appl
553	27.5	13.0	43	2	US-08-453-702A-85	Sequence 85, Appl	626	27	12.7	45	1	US-08-062-472B-8	Sequence 8, Appl
554	27.5	13.0	43	4	US-09-099-639-85	Sequence 85, Appl	627	27	12.7	45	4	US-09-209-525-50	Sequence 50, Appl
555	27.5	13.0	43	5	PCT-US93-12588-85	Sequence 85, Appl	628	27	12.7	46	1	US-08-200-016-3	Sequence 3, Appl
556	27.5	13.0	43	5	PCT-US93-08071-85	Sequence 85, Appl	629	27	12.7	46	2	US-08-499-676A-9	Sequence 9, Appl
557	27.5	13.0	46	3	US-08-486-099-97	Sequence 97, Appl	630	27	12.7	46	4	US-09-227-357-563	Sequence 563, App
558	27.5	13.0	46	3	US-08-360-107A-107	Sequence 107, App	631	27	12.7	46	4	US-09-244-592-3	Sequence 3, Appl
559	27.5	13.0	46	3	US-08-484-223B-97	Sequence 97, Appl	632	27	12.7	47	5	PCT-US95-06266-112	Sequence 112, App
560	27.5	13.0	46	3	US-08-919-597-97	Sequence 97, Appl	633	27	12.7	47	1	US-07-653-091A-1	Sequence 1, Appl
561	27.5	13.0	46	3	US-08-475-668A-97	Sequence 97, Appl	634	27	12.7	47	1	US-08-485-068-1	Sequence 1, Appl
562	27.5	13.0	46	3	US-08-485-551A-97	Sequence 97, Appl	635	27	12.7	47	2	US-08-481-598-1	Sequence 1, Appl
563	27.5	13.0	46	3	US-08-471-913A-97	Sequence 97, Appl	636	27	12.7	47	2	US-08-483-353-1	Sequence 1, Appl
564	27.5	13.0	46	4	US-08-485-264A-97	Sequence 97, Appl	637	27	12.7	48	1	US-08-473-702-1	Sequence 1, Appl
565	27.5	13.0	46	4	US-08-474-349A-97	Sequence 97, Appl	638	27	12.7	48	3	US-08-236-886-4	Sequence 3, Appl
566	27.5	13.0	54	4	US-08-565-056-75	Sequence 75, Appl	639	27	12.7	49	2	US-08-248-839C-81	Sequence 81, Appl
567	27.5	13.0	55	1	US-08-394-328-7	Sequence 7, Appl	640	27	12.7	49	4	US-09-261-855-18	Sequence 18, Appl
568	27.5	13.0	55	3	US-09-082-308-7	Sequence 7, Appl	641	27	12.7	49	4	US-09-542-749A-4	Sequence 4, Appl
569	27.5	13.0	56	4	US-09-058-453-67	Sequence 67, Appl	642	27	12.7	50	2	US-08-980-071-51	Sequence 51, Appl
570	27.5	13.0	56	4	US-09-058-453-70	Sequence 70, Appl	643	27	12.7	50	2	US-08-757-536-51	Sequence 51, Appl
571	27.5	13.0	56	4	US-09-127-926-67	Sequence 67, Appl	644	27	12.7	50	3	US-08-314-093-51	Sequence 51, Appl
572	27.5	13.0	56	4	US-09-127-926-70	Sequence 70, Appl	645	27	12.7	50	3	US-08-314-093-51	Sequence 51, Appl
573	27.5	13.0	60	4	US-09-442-099A-15	Sequence 15, Appl	646	27	12.7	50	4	US-09-250-848-51	Sequence 51, Appl
574	27.5	13.0	64	1	US-08-091-569-22	Sequence 22, Appl	647	27	12.7	50	4	US-09-251-885-51	Sequence 51, Appl
575	27.5	13.0	64	1	US-08-203-676-22	Sequence 22, Appl	648	27	12.7	50	4	US-09-337-635-51	Sequence 51, Appl
576	27.5	13.0	64	1	US-08-385-375-2	Sequence 22, Appl	649	27	12.7	50	4	US-09-337-635-51	Sequence 51, Appl
577	27.5	13.0	64	2	US-08-822-238-22	Sequence 22, Appl	650	27	12.7	51	4	US-09-174-465D-10	Sequence 10, Appl
578	27.5	13.0	65	4	US-09-134-001C-5364	Sequence 5364, Ap	651	27	12.7	51	4	US-09-599-564A-10	Sequence 10, Appl
579	27.5	13.0	72	1	US-08-280-443-11	Sequence 11, Appl	652	27	12.7	51	4	US-07-757-022B-100	Sequence 100, App
580	27.5	13.0	72	1	US-08-457-459-11	Sequence 11, Appl	653	27	12.7	51	4	US-07-757-022B-112	Sequence 112, App
581	27.5	13.0	72	1	US-08-555-678-11	Sequence 11, Appl	654	27	12.7	52	3	US-08-824-800D-12	Sequence 12, App
582	27.5	13.0	72	4	US-08-558-207A-412	Sequence 412, App	655	27	12.7	52	4	US-08-927-219-45	Sequence 45, Appl
583	27.5	13.0	72	4	US-09-149-476-566	Sequence 566, App	656	27	12.7	52	4	US-09-588-751-12	Sequence 12, Appl
584	27.5	13.0	75	2	PCT-US95-02275-11	Sequence 11, Appl	657	27	12.7	53	2	US-08-942-423-31	Sequence 31, Appl
585	27.5	13.0	75	2	US-08-332-562A-29	Sequence 29, Appl	658	27	12.7	53	3	US-08-726-306A-144	Sequence 144, App
586	27.5	13.0	76	2	US-08-469-537A-42	Sequence 42, Appl	659	27	12.7	53	3	US-08-851-843A-20	Sequence 20, Appl
587	27.5	13.0	76	2	US-08-284-391B-53	Sequence 53, Appl	660	27	12.7	53	4	US-08-854-050-20	Sequence 20, Appl
588	27.5	13.0	76	4	US-09-218-950-53	Sequence 53, Appl	661	27	12.7	53	4	US-09-230-637-57	Sequence 57, Appl
589	27.5	13.0	80	1	US-08-100-247-3	Sequence 3, Appl	662	27	12.7	53	4	US-09-430-323-20	Sequence 20, Appl
590	27.5	13.0	80	1	US-08-483-146A-3	Sequence 3, Appl	663	27	12.7	56	1	US-08-182-173A-59	Sequence 59, Appl
591	27.5	13.0	80	1	US-08-232-513A-4	Sequence 4, Appl	664	27	12.7	56	1	US-08-474-633A-77	Sequence 77, Appl
592	27.5	13.0	80	1	US-08-484-594A-3	Sequence 3, Appl	665	27	12.7	56	4	US-09-058-459-38	Sequence 38, Appl
593	27.5	13.0	81	2	US-08-353-476-84	Sequence 84, Appl	666	27	12.7	56	4	US-09-058-459-41	Sequence 41, Appl
594	27.5	13.0	81	4	US-08-679-493A-103	Sequence 103, App	667	27	12.7	56	4	US-09-058-459-42	Sequence 42, Appl
595	27.5	13.0	83	4	US-09-261-853-1	Sequence 1, Appl	668	27	12.7	56	4	US-09-058-459-43	Sequence 43, Appl
596	27.5	13.0	84	1	US-08-510-039-2	Sequence 2, Appl	669	27	12.7	56	4	US-09-058-459-44	Sequence 44, Appl
597	27.5	13.0	84	1	US-07-748-510-2	Sequence 2, Appl	670	27	12.7	56	4	US-09-058-459-45	Sequence 45, Appl
598	27.5	13.0	84	4	US-09-247-155-119	Sequence 119, App	671	27	12.7	56	4	US-09-058-459-46	Sequence 46, Appl
599	27.5	13.0	85	4	US-09-103-478-27	Sequence 27, Appl	672	27	12.7	56	4	US-09-058-459-47	Sequence 47, Appl
600	27.5	13.0	85	4	US-09-193-931C-27	Sequence 27, Appl	673	27	12.7	56	4	US-09-058-459-50	Sequence 50, Appl
601	27.5	13.0	86	4	US-09-442-099A-14	Sequence 14, Appl	674	27	12.7	56	4	US-09-058-459-51	Sequence 51, Appl
602	27.5	13.0	87	3	US-08-554-840-18	Sequence 18, Appl	675	27	12.7	56	4	US-09-058-459-52	Sequence 52, Appl
603	27.5	13.0	87	4	US-08-925-339-18	Sequence 18, Appl	676	27	12.7	56	4	US-09-058-459-53	Sequence 53, Appl
604	27.5	13.0	88	1	US-07-987-272A-1	Sequence 1, Appl	677	27	12.7	56	4	US-09-058-459-54	Sequence 54, Appl
605	27.5	13.0	88	1	US-08-576-626A-43	Sequence 43, Appl	678	27	12.7	56	4	US-09-058-459-55	Sequence 55, Appl
606	27.5	13.0	89	2	US-07-987-272A-14	Sequence 14, Appl	679	27	12.7	56	4	US-09-058-459-56	Sequence 56, Appl
607	27.5	13.0	90	2	US-08-642-406A-10	Sequence 10, Appl	680	27	12.7	56	4	US-09-058-459-57	Sequence 57, Appl
608	27.5	13.0	90	2	US-08-642-406A-11	Sequence 11, Appl	681	27	12.7	56	4	US-09-058-459-58	Sequence 58, Appl
609	27.5	13.0	90	4	US-09-199-534-10	Sequence 10, Appl	682	27	12.7	56	4	US-09-058-459-59	Sequence 59, Appl
610	27.5	13.0	90	4	US-09-199-534-11	Sequence 11, Appl	683	27	12.7	56	4	US-09-058-459-60	Sequence 60, Appl
611	27.5	13.0	90	4	US-09-199-534-10	Sequence 10, Appl	684	27	12.7	56	4	US-09-058-459-61	Sequence 61, Appl
												US-09-058-459-62	Sequence 62, Appl

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685	27	12.7	56	4	US-09-058-459-63	Sequence 63, Appl	758	27	12.7	57	4	US-09-605-785-565	Sequence 565, Appl
686	27	12.7	56	4	US-09-058-459-64	Sequence 64, Appl	759	27	12.7	57	4	US-08-474-349A-158	Sequence 158, Appl
687	27	12.7	56	4	US-09-058-459-65	Sequence 65, Appl	760	27	12.7	58	4	US-08-963-851-23	Sequence 23, Appl
688	27	12.7	56	4	US-09-058-459-66	Sequence 66, Appl	761	27	12.7	58	4	US-08-598-873-59	Sequence 59, Appl
689	27	12.7	56	4	US-09-058-459-67	Sequence 67, Appl	762	27	12.7	59	4	US-08-468-011A-9	Sequence 9, Appl
690	27	12.7	56	4	US-09-058-459-68	Sequence 68, Appl	763	27	12.7	60	4	US-08-961-564A-6	Sequence 6, Appl
691	27	12.7	56	4	US-09-058-459-69	Sequence 69, Appl	764	27	12.7	60	4	US-08-605-430-59	Sequence 59, Appl
692	27	12.7	56	4	US-09-058-459-70	Sequence 70, Appl	765	27	12.7	60	4	US-09-236-468A-9	Sequence 9, Appl
693	27	12.7	56	4	US-09-058-459-71	Sequence 71, Appl	766	27	12.7	61	1	US-08-444-418-2	Sequence 2, Appl
694	27	12.7	56	4	US-09-058-459-72	Sequence 72, Appl	767	27	12.7	61	1	US-08-444-418-4	Sequence 4, Appl
695	27	12.7	56	4	US-09-058-459-73	Sequence 73, Appl	768	27	12.7	61	2	US-08-993-172-6	Sequence 15, Appl
696	27	12.7	56	4	US-09-058-459-74	Sequence 74, Appl	769	27	12.7	61	2	US-08-993-172-7	Sequence 6, Appl
697	27	12.7	56	4	US-09-058-459-75	Sequence 75, Appl	770	27	12.7	61	4	US-08-993-172-8	Sequence 54, Appl
698	27	12.7	56	4	US-09-058-459-76	Sequence 76, Appl	771	27	12.7	61	5	PCT-US93-01669-54	Sequence 11, Appl
699	27	12.7	56	4	US-09-058-459-77	Sequence 77, Appl	772	27	12.7	62	1	US-08-464-531-111	Sequence 116, Appl
700	27	12.7	56	4	US-09-058-459-78	Sequence 78, Appl	773	27	12.7	62	1	US-08-464-531-116	Sequence 116, Appl
701	27	12.7	56	4	US-09-058-459-79	Sequence 79, Appl	774	27	12.7	62	2	US-08-461-598-111	Sequence 116, Appl
702	27	12.7	56	4	US-09-127-926-38	Sequence 38, Appl	775	27	12.7	62	2	US-08-461-598-116	Sequence 116, Appl
703	27	12.7	56	4	US-09-127-926-41	Sequence 41, Appl	776	27	12.7	62	3	US-08-322-137-111	Sequence 116, Appl
704	27	12.7	56	4	US-09-127-926-42	Sequence 42, Appl	777	27	12.7	62	3	US-08-322-137-116	Sequence 2, Appl
705	27	12.7	56	4	US-09-127-926-43	Sequence 43, Appl	778	27	12.7	63	4	US-08-894-626-2	Sequence 11, Appl
706	27	12.7	56	4	US-09-127-926-44	Sequence 44, Appl	779	27	12.7	63	4	US-09-106-568E-139	Sequence 21, Appl
707	27	12.7	56	4	US-09-127-926-45	Sequence 45, Appl	780	27	12.7	64	2	US-08-209-521-21	Sequence 131, Appl
708	27	12.7	56	4	US-09-127-926-46	Sequence 46, Appl	781	27	12.7	64	4	US-08-961-810-131	Sequence 131, Appl
709	27	12.7	56	4	US-09-127-926-47	Sequence 47, Appl	782	27	12.7	64	4	US-08-352-902D-131	Sequence 414, Appl
710	27	12.7	56	4	US-09-127-926-50	Sequence 50, Appl	783	27	12.7	65	2	US-07-808-457-1	Sequence 1, Appl
711	27	12.7	56	4	US-09-127-926-51	Sequence 51, Appl	784	27	12.7	65	2	US-07-808-457-7	Sequence 9, Appl
712	27	12.7	56	4	US-09-127-926-52	Sequence 52, Appl	785	27	12.7	65	2	US-07-808-457-9	Sequence 7, Appl
713	27	12.7	56	4	US-09-127-926-53	Sequence 53, Appl	786	27	12.7	65	3	PCT-US92-10178-1	Sequence 1, Appl
714	27	12.7	56	4	US-09-127-926-54	Sequence 54, Appl	787	27	12.7	65	3	PCT-US92-10178-9	Sequence 9, Appl
715	27	12.7	56	4	US-09-127-926-55	Sequence 55, Appl	788	27	12.7	65	5	PCT-US92-10178-9	Sequence 9, Appl
716	27	12.7	56	4	US-09-127-926-56	Sequence 56, Appl	789	27	12.7	65	5	PCT-US92-10178-9	Sequence 9, Appl
717	27	12.7	56	4	US-09-127-926-57	Sequence 57, Appl	790	27	12.7	66	4	US-09-134-001C-5385	Sequence 5385, Ap
718	27	12.7	56	4	US-09-127-926-58	Sequence 58, Appl	791	27	12.7	66	4	US-09-010-928B-5	Sequence 5, Appl
719	27	12.7	56	4	US-09-127-926-59	Sequence 59, Appl	792	27	12.7	67	2	US-09-120-365-99	Sequence 99, Appl
720	27	12.7	56	4	US-09-127-926-60	Sequence 60, Appl	793	27	12.7	67	3	US-09-102-528-19	Sequence 19, Appl
721	27	12.7	56	4	US-09-127-926-61	Sequence 61, Appl	794	27	12.7	67	4	US-09-515-039-99	Sequence 99, Appl
722	27	12.7	56	4	US-09-127-926-62	Sequence 62, Appl	795	27	12.7	68	2	US-08-456-647B-31	Sequence 31, Appl
723	27	12.7	56	4	US-09-127-926-63	Sequence 63, Appl	796	27	12.7	68	2	US-08-237-401A-31	Sequence 31, Appl
724	27	12.7	56	4	US-09-127-926-64	Sequence 64, Appl	797	27	12.7	68	3	US-08-912-273-23	Sequence 23, Appl
725	27	12.7	56	4	US-09-127-926-65	Sequence 65, Appl	798	27	12.7	68	4	US-09-026-039-23	Sequence 23, Appl
726	27	12.7	56	4	US-09-127-926-66	Sequence 66, Appl	799	27	12.7	69	1	US-08-193-863-1	Sequence 1, Appl
727	27	12.7	56	4	US-09-127-926-67	Sequence 67, Appl	800	27	12.7	69	1	US-08-377-833-1	Sequence 1, Appl
728	27	12.7	56	4	US-09-127-926-68	Sequence 68, Appl	801	27	12.7	69	1	US-08-324-503-1	Sequence 1, Appl
729	27	12.7	56	4	US-09-127-926-69	Sequence 69, Appl	802	27	12.7	69	1	US-08-083-501-1	Sequence 1, Appl
730	27	12.7	56	4	US-09-127-926-70	Sequence 70, Appl	803	27	12.7	69	1	US-08-415-935-1	Sequence 1, Appl
731	27	12.7	56	4	US-09-127-926-71	Sequence 71, Appl	804	27	12.7	69	1	US-08-548-153-1	Sequence 1, Appl
732	27	12.7	56	4	US-09-127-926-72	Sequence 72, Appl	805	27	12.7	69	4	US-09-134-001C-4592	Sequence 4592, Ap
733	27	12.7	56	4	US-09-127-926-73	Sequence 73, Appl	806	27	12.7	70	4	US-08-965-056-102	Sequence 102, App
734	27	12.7	56	4	US-09-127-926-74	Sequence 74, Appl	807	27	12.7	70	4	US-09-187-789-12	Sequence 12, Appl
735	27	12.7	56	4	US-09-127-926-75	Sequence 75, Appl	808	27	12.7	70	4	US-09-139-600-7	Sequence 7, Appl
736	27	12.7	56	4	US-09-127-926-76	Sequence 76, Appl	809	27	12.7	72	4	US-08-968-056-83	Sequence 83, Appl
737	27	12.7	56	4	US-09-127-926-77	Sequence 77, Appl	810	27	12.7	72	4	US-09-209-525-51	Sequence 51, Appl
738	27	12.7	56	4	US-09-127-926-78	Sequence 78, Appl	811	27	12.7	74	4	US-09-244-592-4	Sequence 4, Appl
739	27	12.7	56	4	US-09-127-926-79	Sequence 79, Appl	812	27	12.7	75	4	US-09-244-592-5	Sequence 5, Appl
740	27	12.7	56	4	US-09-127-926-80	Sequence 80, Appl	813	27	12.7	76	2	US-08-244-537-6	Sequence 6, Appl
741	27	12.7	56	4	US-09-127-926-81	Sequence 81, Appl	814	27	12.7	76	4	US-09-106-568E-153	Sequence 153, App
742	27	12.7	56	4	US-09-127-926-82	Sequence 82, Appl	815	27	12.7	76	6	5273901-11	Patent No. 5273901
743	27	12.7	56	4	US-09-127-926-83	Sequence 83, Appl	816	27	12.7	76	6	5482709-10	Patent No. 5482709
744	27	12.7	56	4	US-09-127-926-84	Sequence 84, Appl	817	27	12.7	77	1	US-08-014-153D-40	Sequence 40, Appl
745	27	12.7	56	4	US-09-127-926-85	Sequence 85, Appl	818	27	12.7	77	1	US-08-325-547-8	Sequence 8, Appl
746	27	12.7	56	4	US-09-127-926-86	Sequence 86, Appl	819	27	12.7	77	2	US-08-469-537A-47	Sequence 47, Appl
747	27	12.7	56	4	US-09-127-926-87	Sequence 87, Appl	820	27	12.7	77	2	US-08-469-537A-48	Sequence 48, Appl
748	27	12.7	56	4	US-09-127-926-88	Sequence 88, Appl	821	27	12.7	77	4	US-09-100-802-3	Sequence 3, Appl
749	27	12.7	56	4	US-09-127-926-89	Sequence 89, Appl	822	27	12.7	77	4	US-09-100-802-4	Sequence 4, Appl
750	27	12.7	56	4	US-09-127-926-90	Sequence 90, Appl	823	27	12.7	79	4	US-08-905-223-470	Sequence 470, App
751	27	12.7	56	4	US-09-127-926-91	Sequence 91, Appl	824	27	12.7	80	4	US-09-209-525-54	Sequence 54, Appl
752	27	12.7	56	4	US-09-127-926-92	Sequence 92, Appl	825	27	12.7	80	4	US-08-370-225-24	Sequence 24, Appl
753	27	12.7	56	4	US-09-127-926-93	Sequence 93, Appl	826	27	12.7	83	1	US-08-244-563-2	Sequence 2, Appl
754	27	12.7	56	4	US-09-127-926-94	Sequence 94, Appl	827	27	12.7	83	1	US-08-461-859-24	Sequence 24, Appl
755	27	12.7	56	4	US-09-127-926-95	Sequence 95, Appl	828	27	12.7	83	2	US-08-852-933-2	Sequence 2, Appl
756	27	12.7	56	4	US-09-127-926-96	Sequence 96, Appl	829	27	12.7	83	2	US-08-852-933-2	Sequence 2, Appl
757	27	12.7	56	4	US-09-127-926-97	Sequence 97, Appl	830	27	12.7	83	2	US-08-853-021-2	Sequence 2, Appl

831	27	12.7	83	3	US-08-852-865-2	Sequence 2, Appl	904	26.5	12.5	90	4	US-09-193-931C-20	Sequence 20, Appl
832	27	12.7	83	3	US-08-981-988A-6	Sequence 6, Appl	905	26	12.3	40	1	US-08-179-632-4	Sequence 4, Appl
833	27	12.7	83	5	PCR-US92-10069-24	Sequence 24, Appl	906	26	12.3	40	1	US-08-440-174A-4	Sequence 4, Appl
834	27	12.7	83	2	US-08-592-506A-18	Sequence 18, Appl	907	26	12.3	40	4	US-09-082-279B-786	Sequence 786, Appl
835	27	12.7	83	3	US-08-236-886-7	Sequence 7, Appl	908	26	12.3	40	4	US-08-630-915A-68	Sequence 68, Appl
836	27	12.7	85	3	US-09-165-422-16	Sequence 16, Appl	909	26	12.3	40	4	US-09-227-357-580	Sequence 580, Appl
837	27	12.7	86	1	US-08-149-839B-14	Sequence 14, Appl	910	26	12.3	40	4	US-09-315-304B-786	Sequence 786, Appl
838	27	12.7	86	1	US-07-956-700B-24	Sequence 24, Appl	911	26	12.3	40	5	PCR-US93-00062-4	Sequence 4, Appl
839	27	12.7	86	1	US-08-451-568-14	Sequence 14, Appl	912	26	12.3	41	2	US-08-997-080-187	Sequence 187, Appl
840	27	12.7	86	1	US-08-451-568-14	Sequence 14, Appl	913	26	12.3	41	2	US-08-997-080-187	Sequence 187, Appl
841	27	12.7	86	1	US-08-476-537-24	Sequence 24, Appl	914	26	12.3	41	3	US-08-467-023-136	Sequence 136, Appl
842	27	12.7	86	1	US-08-485-607-24	Sequence 24, Appl	915	26	12.3	41	3	US-09-095-855-187	Sequence 187, Appl
843	27	12.7	86	2	US-08-459-568-82	Sequence 82, Appl	916	26	12.3	41	4	US-09-324-542-187	Sequence 187, Appl
844	27	12.7	86	2	US-08-399-411-82	Sequence 82, Appl	917	26	12.3	41	4	US-09-205-426-187	Sequence 187, Appl
845	27	12.7	86	2	US-08-343-443B-7	Sequence 7, Appl	918	26	12.3	41	4	US-09-149-476-386	Sequence 386, Appl
846	27	12.7	86	2	US-08-475-879-24	Sequence 24, Appl	919	26	12.3	42	1	US-07-651-710A-25	Sequence 25, Appl
847	27	12.7	86	2	US-08-777-113-14	Sequence 14, Appl	920	26	12.3	42	1	US-08-182-175A-37	Sequence 37, Appl
848	27	12.7	86	3	US-08-516-859A-82	Sequence 82, Appl	921	26	12.3	42	1	US-08-474-633A-34	Sequence 34, Appl
849	27	12.7	86	4	US-08-441-507-8	Sequence 8, Appl	922	26	12.3	42	2	US-08-348-353-35	Sequence 35, Appl
850	27	12.7	86	4	US-09-586-472-82	Sequence 82, Appl	923	26	12.3	42	2	US-08-465-965-35	Sequence 35, Appl
851	27	12.7	86	4	US-09-433-043B-24	Sequence 24, Appl	924	26	12.3	42	3	US-08-465-966-35	Sequence 35, Appl
852	27	12.7	86	4	US-07-969-875A-8	Sequence 8, Appl	925	26	12.3	42	4	US-09-082-279B-746	Sequence 746, Appl
853	27	12.7	85	4	US-09-528-706-82	Sequence 82, Appl	926	26	12.3	42	4	US-09-082-279B-1091	Sequence 1091, Appl
854	27	12.7	87	1	US-08-062-472B-10	Sequence 10, Appl	927	26	12.3	42	4	US-09-315-304B-746	Sequence 746, Appl
855	27	12.7	87	1	US-09-134-001C-3097	Sequence 3097, Appl	928	26	12.3	42	4	US-09-315-304B-1091	Sequence 1091, Appl
856	27	12.7	88	1	US-08-885-440-27	Sequence 27, Appl	929	26	12.3	42	4	US-09-116-92A-7	Sequence 7, Appl
857	27	12.7	88	1	US-08-630-349-27	Sequence 27, Appl	930	26	12.3	42	4	US-08-823-771-34	Sequence 34, Appl
858	27	12.7	88	2	US-08-391-916A-10	Sequence 10, Appl	931	26	12.3	42	5	PCR-US92-08412-37	Sequence 37, Appl
859	27	12.7	88	3	US-08-851-843A-204	Sequence 204, Appl	932	26	12.3	43	4	US-09-461-697-127	Sequence 127, Appl
860	27	12.7	89	4	US-08-974-549A-323	Sequence 323, Appl	933	26	12.3	44	4	US-09-082-279B-997	Sequence 997, Appl
861	27	12.7	89	4	US-08-854-050-204	Sequence 204, Appl	934	26	12.3	44	4	US-09-082-279B-999	Sequence 999, Appl
862	27	12.7	89	4	US-09-430-323-204	Sequence 204, Appl	935	26	12.3	44	4	US-09-082-279B-1092	Sequence 1092, Appl
863	27	12.7	89	4	US-09-056-556-238	Sequence 238, Appl	936	26	12.3	44	4	US-09-082-279B-1118	Sequence 1118, Appl
864	27	12.7	89	4	US-09-187-859-29	Sequence 29, Appl	937	26	12.3	44	4	US-09-315-304B-997	Sequence 997, Appl
865	27	12.7	89	4	US-09-072-596-233	Sequence 233, Appl	938	26	12.3	44	4	US-09-315-304B-999	Sequence 999, Appl
866	27	12.7	90	1	US-08-285-440-25	Sequence 25, Appl	939	26	12.3	44	4	US-09-315-304B-1092	Sequence 1092, Appl
867	27	12.7	90	1	US-08-630-349-25	Sequence 25, Appl	940	26	12.3	44	4	US-09-315-304B-1118	Sequence 1118, Appl
868	27	12.7	90	4	US-09-244-592-2	Sequence 2, Appl	941	26	12.3	45	2	US-08-348-353-5	Sequence 5, Appl
869	26.5	12.5	40	4	US-08-516-165A-427	Sequence 427, Appl	942	26	12.3	45	2	US-08-348-353-6	Sequence 6, Appl
870	26.5	12.5	41	1	US-08-468-674B-69	Sequence 69, Appl	943	26	12.3	45	2	US-08-465-965-5	Sequence 5, Appl
871	26.5	12.5	41	1	US-08-780-571-69	Sequence 69, Appl	944	26	12.3	45	2	US-08-465-965-6	Sequence 6, Appl
872	26.5	12.5	41	3	US-08-888-381-1	Sequence 1, Appl	945	26	12.3	45	3	US-08-465-966-5	Sequence 5, Appl
873	26.5	12.5	43	4	US-08-630-915A-108	Sequence 108, Appl	946	26	12.3	45	3	US-08-465-966-6	Sequence 6, Appl
874	26.5	12.5	44	4	US-08-988-858B-16	Sequence 16, Appl	947	26	12.3	45	4	US-09-082-279B-954	Sequence 954, Appl
875	26.5	12.5	50	4	US-09-605-785-585	Sequence 585, Appl	948	26	12.3	45	4	US-09-082-279B-996	Sequence 996, Appl
876	26.5	12.5	51	1	US-07-562-193-6	Sequence 6, Appl	949	26	12.3	45	4	US-09-315-304B-954	Sequence 954, Appl
877	26.5	12.5	51	3	US-08-300-928C-15	Sequence 15, Appl	950	26	12.3	45	4	US-09-315-304B-996	Sequence 996, Appl
878	26.5	12.5	51	3	US-08-430-944D-15	Sequence 15, Appl	951	26	12.3	46	2	US-08-480-473B-54	Sequence 54, Appl
879	26.5	12.5	51	3	US-08-431-184-15	Sequence 15, Appl	952	26	12.3	46	3	US-08-915-213-54	Sequence 54, Appl
880	26.5	12.5	51	3	US-08-431-184-15	Sequence 15, Appl	953	26	12.3	46	3	US-09-235-217-54	Sequence 54, Appl
881	26.5	12.5	52	1	US-08-203-905B-7	Sequence 7, Appl	954	26	12.3	46	4	US-09-082-279B-995	Sequence 995, Appl
882	26.5	12.5	54	1	US-08-321-071A-20	Sequence 20, Appl	955	26	12.3	46	4	US-09-082-279B-998	Sequence 998, Appl
883	26.5	12.5	54	2	US-08-319-866-3	Sequence 3, Appl	956	26	12.3	46	4	US-09-082-279B-1089	Sequence 1089, Appl
884	26.5	12.5	54	4	US-09-306-446C-13	Sequence 13, Appl	957	26	12.3	46	4	US-08-965-056-112	Sequence 112, Appl
885	26.5	12.5	58	2	US-08-152-721B-20	Sequence 20, Appl	958	26	12.3	46	4	US-09-315-304B-995	Sequence 995, Appl
886	26.5	12.5	59	4	US-09-300-672-7	Sequence 7, Appl	959	26	12.3	46	4	US-09-315-304B-998	Sequence 998, Appl
887	26.5	12.5	60	4	US-09-605-785-586	Sequence 586, Appl	960	26	12.3	46	4	US-09-315-304B-1089	Sequence 1089, Appl
888	26.5	12.5	63	4	US-09-149-476-671	Sequence 671, Appl	961	26	12.3	46	6	5304637-13	Patent No. 5304637
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891	26.5	12.5	64	4	US-09-134-001C-2888	Sequence 2888, Appl	964	26	12.3	47	3	US-08-484-223B-219	Sequence 219, Appl
892	26.5	12.5	65	3	US-08-331-625A-39	Sequence 39, Appl	965	26	12.3	47	4	US-09-082-279B-994	Sequence 994, Appl
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898	26.5	12.5	67	4	US-09-515-039-95	Sequence 95, Appl	971	26	12.3	48	4	US-09-082-279B-1090	Sequence 1090, Appl
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901	26.5	12.5	81	2	US-08-244-537-8	Sequence 8, Appl	974	26	12.3	50	2	US-08-980-071-44	Sequence 44, Appl
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# ALIGNMENTS

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RESULT 1
US-09-331-930A-22
; Sequence 22, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-20007.00
; CURRENT APPLICATION NUMBER: US/09/331,930A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/AU98/00902
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: AU PP0117/97
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: AU PP0323/97
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-331-930A-22

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Query Match      21.5%; Score 45.5; DB 4; Length 73;
Best Local Similarity 29.4%; Pred. No. 8.6;
Matches 10; Conservative 7; Mismatches 12; Indels 5; Gaps 1;
QY 14 DFGSGKSRVIENTEALS-----VAVEGLAWRK 42
DB 8 DRLGKVKIKNFSDTIGDLKLIAAQTGRWEK 41

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RESULT 2
US-08-776-059-18
; Sequence 18, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jurgen
; APPLICANT: BAUR, Axel
; APPLICANT: ZINKE, Holger
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)

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; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776,059B
; CURRENT FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: PCT/EP96/02273
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 95109949.8
; EARLIER FILING DATE: 1995-06-26
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Saponaria officinalis
US-08-776-059-18

Query Match      20.8%; Score 44; DB 4; Length 47;
Best Local Similarity 34.8%; Pred. No. 8;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 13 MDFSQKSRVIENTEALSVAVE 35
DB 6 MDVNVKKARVVKNEARELLAIQ 28

RESULT 3
US-09-081-320-20
; Sequence 20, Application US/09081320
; Patent No. 6093544
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Meng, Baozhong
; TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,320
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,147
; FILING DATE: 20-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,902
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1722
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-081-320-20

Query Match      20.8%; Score 44; DB 3; Length 80;

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Best Local Similarity 50.0%; Pred. No. 17;  
Matches 13; Conservative 4; Mismatches

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Db	40	ESIVIENCGPSEALAAATVKEVLGGLK	65

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RESULT 4
US-09-574-141A-20
; Sequence 20, Application US/09574141A
; Patent No. 6393490
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Meng, Baozhong
; TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
; FILE REFERENCE: 07678/035005
; CURRENT APPLICATION NUMBER: US/09/574,141A
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/047,147
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: 60/069,902
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 09/081,320
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Rupestris stem pitting associated virus
US-09-574-141A-20

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Query Match 20.8%; Score 44; DB 4; Length 80;  
Best Local Similarity 50.0%; Pred. NO. 17;  
Matches 13; Conservative 4; Mismatches 7; Indels

QY 19 KSRVIEN--PTEALSVAVEEGLAWRK 42  
:| |||| |:||: |:|| |  
Db 40 ESIVIENCGPSEALAAATVKEVLGGLK 65

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RESULT 5
US-09-707-780-20
; Sequence 20, Application US/09707780
; Patent No. 639308
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Meng, Baozhong
; TITLE OF INVENTION: RUPESTRIS STEM FITTING ASSOCIATED VIRUS
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
; FILE REFERENCE: 07678/035006
; CURRENT APPLICATION NUMBER: US/09/707,780
; CURRENT FILING DATE: 2000-11-07
; PRIORITY APPLICATION NUMBER: 09/081,320
; PRIORITY FILING DATE: 1998-05-19
; PRIORITY APPLICATION NUMBER: 60/047,147
; PRIORITY FILING DATE: 1997-05-20
; PRIORITY APPLICATION NUMBER: 60/069,902
; PRIORITY FILING DATE: 1997-12-17
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
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; TYPE: PRT
; ORGANISM: Rupestris stem fitting associated virus
US-09-707-780-20

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Query Match 20.8%; Score 44; DB 4; Length 80;  
Best Local Similarity 50.0%; Pred. No. 17;  
Matches 13; Conservative 4; Mismatches 7; Indels

QY 19 KSRVIEN--PTEALSVAVEEGLAWRK 42  
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Db 40 ESIVIENCGPSEALAAATVKEVLGGLK 65

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Query Match 20.5%; Score 43.5; DB 4; Length 55;  
Best Local Similarity 41.4%; Pred. No. 12;  
Matches 12; Conservative 8; Mismatches 4; Indels 5; Gaps 2;

Qy	4	SISENSLVAMDFS-GQKSRVIENPTEALS	31
		:::    :      :	:
Db	23	TVNKGSLVALGFSGDGEAR---	PEEILN 47

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RESULT 7
US-08-776-059-16
; Sequence 16, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jurgen
; APPLICANT: BAUR, Axel
; APPLICANT: ZINKE, Holger
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776.059B

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; CURRENT FILING DATE: 1999-06-19  
; EARLIER APPLICATION NUMBER: PCT/EP96/02273  
; EARLIER FILING DATE: 1996-06-25  
; EARLIER APPLICATION NUMBER: 95109949.8  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Saponaria officinalis  
US-08-776-059-16

Query Match 19.8%; Score 42; DB 4; Length 47;  
Best Local Similarity 30.8%; Pred. No. 16;  
Matches 8; Conservative 10; Indels 0; Gaps 0;

QY 10 LVAMDFSGOKSRVIENTALSVAVE 35  
DB 3 LTFMEAVNKARVVKNREFLIATQ 28

RESULT 8  
US-07-641-971B-5  
; Sequence 5, Application US/07641971B  
; Patent No. 5236706  
; GENERAL INFORMATION:  
; APPLICANT: Debre, Patrice  
; APPLICANT: Mossalayi, Mohammed D  
; TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE  
; TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation  
; STREET: 556 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/641,971B  
; FILING DATE: 19910116  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 90016254  
; FILING DATE: 24-JAN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fishman, Irving M  
; REGISTRATION NUMBER: 30258  
; REFERENCE/DOCKET NUMBER: 4-17921/+/DEB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-277-4832  
; TELEFAX: 908-277-4306  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-07-641-971B-5

Query Match 19.3%; Score 41; DB 1; Length 40;  
Best Local Similarity 39.3%; Pred. No. 19;  
Matches 11; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 PMRISLNSLVAMDFSGOKSRVIENTPTE 28  
DB 2 PVRSNLN----CTLRDSGOKSLVMSGPYE 25  
RESULT 9  
US-07-781-248A-5  
; Sequence 5, Application US/07781248A  
; Patent No. 5246699  
; GENERAL INFORMATION:  
; APPLICANT: Debre, Patrice  
; APPLICANT: Mossalayi, Mohammed D  
; TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation  
; STREET: 556 Morris Avenue  
; CITY: Summit  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07901  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/781,248A  
; FILING DATE: 19911230  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 90103565  
; FILING DATE: 05-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ikeiger, Barbara J.  
; REGISTRATION NUMBER: 36,170  
; REFERENCE/DOCKET NUMBER: 4-18065/A/DEB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-277-3368  
; TELEFAX: 908-277-4306  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-07-781-248A-5

Query Match 19.3%; Score 41; DB 1; Length 40;  
Best Local Similarity 39.3%; Pred. No. 19;  
Matches 11; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 PMRISLNSLVAMDFSGOKSRVIENTPTE 28  
DB 2 PVRSNLN----CTLRDSGOKSLVMSGPYE 25

RESULT 10  
US-08-459-568-52  
; Sequence 52, Application US/08459568  
; Patent No. 5811304  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Shi  
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
; TITLE OF INVENTION: Zinc Finger Proteins  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA: US 08/399,411  
FILING DATE: 06-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1264  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-459-568-52

Query Match 19.1%; Score 40.5; DB 2; Length 66;  
Best Local Similarity 47.4%; Pred. No. 44;  
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 4 SISENSLVAMDFS-GOKSR 21  
DB 22 TVNKGSLVALGFSGQEAR 40

RESULT 11  
US-08-399-411-52  
Sequence 52, Application US/08399411  
Patent No. 5831008  
GENERAL INFORMATION:  
APPLICANT: Huang, Shi  
TITLE OF INVENTION: Retinoblastoma protein - Interacting  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 06-MAR-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1264  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-399-411-52

Query Match 19.1%; Score 40.5; DB 2; Length 66;  
Best Local Similarity 47.4%; Pred. No. 44;  
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 4 SISENSLVAMDFS-GOKSR 21  
DB 22 TVNKGSLVALGFSGQEAR 40

RESULT 12  
US-08-516-859A-52  
Sequence 52, Application US/08516859A  
Patent No. 6069231  
GENERAL INFORMATION:  
APPLICANT: Huang, Shi  
TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 18-AUG-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/399,411  
FILING DATE: 06-MAR-1995  
APPLICATION DATA: US 08/292,683  
FILING DATE: 18-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1776  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-516-859A-52

Query Match 19.1%; Score 40.5; DB 3; Length 66;  
Best Local Similarity 47.4%; Pred. No. 44;  
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 4 SISENSLVAMDFS-GOKSR 21  
DB 22 TVNKGSLVALGFSGQEAR 40

RESULT 13  
US-09-586-472-52  
Sequence 52, Application US/09586472  
Patent No. 6323335



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;
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA: US 09/528,706
; FILING DATE: 01-Jun-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-586-472-52

Query Match 19.1%; Score 40.5; DB 4; Length 66;
Best Local Similarity 47.4%; Pred. No. 44;
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Qy 4 SISENSLVAMDFS-GQKSR 21
Db 22 TVNKGSLVALGFSGQEAR 40
::: ||||: || ||::|

RESULT 14
US-09-528-706-52
; Sequence 52, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-528-706-52

Query Match 19.1%; Score 40.5; DB 4; Length 66;
Best Local Similarity 47.4%; Pred. No. 44;
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Qy 4 SISENSLVAMDFS-GQKSR 21
Db 22 TVNKGSLVALGFSGQEAR 40
::: ||||: || ||::|

RESULT 15
US-09-006-428A-14
; Sequence 14, Application US/09006428A
; Patent No. 6441439
; GENERAL INFORMATION:
; APPLICANT: Jing Li
; APPLICANT: Kazuhisa Nishizawa
; APPLICANT: Wenqian An
; APPLICANT: Ellis L. Reinherz
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A
; FILE REFERENCE: CGC15-LIKE ADAPTOR PROTEIN (CD2BP1)
; CURRENT APPLICATION NUMBER: US/09/006,428A
; CURRENT FILING DATE: 1998-01-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-006-428A-14

Query Match 19.1%; Score 40.5; DB 4; Length 79;
Best Local Similarity 47.4%; Pred. No. 57;
Matches 9; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Qy 4 SISENSLVAMDFS-GQKSR 21
Db 31 TVNKGSLVALGFSGQEAR 49
::: ||||: || ||::|

RESULT 16
US-08-905-223-420
; Sequence 420, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric

```

APPLICANT: Lacroix, Bruno  
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS  
NUMBER OF SEQUENCES: 503  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 501 West Broadway  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-3505  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israel, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 420:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -26...-1  
IDENTIFICATION METHOD: Von Heijne matrix  
OTHER INFORMATION: score 4.5  
OTHER INFORMATION: seq ENSLILLLQLGQ/RV  
US-08-905-223-420

Query Match 19.1%; Score 40.5; DB 4; Length 86;  
Best Local Similarity 50.0%; Pred. No. 64;  
Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 3 RISENSLVAMDFSGQKSRV 22  
Db 10 RTISENSLILLL-LQLGQGRV 28

RESULT 17  
US-09-227-357-611  
Sequence 611, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischer et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08  
EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803

EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 611  
LENGTH: 63  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-227-357-611

Query Match 18.9%; Score 40; DB 4; Length 63;  
Best Local Similarity 47.1%; Pred. No. 50;  
Matches 8; Conservative 3; Mismatches 6; Indels; 0; Gaps 0;

QY 5 ISENSLVAMDFSGQKSR 21  
Db 20 VSSNLFSPFFGQKAR 36

RESULT 18

US-09-331-930A-2

; Sequence 2, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:  
; APPLICANT: ZIMMET, PAUL Z.  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Amino acid  
; OTHER INFORMATION: sequence for beacon from unknown organism

US-09-331-930A-2

Query Match 18.6%; Score 39.5; DB 4; Length 73;  
Best Local Similarity 28.9%; Pred. No. 73;  
Matches 11; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

QY 10 LVAMDFSGQKSRVIENPTREALS-----VAVEEGLAWRK 42  
Db 4 VVCNDRLGKVKRVKNCNTDITGDLKLLIAAQTGRWKK 41

RESULT 19

US-09-331-930A-19  
; Sequence 19, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL Z.  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Amino acid  
; OTHER INFORMATION: sequence for beacon from unknown organism

US-09-331-930A-19

Query Match 18.6%; Score 39.5; DB 4; Length 73;  
Best Local Similarity 28.9%; Pred. No. 73;  
Matches 11; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

QY 10 LVAMDFSGQKSRVIENPTREALS-----VAVEEGLAWRK 42  
Db 4 VVCNDRLGKVKRVKNCNTDITGDLKLLIAAQTGRWKK 41

RESULT 20

US-09-331-930A-20  
; Sequence 20, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL Z.  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: sequence for beacon from unknown organism

US-09-331-930A-20

Query Match 18.6%; Score 39.5; DB 4; Length 73;  
Best Local Similarity 28.9%; Pred. No. 73;  
Matches 11; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

QY 10 LVAMDFSGQKSRVIENPTREALS-----VAVEEGLAWRK 42  
Db 4 VVCNDRLGKVKRVKNCNTDITGDLKLLIAAQTGRWKK 41

RESULT 21

US-09-331-930A-21  
; Sequence 21, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:

; APPLICANT: ZIMMET, PAUL Z.  
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
; FILE REFERENCE: 22975-20007.00  
; CURRENT APPLICATION NUMBER: US/09/331,930A  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: PCT/AU98/00902  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: AU PP0117/97  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: AU PP0323/97  
; PRIOR FILING DATE: 1997-11-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Murine sp.  
; OTHER INFORMATION: sequence for beacon from unknown organism

US-09-331-930A-21

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Best Local Similarity 28.9%; Pred. No. 73;  
Matches 11; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

QY 10 LVAMDFSGQKSRVIENPTREALS-----VAVEEGLAWRK 42  
Db 4 VVCNDRLGKVKRVKNCNTDITGDLKLLIAAQTGRWKK 41

RESULT 22

US-09-331-930A-24  
; Sequence 24, Application US/09331930A  
; Patent No. 6436670  
; GENERAL INFORMATION:

US-09-331-930A-24

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; APPLICANT: ZIMMET, PAUL Z.
; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-2007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR FILING DATE: 1998-10-30
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-331-930A-24

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Query Match      18.6%; Score 39.5; DB 4; Length 73;
Best Local Similarity 28.9%; Pred. No. 73;
Matches 11; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

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OY 10 LVAMDFSGQSRVIENTPTALS-----VAVEEGLAWRK 42
Db 4 VVCDRLGKVRVKCNDTDTIGDLKKLIAAQTGTNRNK 41

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RESULT 23
US-09-331-930A-25
; Sequence 25, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
; APPLICANT: ZIMMET, PAUL Z.

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; TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
; FILE REFERENCE: 22975-2007.00
; CURRENT APPLICATION NUMBER: US/09/331.930A
; PRIOR FILING DATE: 1999-06-30
; PRIOR FILING DATE: 1998-10-30
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-11-11
; NUMBER OF SEQ ID NOS: 27
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; LENGTH: 73
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-331-930A-25

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Matches 11; Conservative 6; Mismatches 16; Indels 5; Gaps 1;

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OY 10 LVAMDFSGQSRVIENTPTALS-----VAVEEGLAWRK 42
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RESULT 24
US-09-100-804-30
; Sequence 30, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

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; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100.804
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: L0461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:

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; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-09-100-804-30

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Best Local Similarity 30.4%; Pred. No. 79;
Matches 14; Conservative 9; Mismatches 19; Indels 4; Gaps 1;

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RESULT 25
US-09-081-320-9
; Sequence 9, Application US/09081320
; Patent No. 6093544
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Meng, Baozhong
; TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:

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us-09-936-697-5.max.rai

Page 16

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;; APPLICATION NUMBER: US 60/047,147  
;; FILING DATE: 20-MAY-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/069,902  
;; FILING DATE: 17-DEC-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldman, Michael L.  
;; REGISTRATION NUMBER: 30,727  
;; REFERENCE/DOCKET NUMBER: 19603/1722  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (716) 263-1304  
;; TELEFAX: (716) 263-1600  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 80 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-081-320-9

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Best Local Similarity 46.2%; Pred No 98;  
Matches 12; Conservative 5; Mismatches 7; Indels 2; Gaps 1;  
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Db 40 ESILINCPSALASTVKEVLGLK 65

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Job time : 30.5276 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: March 28, 2003, 08:55:25 ; Search time 33.8583 Seconds  
(without alignments)

169.228 Million cell updates/sec

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Searched: 908470 seqs, 133250620 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

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## SUMMARIES

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3	205	96.7	43	AA1893.7	Peptide derived fr
4	205	96.7	84	AA1893.8	Peptide derived fr
5	159	79.7	43	AA1894.9	Peptide derived fr
6	159	79.7	82	AA1895.0	Peptide derived fr
7	162	76.4	43	AA1895.7	Peptide derived fr
8	162	76.4	80	AA1895.8	Peptide derived fr
9	161	75.9	43	AA1894.5	Peptide derived fr
10	161	75.9	82	AA1894.6	Peptide derived fr

11	159	75.0	43	21	AA1895.3	Peptide derived fr
12	159	75.0	43	21	AA1896.1	Peptide derived fr
13	159	75.0	80	21	AA1895.4	Peptide derived fr
14	159	75.0	80	21	AA1896.2	Peptide derived fr
15	49	23.1	67	23	ABP08708	Human ORFX protein
16	48	22.6	72	22	AAU30892	Novel human secret
17	47.5	22.4	73	22	AAU30892	Human colon cancer
18	45.5	21.5	57	23	ABP02324	Human ORFX protein
19	45	21.2	84	23	ABG47266	Human ORFX protein
20	44.5	21.0	72	21	AAU03340	Human peptide enco
21	44.5	21.0	74	22	AAU87480	Human secreted pro
22	44.5	21.0	74	22	AAU87480	Novel central nerv
23	44.5	21.0	79	22	AAU41349	Novel central nerv
24	44.5	21.0	90	22	AAU62249	Protonibacterium
25	44	20.8	47	22	AAU94366	Protonibacterium
26	44	20.8	62	22	AAU94366	Human reproductive
27	44	20.8	80	20	AAU97732	Novel human diagno
28	44	20.8	82	22	AAU97732	RSPV strain RSP47
29	42	19.8	45	22	AAU86158	Drosophila melanog
30	42	19.8	63	22	AAU86158	Human immune/haema
31	42	19.8	63	22	AAU86158	Human peptide #979
32	42	19.8	63	22	AAU86158	Peptide #1011 enco
33	42	19.8	63	22	AAU86158	Protein #963 enco
34	42	19.8	63	22	AAU86158	Human brain expres
35	42	19.8	63	22	AAU86158	Human bone marrow
36	42	19.8	63	22	AAU86158	Peptide #981 enco
37	42	19.8	63	22	AAU86158	Peptide #1002 enco
38	42	19.8	63	22	AAU86158	Peptide #955 enco
39	42	19.8	64	22	AAU86158	Human immune/haema
40	42	19.8	72	22	AAU86158	Human immune/haema
41	42	19.8	81	20	AAU35749	C glutamyl prote
42	42	19.8	87	23	ABP11032	Chlamydia pneumoni
43	42	19.8	89	22	AAU41466	Human ORFX protein
44	41.5	19.6	51	22	AAU96493	Human polypeptide
45	41.5	19.6	71	22	AAU96493	Human reproductive
46	41.5	19.6	83	22	ABU16786	Protonibacterium
47	41	19.3	52	22	ABU16786	Human nervous syst
48	41	19.3	63	22	ABU16786	Protonibacterium
49	41	19.3	89	22	ABU16786	Human ORFX protein
50	40.5	19.1	51	21	AAU59414	Protonibacterium
51	40.5	19.1	56	21	AAU59414	Bacteriophage Dp-1
52	40.5	19.1	66	21	AAU59414	SH3 domain from P8
53	40.5	19.1	74	21	AAU59414	Arabidopsis thalia
54	40.5	19.1	82	20	AAU59414	Human secreted pro
55	40	18.9	49	22	ABU42761	Peptide #10267 enc
56	40	18.9	49	22	ABU42761	Protein #8053 enco
57	40	18.9	49	22	AAU63652	Human brain expres
58	40	18.9	49	22	AAU63652	Human bone marrow
59	40	18.9	49	22	AAU63652	Peptide #10610 enc
60	40	18.9	49	22	AAU63652	Human peptide enco
61	40	18.9	49	22	AAU63652	Human secreted pro
62	40	18.9	63	20	AAU02955	Fragment of human
63	40	18.9	70	19	AAU98525	H. pylori GHPO 138
64	40	18.9	71	22	AAU45158	Protonibacterium
65	40	18.9	71	22	AAU45158	Novel human colon
66	40	18.9	71	22	AAU45158	Human digestive sy
67	40	18.9	72	21	AAU45158	Arabidopsis thalia
68	40	18.9	74	21	AAU45158	Arabidopsis thalia
69	39.5	18.6	54	20	AAU66664	Magnaporthe grisea
70	39.5	18.6	61	23	AAU66664	Lactococcus lactis
71	39.5	18.6	68	22	AAU73013	Human bone marrow
72	39.5	18.6	68	22	AAU73013	Peptide #7275 enco
73	39.5	18.6	68	22	AAU73013	Human peptide enco
74	39.5	18.6	73	20	AAU08413	P. obesus beaon p
75	39.5	18.6	73	21	AAU08413	Israeli sand rat b
76	39.5	18.6	73	22	AAU36290	Human polypeptide
77	39.5	18.6	78	22	AAU92935	Human digestive sy
78	39.5	18.6	78	22	AAU20031	Human liver associ
79	39.5	18.6	78	22	ABP40892	Human liver associ
80	39.5	18.6	83	22	ABG28281	Novel human diagno
81	39.5	18.6	86	21	AAU19836	Arabidopsis thalia
82	39.5	18.6	89	22	AAU33422	Enterococcus faeca
83	39	18.4	40	22	AAU99833	ERA binding domain

84	39	18.4	42	22	AAG99788	ERA binding domain	157	38	17.9	62	19	AAW77541	Ornithine carbamoy
85	39	18.4	42	22	AAG99797	ERA binding domain	158	38	17.9	68	21	AAB56982	Human prostate can
86	39	18.4	46	22	AAG99806	ERA binding domain	159	38	17.9	71	23	ABP31329	Human dehydrogenas
87	39	18.4	46	22	AAG99854	ERA binding domain	160	38	17.9	78	20	AAI36873	Protein involved i
88	39	18.4	47	22	AAM59858	Human brain expres	161	38	17.9	79	23	ABP32367	Human phosphatase-
89	39	18.4	47	22	AAW72447	Human bone marrow	162	38	17.9	79	23	ABP03245	Human ORFX protein
90	39	18.4	47	22	AAW72447	Human bone marrow	163	38	17.9	80	20	AAW87737	RSPV strain RSP15
91	39	18.4	47	22	ABG42267	Human peptide enco	164	38	17.9	84	13	AAW25872	HCV polypeptide 19
92	39	18.4	49	22	AAG99770	ERA binding domain	165	38	17.9	84	14	AAW41750	Hepatitis C virus
93	39	18.4	50	22	AAG99842	ERA binding domain	166	38	17.9	85	22	AAU03385	Human partial fsh2
94	39	18.4	52	22	AAO53735	Human polypeptide	167	37.5	17.7	40	22	AAO11871	Human polypeptide
95	39	18.4	52	22	AAO53735	Human polypeptide	168	37.5	17.7	43	22	AAG64824	Chronic hepatitis
96	39	18.4	54	22	AAG99818	ERA binding domain	169	37.5	17.7	51	21	AAG57616	Arabidopsis thalia
97	39	18.4	54	22	AAG99818	ERA binding domain	170	37.5	17.7	51	22	ABP38183	Peptide #5689 enco
98	39	18.4	56	20	AAO24297	Clone selected aft	171	37.5	17.7	51	22	AAW58817	Human brain expres
99	39	18.4	58	22	AAG99860	ERA binding domain	172	37.5	17.7	51	22	AAW71333	Human bone marrow
100	39	18.4	58	22	ABP10541	Human ORFX protein	173	37.5	17.7	51	22	AAW31612	Peptide #5649 enco
101	39	18.4	58	22	AAW41107	Human ORFX ORF871	174	37.5	17.7	51	22	ABG3742	Chaperone cpn60 pr
102	39	18.4	59	22	AAG99662	ERA binding domain	175	37.5	17.7	51	23	ABG41136	Human peptide can
103	39	18.4	59	22	AAG99662	ERA binding domain	176	37.5	17.7	64	21	ABG57187	Human prostate can
104	39	18.4	59	22	AAG99812	ERA binding domain	177	37.5	17.7	65	22	AAU86670	Novel human connec
105	39	18.4	59	22	AAG99812	ERA binding domain	178	37.5	17.7	67	21	AAW52244	H. pylori yjpb pro
106	39	18.4	59	22	AAG99818	ERA binding domain	179	37.5	17.7	71	21	AAW35100	Arabidopsis thalia
107	39	18.4	59	22	ABP02829	Human ORFX protein	180	37.5	17.7	73	21	AAW57615	Arabidopsis thalia
108	39	18.4	60	22	ABW42044	Peptide #9550 enco	181	37.5	17.7	74	21	AAW57614	Arabidopsis thalia
109	39	18.4	60	22	AAW62925	Human brain expres	182	37.5	17.7	74	21	ABG57614	Arabidopsis thalia
110	39	18.4	60	22	AAW75737	Human bone marrow	183	37.5	17.7	80	22	ABG57614	Human testicular a
111	39	18.4	60	22	AAW35846	Peptide #9883 enco	184	37.5	17.7	80	22	AAW95703	Human reproductive
112	39	18.4	60	22	AAG99661	ERA binding domain	185	37.5	17.7	82	23	ABP11289	Human ORFX protein
113	39	18.4	60	22	AAG99661	ERA binding domain	186	37.5	17.7	82	19	AAW62708	Streptococcus pneu
114	39	18.4	60	22	AAG99713	ERA binding domain	187	37.5	17.7	86	22	AAU46593	Propionibacterium
115	39	18.4	60	22	AAG99713	ERA binding domain	188	37.5	17.7	86	22	AAW49550	Bovine P13-SH3 ami
116	39	18.4	60	22	AAG99713	ERA binding domain	189	37.5	17.7	86	22	AAW49550	Bovine P13-SH3 ami
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121	39	18.4	62	21	AAW325011	Plant SDF encoded	194	37.5	17.7	93	13	AAW30080	Human reproductive
122	39	18.4	64	22	AAW99328	Human polypeptide	195	37.5	17.7	43	22	AAW94625	Human breast or ov
123	39	18.4	64	22	AAW99328	Human polypeptide	196	37.5	17.7	43	22	AAW94625	pH-dependent membr
124	39	18.4	67	22	AAW93179	Human ORFX protein	197	37.5	17.7	44	11	AAW03437	Human immune/haema
125	39	18.4	76	23	ABP34719	Human ORFX protein	198	37.5	17.7	45	22	AAW86438	Novel human diagno
126	39	18.4	77	23	ABP34719	Human ORFX protein	199	37.5	17.7	50	23	ABP34466	Human ORF3439 prot
127	39	18.4	80	22	AAW87727	RSPV-1 triple gen	200	37.5	17.7	55	22	ABG20798	Polypeptide fragme
128	39	18.4	81	22	AAW87727	RSPV-1 triple gen	201	37.5	17.7	55	22	ABG20798	Novel human diagno
129	39	18.4	87	22	ABP03287	Propionibacterium	202	37.5	17.7	55	22	ABG20798	Human secreted PRO
130	39	18.4	87	22	ABP03287	Propionibacterium	203	37.5	17.7	55	22	ABG20798	Novel human diagno
131	39	18.4	89	22	AAW99699	Human immune/haema	204	37.5	17.7	59	22	ABG25325	Human polypeptide
132	39	18.4	90	22	AAW99699	Human immune/haema	205	37.5	17.7	59	22	ABG25325	Propionibacterium
133	39	18.4	92	22	AAW99699	Human immune/haema	206	37.5	17.7	64	22	AAW99699	Arabidopsis thalia
134	39	18.4	92	22	AAW99699	Human immune/haema	207	37.5	17.7	69	21	AAW99699	Human ORFX ORF3037
135	39	18.4	92	22	AAW99699	Human immune/haema	208	37.5	17.7	69	21	AAW99699	Novel human diagno
136	39	18.4	92	22	AAW99699	Human immune/haema	209	37.5	17.7	69	21	AAW99699	Human nervous syst
137	39	18.4	92	22	AAW99699	Human immune/haema	210	37.5	17.7	70	22	ABG18788	Arabidopsis thalia
138	39	18.4	92	22	AAW99699	Human immune/haema	211	37.5	17.7	71	21	AAW58131	Rat giig15B protei
139	39	18.4	92	22	AAW99699	Human immune/haema	212	37.5	17.7	73	21	AAW58131	Arabidopsis thalia
140	39	18.4	92	22	AAW99699	Human immune/haema	213	37.5	17.7	73	21	AAW58131	Arabidopsis thalia
141	39	18.4	92	22	AAW99699	Human immune/haema	214	37.5	17.7	75	22	AAW58131	Human immune/haema
142	39	18.4	92	22	AAW99699	Human immune/haema	215	37.5	17.7	76	21	AAW58131	Arabidopsis thalia
143	39	18.4	92	22	AAW99699	Human immune/haema	216	37.5	17.7	78	23	ABP00955	Human ORFX protein
144	39	18.4	92	22	AAW99699	Human immune/haema	217	37.5	17.7	80	21	AAW55464	Arabidopsis thalia
145	39	18.4	92	22	AAW99699	Human immune/haema	218	37.5	17.7	81	22	AAU51964	Propionibacterium
146	39	18.4	92	22	AAW99699	Human immune/haema	219	37.5	17.7	81	22	AAU51964	Propionibacterium
147	39	18.4	92	22	AAW99699	Human immune/haema	220	37.5	17.7	84	22	AAW91403	Human reproductive
148	39	18.4	92	22	AAW99699	Human immune/haema	221	37.5	17.7	84	22	AAW91403	Human peroxidase p
149	39	18.4	92	22	AAW99699	Human immune/haema	222	37.5	17.7	85	22	AAW91403	Arabidopsis thalia
150	39	18.4	92	22	AAW99699	Human immune/haema	223	37.5	17.7	85	22	AAW91403	Human musculoskele
151	39	18.4	92	22	AAW99699	Human immune/haema	224	37.5	17.7	85	22	AAW91403	T. intermedius phe
152	39	18.4	92	22	AAW99699	Human immune/haema	225	37.5	17.7	89	20	AAW90044	Arabidopsis thalia
153	39	18.4	92	22	AAW99699	Human immune/haema	226	37.5	17.7	90	21	AAW90044	Human ORFX protein
154	39	18.4	92	22	AAW99699	Human immune/haema	227	37.5	17.7	90	21	AAW90044	SH3 domain B of hu
155	39	18.4	92	22	AAW99699	Human immune/haema	228	37.5	17.7	90	21	AAW90044	Arabidopsis thalia
156	39	18.4	92	22	AAW99699	Human immune/haema	229	37.5	17.7	90	21	AAW90044	Human ORFX protein

330	36.5	17.2	64	21	AAG57725	Arabidopsis thalia	303	36	17.0	66	23	ABB07338	S. clavuligerus CS
231	36.5	17.2	64	22	AAU50978	Propionibacterium	304	36	17.0	69	21	AAG17411	Arabidopsis thalia
232	36.5	17.2	67	22	AAU62012	Propionibacterium	305	36	17.0	69	22	ABG23020	Novel human thalio
233	36.5	17.2	68	21	AAG57152	Arabidopsis thalia	306	36	17.0	69	22	AAU89883	Human immune/haema
234	36.5	17.2	71	23	ABB81379	Human prostate spe	307	36	17.0	70	22	AAU46289	Propionibacterium
235	36.5	17.2	72	21	AAG55247	Arabidopsis thalia	308	36	17.0	71	22	AAG12510	Zea mays protein f
236	36.5	17.2	72	21	AAG56940	Arabidopsis thalia	309	36	17.0	71	22	AAU52778	Propionibacterium
237	36.5	17.2	72	21	AAG57986	Arabidopsis thalia	310	36	17.0	71	22	ABP32328	Human ORF1301 prot
238	36.5	17.2	74	21	AAU32807	Eucalyptus grandis	311	36	17.0	72	22	AAU52732	Propionibacterium
239	36.5	17.2	74	23	ABP06571	Human ORFX protein	312	36	17.0	74	22	AAG91043	C glutamicum prote
240	36.5	17.2	77	22	ABU14915	Human nervous syst	313	36	17.0	74	22	AAG91043	Human protein kina
241	36.5	17.2	78	21	AAG21116	Arabidopsis thalia	314	36	17.0	76	20	AAU26802	Human myometrium t
242	36.5	17.2	79	22	ABB38008	Peptide #5514 enco	315	36	17.0	76	20	AAU59921	Human CAMP-depende
243	36.5	17.2	79	22	ABB23244	Protein #5243 enco	316	36	17.0	76	21	AAU21798	Human CAMP-depende
244	36.5	17.2	79	22	AAU58635	Human brain expres	317	36	17.0	76	22	AAG04114	Arabidopsis thalia
245	36.5	17.2	79	22	AAU71141	Human bone marrow	318	36	17.0	76	22	AAU74309	Human protein kina
246	36.5	17.2	79	22	AAU18888	Peptide #5322 enco	319	36	17.0	76	22	AAU74311	Murine protein kina
247	36.5	17.2	79	22	AAU31422	Peptide #5459 enco	320	36	17.0	78	22	ABU27673	Human peptide #324
248	36.5	17.2	79	23	ABG40938	Human peptide enco	321	36	17.0	78	22	ABU27673	Human peptide #324
249	36.5	17.2	80	22	AAU88730	Human immune/haema	322	36	17.0	78	22	ABU18325	Protein #324 enco
250	36.5	17.2	82	22	AAU56054	Propionibacterium	323	36	17.0	78	22	AAU53648	Human brain expres
251	36.5	17.2	83	23	AAU20047	Staphylococcus aur	324	36	17.0	78	22	AAU566029	Human bone marrow
252	36.5	17.2	83	23	AAU20088	Staphylococcus aur	325	36	17.0	78	22	AAU566029	Human bone marrow
253	36.5	17.2	85	22	AAU61278	Propionibacterium	326	36	17.0	78	22	AAU07030	Human polypeptide
254	36.5	17.2	87	22	AAU54565	Propionibacterium	327	36	17.0	78	22	AAU13898	Peptide #332 enco
255	36.5	17.2	88	20	AAU35795	Amino acid sequenc	328	36	17.0	78	22	AAU26304	Peptide #341 enco
256	36.5	17.2	88	23	ABU53119	Streptococcus poly	329	36	17.0	79	22	AAU01641	Peptide #323 enco
257	36.5	17.2	89	23	ABU29332	Streptococcus poly	330	36	17.0	88	23	ABU35677	Human peptide enco
258	36.5	17.2	90	21	AAU55905	Arabidopsis thalia	331	36	17.0	89	20	AAU29439	Propionibacterium
259	36.5	17.2	90	21	AAU60917	Arabidopsis thalia	332	36	17.0	89	20	AAU90045	Streptococcus poly
260	36.5	17.2	90	22	AAU29597	Novel human colon	333	36	17.0	89	22	AAU90046	B. sphaericus phen
261	36.5	17.2	90	22	AAU93571	Human digestive sy	334	36	17.0	89	23	AAU33444	S. ureae phenylala
262	36	17.0	45	21	ABU32392	Human secreted pro							



376	35	16.5	43	22	AAH82601	Human immune/haema	449	35	16.5	82	22	ABG03961	Novel human diago
377	35	16.5	43	22	AAH45716	Human 7TM clone H7	450	35	16.5	84	20	AAW97738	Wheat threonine sy
378	35	16.5	46	22	ABH95694	Human testicular a	451	35	16.5	84	22	AAU43383	Propionibacterium
379	35	16.5	46	22	ABH95694	Human reproductive	452	35	16.5	84	22	AAU43383	Canine interleukin
380	35	16.5	48	22	ABG28786	Novel human diago	453	35	16.5	84	22	ABP35210	Human ORF183 prot
381	35	16.5	49	22	AAH83590	Human immune/haema	454	35	16.5	84	23	ABP03741	Human ORF183 prot
382	35	16.5	52	21	AAH14887	Arabidopsis thalia	455	35	16.5	85	23	ABP04531	Human ORF183 prot
383	35	16.5	52	22	AAU58539	Propionibacterium	456	35	16.5	85	23	ABP04531	Human ORF183 prot
384	35	16.5	53	22	AAU58539	Human digestive sy	457	35	16.5	86	21	AAU58539	Human ORF183 prot
385	35	16.5	54	21	AAU58539	Human secreted pro	458	35	16.5	86	21	AAU58539	Human ORF183 prot
386	35	16.5	54	21	AAU58539	Human ORF183 prot	459	35	16.5	86	22	ABG23045	Novel human diago
387	35	16.5	56	21	AAU58539	Human ORF183 prot	460	35	16.5	86	22	ABG23045	Novel human diago
388	35	16.5	56	21	AAU58539	Cone snail alpha-c	461	35	16.5	86	22	ABG23045	Novel human diago
389	35	16.5	57	22	AAU58539	Human colon cancer	462	35	16.5	86	22	ABG23045	Novel human diago
390	35	16.5	58	21	AAU58539	Eglin based protei	463	35	16.5	86	22	ABG23045	Novel human diago
391	35	16.5	58	21	AAU58539	Lung cancer associ	464	35	16.5	86	22	ABG23045	Novel human diago
392	35	16.5	58	22	AAU58539	Arabidopsis thalia	465	35	16.5	86	22	ABG23045	Novel human diago
393	35	16.5	58	22	AAU58539	Propionibacterium	466	35	16.5	86	22	ABG23045	Novel human diago
394	35	16.5	59	22	AAU58539	Propionibacterium	467	35	16.5	86	22	ABG23045	Novel human diago
395	35	16.5	59	22	AAU58539	Peptide #6909 enco	468	35	16.5	86	22	ABG23045	Novel human diago
396	35	16.5	59	22	AAU58539	Protein #6184 enco	469	35	16.5	86	22	ABG23045	Novel human diago
397	35	16.5	59	22	AAU58539	Human brain expres	470	35	16.5	86	22	ABG23045	Novel human diago
398	35	16.5	59	22	AAU58539	Human bone marrow	471	35	16.5	86	22	ABG23045	Novel human diago
399	35	16.5	59	22	AAU58539	Peptide #6120 enco	472	35	16.5	86	22	ABG23045	Novel human diago
400	35	16.5	59	22	AAU58539	Peptide #6960 enco	473	35	16.5	86	22	ABG23045	Novel human diago
401	35	16.5	59	22	AAU58539	Human peptide enco	474	35	16.5	86	22	ABG23045	Novel human diago
402	35	16.5	60	22	AAU58539	Propionibacterium	475	35	16.5	86	22	ABG23045	Novel human diago
403	35	16.5	61	18	AAU58539	Amino acid sequenc	476	35	16.5	86	22	ABG23045	Novel human diago
404	35	16.5	61	21	AAU58539	Arabidopsis thalia	477	35	16.5	86	22	ABG23045	Novel human diago
405	35	16.5	61	21	AAU58539	Arabidopsis thalia	478	35	16.5	86	22	ABG23045	Novel human diago
406	35	16.5	61	21	AAU58539	Arabidopsis thalia	479	35	16.5	86	22	ABG23045	Novel human diago
407	35	16.5	62	22	AAU58539	Propionibacterium	480	35	16.5	86	22	ABG23045	Novel human diago
408	35	16.5	62	22	AAU58539	Human musculoskele	481	35	16.5	86	22	ABG23045	Novel human diago
409	35	16.5	62	22	AAU58539	Human ORF183 prot	482	35	16.5	86	22	ABG23045	Novel human diago
410	35	16.5	63	22	AAU58539	Human ORF183 prot	483	35	16.5	86	22	ABG23045	Novel human diago
411	35	16.5	64	22	AAU58539	Peptide #1153 enco	484	35	16.5	86	22	ABG23045	Novel human diago
412	35	16.5	64	22	AAU58539	Leech eglin C as e	485	35	16.5	86	22	ABG23045	Novel human diago
413	35	16.5	65	23	AAU58539	N-terminally short	486	35	16.5	86	22	ABG23045	Novel human diago
414	35	16.5	66	22	AAU58539	Propionibacterium	487	35	16.5	86	22	ABG23045	Novel human diago
415	35	16.5	66	22	AAU58539	Leech eglin C as e	488	35	16.5	86	22	ABG23045	Novel human diago
416	35	16.5	66	22	AAU58539	Human ORF183 prot	489	35	16.5	86	22	ABG23045	Novel human diago
417	35	16.5	67	21	AAU58539	Arabidopsis thalia	490	35	16.5	86	22	ABG23045	Novel human diago
418	35	16.5	67	21	AAU58539	Arabidopsis thalia	491	35	16.5	86	22	ABG23045	Novel human diago
419	35	16.5	67	21	AAU58539	Arabidopsis thalia	492	35	16.5	86	22	ABG23045	Novel human diago
420	35	16.5	67	23	AAU58539	Human ORF183 prot	493	35	16.5	86	22	ABG23045	Novel human diago
421	35	16.5	67	23	AAU58539	Human ORF183 prot	494	35	16.5	86	22	ABG23045	Novel human diago
422	35	16.5	67	23	AAU58539	Human secreted pro	495	35	16.5	86	22	ABG23045	Novel human diago
423	35	16.5	70	22	AAU58539	Propionibacterium	496	35	16.5	86	22	ABG23045	Novel human diago
424	35	16.5	70	22	AAU58539	Human immune/haema	497	35	16.5	86	22	ABG23045	Novel human diago
425	35	16.5	70	22	AAU58539	Leech protease inh	498	35	16.5	86	22	ABG23045	Novel human diago
426	35	16.5	70	22	AAU58539	Eglin based protei	499	35	16.5	86	22	ABG23045	Novel human diago
427	35	16.5	70	22	AAU58539	Eglin based protei	500	35	16.5	86	22	ABG23045	Novel human diago
428	35	16.5	70	22	AAU58539	Leech N-acetyl-egl	501	35	16.5	86	22	ABG23045	Novel human diago
429	35	16.5	71	6	AAU58539	Sequence of new eg	502	35	16.5	86	22	ABG23045	Novel human diago
430	35	16.5	71	19	AAU58539	Streptococcus pneu	503	35	16.5	86	22	ABG23045	Novel human diago
431	35	16.5	71	19	AAU58539	Human nervous syst	504	35	16.5	86	22	ABG23045	Novel human diago
432	35	16.5	71	22	AAU58539	Eglin C based prot	505	35	16.5	86	22	ABG23045	Novel human diago
433	35	16.5	71	22	AAU58539	Eglin B based prot	506	35	16.5	86	22	ABG23045	Novel human diago
434	35	16.5	71	22	AAU58539	Human ORF183 prot	507	35	16.5	86	22	ABG23045	Novel human diago
435	35	16.5	72	22	AAU58539	Peptide #8939 enco	508	35	16.5	86	22	ABG23045	Novel human diago
436	35	16.5	75	22	AAU58539	Human nervous syst	509	35	16.5	86	22	ABG23045	Novel human diago
437	35	16.5	75	22	AAU58539	Human brain expres	510	35	16.5	86	22	ABG23045	Novel human diago
438	35	16.5	75	22	AAU58539	Human bone marrow	511	35	16.5	86	22	ABG23045	Novel human diago
439	35	16.5	75	22	AAU58539	Peptide #9262 enco	512	35	16.5	86	22	ABG23045	Novel human diago
440	35	16.5	75	22	AAU58539	Human peptide enco	513	35	16.5	86	22	ABG23045	Novel human diago
441	35	16.5	76	22	AAU58539	Novel human connec	514	35	16.5	86	22	ABG23045	Novel human diago
442	35	16.5	76	22	AAU58539	Human ribosomal pr	515	35	16.5	86	22	ABG23045	Novel human diago
443	35	16.5	77	21	AAU58539	Human secreted pro	516	35	16.5	86	22	ABG23045	Novel human diago
444	35	16.5	77	21	AAU58539	Propionibacterium	517	35	16.5	86	22	ABG23045	Novel human diago
445	35	16.5	78	22	AAU58539	Human polypeptide	518	35	16.5	86	22	ABG23045	Novel human diago
446	35	16.5	78	22	AAU58539	Human gene 22 enco	519	35	16.5	86	22	ABG23045	Novel human diago
447	35	16.5	80	21	AAU58539	Virulence gene pro	520	35	16.5	86	22	ABG23045	Novel human diago
448	35	16.5	81	19	AAU58539	Human PEA-15 prote	521	35	16.5	86	22	ABG23045	Novel human diago
													Novel human diago
													Wheat threonine sy
													Propionibacterium
													Canine interleukin
													Human ORF183 prot
													Human ORF183 prot
													Human ORF183 prot
													Human ORF183 prot
													Novel human diago
													Peptide #2112 enco
													Peptide #2144 enco
													Protein #2046 enco
													Peptide #2067 enco
													Peptide #2168 enco
													Peptide #2058 enco
													Peptide #6489 enco
													Human brain expres
													Human bone marrow
													Human immune/haema
													Peptide #6505 enco
													Human peptide enco
													Novel human diago
													Human immune/haema
													Human ORF183 prot
													Human polypeptide
													Human polypeptide
													Human polypeptide
													Human pancreatic c
													Human digestive sy
													Human polypeptide
													Lung-specific amin
													Arabidopsis thalia
													Human receptor typ
													Human ORF146 prot
													Partial bPTK7 gene
													Protein tyrosine-k
													Propionibacterium
													Arabidopsis thalia
													Amino acid sequenc
													Propionibacterium
													Propionibacterium
													Human secreted pro
													Human immune/haema
													Human ORF2331 prot
													Human secreted pro

522	34.5	16.3	80	21	AMG50527	Arabidopsis thalia	595	34	16.0	66	22	AAU56872	Propionibacterium
523	34.5	16.3	80	22	AAU50764	Propionibacterium	596	34	16.0	66	22	AAU59149	Propionibacterium
524	34.5	16.3	81	22	AAU67451	Propionibacterium	597	34	16.0	66	22	AAU59149	Human reproductive
525	34.5	16.3	82	22	AAU47452	Propionibacterium	598	34	16.0	67	22	ABG04933	Novel human diago
526	34.5	16.3	82	22	ABU12404	Human bone marrow	599	34	16.0	67	22	ABG04933	Human immune/haema
527	34.5	16.3	83	22	ABU69181	Drosophila melanog	600	34	16.0	67	23	AAU99205	N-terminally short
528	34.5	16.3	83	22	ABU2537	Peptide #10043 enc	601	34	16.0	67	23	ABP32690	Human ORF1663 prot
529	34.5	16.3	83	22	ABU25936	Protein #7935 enco	602	34	16.0	67	23	ABP05497	Human ORFX protein
530	34.5	16.3	83	22	ABU6427	Human brain expres	603	34	16.0	68	22	AAU59624	Propionibacterium
531	34.5	16.3	83	22	AAU6240	Human bone marrow	604	34	16.0	68	22	AAU09776	Aminotransferase d
532	34.5	16.3	83	22	AAU63630	Peptide #10387 enc	605	34	16.0	68	23	ABF033119	Human isomerase-ll
533	34.5	16.3	83	23	ABG45566	Human ORFX protein	606	34	16.0	68	23	ABF06632	Human ORFX protein
534	34.5	16.3	85	23	ABP03478	Human MDTT SEQ ID	607	34	16.0	68	23	ABF28415	Streptococcus poly
535	34.5	16.3	85	23	ABP51472	Propionibacterium	608	34	16.0	69	21	AAU12419	Zea mays protein f
536	34.5	16.3	87	22	AAU58059	Propionibacterium	609	34	16.0	69	21	AAU79490	Human testis-speci
537	34.5	16.3	89	22	AAU61978	S. pneumoniae deri	610	34	16.0	69	22	ABG02269	Novel human diago
538	34.5	16.3	90	19	AAU85848	Drosophila melanog	611	34	16.0	69	22	AAU16751	Peptide #3185 enco
539	34.5	16.3	90	22	ABU60712	Arabidopsis thalia	612	34	16.0	69	22	AAU04468	Human peptide enco
540	34	16.0	42	21	AAU04347	pH-dependent membr	613	34	16.0	69	23	ABG38509	Listeria monocytog
541	34	16.0	43	13	AAU30081	Human Machado-Jose	614	34	16.0	69	23	ABG49239	Arabidopsis thalia
542	34	16.0	43	17	AAU96127	pH-dependent membr	615	34	16.0	71	21	AAU371104	Propionibacterium
543	34	16.0	44	11	AAU03438	Human nervous syst	616	34	16.0	71	22	AAU57136	Protein encoded by
544	34	16.0	47	23	AAU47247	Alphavirus replic	617	34	16.0	72	21	AAU84848	Machado-Joseph dis
545	34	16.0	49	22	ABU16525	Human nervous syst	618	34	16.0	72	22	AAU569621	Human ORFX protein
546	34	16.0	50	21	AAU04346	Arabidopsis thalia	619	34	16.0	72	23	ABP06579	Arabidopsis thalia
547	34	16.0	50	23	ABP03263	Human ORFX protein	620	34	16.0	73	21	AAU17641	Human ORFX protein
548	34	16.0	51	20	AAU36084	Extended human sec	621	34	16.0	73	23	ABP09025	Arabidopsis thalia
549	34	16.0	51	20	AAU35945	Extended human sec	622	34	16.0	74	21	AAU08825	Arabidopsis thalia
550	34	16.0	52	22	AAU65996	Propionibacterium	623	34	16.0	74	21	AAU15110	Arabidopsis thalia
551	34	16.0	53	20	AAU13042	Human secreted pro	624	34	16.0	74	21	AAU43077	Arabidopsis thalia
552	34	16.0	55	22	ABU42849	Peptide #10355 enc	625	34	16.0	74	21	AAU51393	Arabidopsis thalia
553	34	16.0	55	22	AAU63741	Human brain expres	626	34	16.0	74	21	AAU51396	Arabidopsis thalia
554	34	16.0	55	22	AAU76555	Human bone marrow	627	34	16.0	75	22	ABU30432	Peptide #3083 enco
555	34	16.0	55	22	AAU88448	Human immune/haema	628	34	16.0	75	22	ABU35600	Peptide #3106 enco
556	34	16.0	55	22	AAU66662	Peptide #10699 enc	629	34	16.0	75	22	ABU21030	Human bone marrow
557	34	16.0	56	20	AAU12783	Human 5' EST secre	630	34	16.0	75	22	AAU56418	Human bone marrow
558	34	16.0	56	21	AAU26882	Zea mays protein f	631	34	16.0	75	22	AAU68798	Peptide #3050 enco
559	34	16.0	56	21	AAU00343	Human secreted pro	632	34	16.0	75	22	AAU16616	Peptide #3139 enco
560	34	16.0	56	22	AAU63055	Propionibacterium	633	34	16.0	75	22	AAU29102	Peptide #3015 enco
561	34	16.0	58	15	AAU53252	Signal peptide of	634	34	16.0	75	23	ABG38377	Human peptide enco
562	34	16.0	58	21	AAU76984	Corn RUBISCO small	635	34	16.0	76	20	AAU00301	SSP polypeptide pr
563	34	16.0	58	23	ABP07759	Human ORFX protein	636	34	16.0	77	19	AAU78258	Ssp 7.7.7.7.7.8.
564	34	16.0	60	21	AAU15111	Arabidopsis thalia	637	34	16.0	77	16	AAU60524	Synthetic storage
565	34	16.0	60	21	AAU08826	Arabidopsis thalia	638	34	16.0	77	19	AAU78258	Synthetic lysine-r
566	34	16.0	60	21	AAU51397	Arabidopsis thalia	639	34	16.0	77	20	AAU07752	Human polypeptide
567	34	16.0	60	21	AAU51397	Arabidopsis thalia	640	34	16.0	78	22	AAU07752	Human immune/haema
568	34	16.0	61	22	AAU23682	Novel human enzyme	641	34	16.0	78	22	AAU07752	Human immune/haema
569	34	16.0	61	22	AAU51496	Propionibacterium	642	34	16.0	78	22	AAU07752	Human immune/haema
570	34	16.0	61	22	ABU17883	Human nervous syst	643	34	16.0	78	22	AAU07752	Human immune/haema
571	34	16.0	61	22	ABU17883	Human nervous syst	644	34	16.0	79	21	AAU07752	Human immune/haema
572	34	16.0	62	22	ABU28703	Human nervous syst	645	34	16.0	79	21	AAU07752	Human immune/haema
573	34	16.0	62	22	ABU15033	Propionibacterium	646	34	16.0	80	22	AAU07752	Human immune/haema
574	34	16.0	63	22	AAU54282	Propionibacterium	647	34	16.0	80	22	AAU07752	Human secreted pro
575	34	16.0	63	22	AAU61408	Human brain expres	648	34	16.0	81	21	AAU07752	Human secreted pro
576	34	16.0	63	22	AAU64613	Human brain expres	649	34	16.0	81	21	AAU07752	Human secreted pro
577	34	16.0	63	22	ABG46420	Human peptide enco	650	34	16.0	81	21	AAU07752	Human secreted pro
578	34	16.0	64	18	AAU19899	Pea rubisco small	651	34	16.0	82	23	ABU10071	Human ORFX ORF919
579	34	16.0	64	21	AAU55661	Pea small subunit	652	34	16.0	84	21	AAU41155	Human ORFX ORF919
580	34	16.0	64	23	ABP03147	Human ORFX protein	653	34	16.0	84	22	AAU56161	Propionibacterium
581	34	16.0	65	21	AAU03105	Human secreted pro	654	34	16.0	84	23	AAU05156	Human ORFX protein
582	34	16.0	65	22	ABU30790	Peptide #2941 enco	655	34	16.0	85	21	AAU26881	Zea mays protein f
583	34	16.0	65	22	ABU34546	Peptide #2962 enco	656	34	16.0	85	22	AAU26881	Zea mays protein f
584	34	16.0	65	22	ABU20896	Protein #2895 enco	657	34	16.0	85	23	AAU09073	Human immune/haema
585	34	16.0	65	22	ABU22515	Protein #4514 enco	658	34	16.0	86	23	AAU09073	Human immune/haema
586	34	16.0	65	22	ABU56279	Human brain expres	659	34	16.0	86	23	AAU09073	Human immune/haema
587	34	16.0	65	22	AAU68654	Human bone marrow	660	34	16.0	88	21	AAU41063	Human colon cancer
588	34	16.0	65	22	AAU70343	Human bone marrow	661	34	16.0	88	21	AAU41063	Human colon cancer
589	34	16.0	65	22	AAU16470	Peptide #2904 enco	662	34	16.0	88	21	AAU41063	Human colon cancer
590	34	16.0	65	22	AAU28963	Peptide #3000 enco	663	34	16.0	88	21	AAU41063	Human colon cancer
591	34	16.0	65	22	AAU28963	Peptide #4717 enco	664	34	16.0	89	21	AAU41063	Human colon cancer
592	34	16.0	65	22	AAU04198	Peptide #2880 enco	665	34	16.0	89	21	AAU41063	Human colon cancer
593	34	16.0	65	22	AAU04198	Peptide #2880 enco	666	34	16.0	89	21	AAU41063	Human colon cancer
594	34	16.0	65	23	ABP05290	Human ORFX protein	667	34	16.0	89	22	AAU45033	Propionibacterium

668 34 16.0 89 22 AAM96539 Human reproductive  
669 34 16.0 90 22 ABE43464 Peptide #10970 enc  
670 34 16.0 90 22 ABE26430 Protein #8429 enc  
671 34 16.0 90 22 AAM64394 Human brain expres  
672 34 16.0 90 22 AAM77214 Human bone marrow  
673 34 16.0 90 22 AAM21147 Peptide #7581 enc  
674 34 16.0 90 22 AAM37352 Peptide #11389 enc  
675 34 16.0 90 22 AAY97674 Partial GLRAV-8 co  
676 34 16.0 90 23 ABG46227 Human ORFX protein  
677 34 16.0 90 23 ABP07811 Human ORFX protein  
678 33.5 15.8 43 20 AAY13110 Protein binding si  
679 33.5 15.8 43 20 AAY13116 Protein binding si  
680 33.5 15.8 43 20 AAY13119 Protein binding si  
681 33.5 15.8 43 20 AAY13121 Protein binding si  
682 33.5 15.8 43 20 AAM10064 Flanking sequence  
683 33.5 15.8 43 21 AAB27078 Human polypeptide  
684 33.5 15.8 47 22 AAO11959 HCV-N (6957-7100)  
685 33.5 15.8 48 12 AAR44921 Human bone marrow  
686 33.5 15.8 49 22 ABB12340 Peptide #9735 enc  
687 33.5 15.8 50 22 ABB24229 Peptide #7758 enc  
688 33.5 15.8 50 22 ABB25759 Human brain expres  
689 33.5 15.8 50 22 AAM63114 Human bone marrow  
690 33.5 15.8 50 22 AAM75925 Human polypeptide  
691 33.5 15.8 50 22 AAO11989 Peptide #10073 enc  
692 33.5 15.8 50 22 AAM36036 Human peptide enc  
693 33.5 15.8 51 21 AAB54056 Human pancreatic c  
694 33.5 15.8 51 21 AAG15819 Human polypeptide  
695 33.5 15.8 51 23 ABO05741 Arabidopsis thalia  
696 33.5 15.8 51 23 ABO11592 Human ORFX protein  
697 33.5 15.8 53 22 ABO11954 Human PRO0663 homo  
698 33.5 15.8 57 22 ABO11954 Propionibacterium  
699 33.5 15.8 57 22 ABO11954 Human immune/haema  
700 33.5 15.8 57 22 ABO11954 Human novel foetal  
701 33.5 15.8 60 22 AAO21254 Propionibacterium  
702 33.5 15.8 61 22 AAO04342 Human ORFX protein  
703 33.5 15.8 61 22 ABO07143 Novel human diagno  
704 33.5 15.8 62 22 ABO18172 Human thyroid horm  
705 33.5 15.8 62 22 ABO09071 Arabidopsis thalia  
706 33.5 15.8 65 21 AAG15818 Propionibacterium  
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708 33.5 15.8 65 22 AAM32960 Peptide #6997 enc  
709 33.5 15.8 65 23 ABE42555 Human peptide enc  
710 33.5 15.8 66 22 AAO61918 Propionibacterium  
711 33.5 15.8 66 22 ABO19188 Protein fragment e  
712 33.5 15.8 67 21 AAB27766 Propionibacterium  
713 33.5 15.8 67 22 ABO69317 Drosophila melanog  
714 33.5 15.8 67 22 AAO65190 Propionibacterium  
715 33.5 15.8 68 22 AAY13085 Human secreted pro  
716 33.5 15.8 68 22 AAG75639 Human colon cancer  
717 33.5 15.8 69 22 AAM88924 Human immune/haema  
718 33.5 15.8 70 22 AAO26263 Propionibacterium  
719 33.5 15.8 70 22 ABO23366 Novel human diagno  
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721 33.5 15.8 71 22 ABO12345 Human polypeptide  
722 33.5 15.8 71 22 ABO50535 Rat C-CAM1 cytopla  
723 33.5 15.8 72 20 AAO10327 Wild-type T7 RNA p  
724 33.5 15.8 72 20 AAO10328 Modified T7 RNA p  
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732 33.5 15.8 73 20 AAO10329 Propionibacterium  
733 33.5 15.8 73 20 AAO10329 Human haematologic  
734 33.5 15.8 74 22 AAM81105 Human haematologic  
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736 33.5 15.8 74 22 AAM81587 Human foetal prote  
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741 33.5 15.8 75 22 AAU43648 Propionibacterium  
742 33.5 15.8 78 20 AAY01323 Wild-type T7 RNA p  
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751 33.5 15.8 78 23 ABP09780 Human ORFX protein  
752 33.5 15.8 80 19 AAM62520 Protease inhibitor  
753 33.5 15.8 80 23 ABG40245 Human peptide enc  
754 33.5 15.8 81 19 AAW38740 Streptococcus pneu  
755 33.5 15.8 81 21 AAG17565 Arabidopsis thalia  
756 33.5 15.8 81 23 AAO84396 HIV VP1 consensus  
757 33.5 15.8 82 21 AAG40903 Zea mays protein f  
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761 33.5 15.8 85 22 AAM91107 Human immune/haema  
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763 33.5 15.8 86 21 AAB93444 HIV-1 non-subtype  
764 33.5 15.8 86 22 AAB93444 Human testicular a  
765 33.5 15.8 86 22 AAM95910 Human reproductive  
766 33.5 15.8 87 22 AAG23709 Novel human diagno  
767 33.5 15.8 88 22 AAO08604 Human polypeptide  
768 33.5 15.8 89 23 ABO01147 Human ORFX protein  
769 33.5 15.8 90 22 ABO00961 Novel human secreto  
770 33.5 15.8 90 22 AAO29975 Human human diagno  
771 33.5 15.8 90 22 AAM95631 Human reproductive  
772 33.5 15.8 90 22 AAO12344 Human polypeptide  
773 33.5 15.8 90 23 ABO09964 Human ORFX protein  
774 33 15.6 40 20 AAY42739 Human alpha-1-anti  
775 33 15.6 40 22 AAG22480 Arabidopsis thalia  
776 33 15.6 40 22 ABO28639 Peptide #1290 enc  
777 33 15.6 40 22 ABO33923 Peptide #1329 enc  
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779 33 15.6 40 22 AAM45485 Human brain expres  
780 33 15.6 40 22 AAM66595 Human bone marrow  
781 33 15.6 40 22 AAM14855 Peptide #1289 enc  
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791 33 15.6 42 23 ABO41640 Human peptide enc  
792 33 15.6 43 21 AAB24578 Human secreted pro  
793 33 15.6 44 22 ABO27755 Novel human diagno  
794 33 15.6 46 22 AAM88148 Human immune/haema  
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797 33 15.6 49 22 AAM00474 Human immune/haema  
798 33 15.6 50 21 AAB12070 SH3 domain from PL  
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800 33 15.6 51 22 ABB50703 Human secreted pro  
801 33 15.6 52 21 AAG00521 Polypeptide frame  
802 33 15.6 52 20 AAM99014 Human secreted pro  
803 33 15.6 52 22 AAB51092 Propionibacterium  
804 33 15.6 53 22 AAB51092 Propionibacterium  
805 33 15.6 53 22 AAB51092 Human nervous syst  
806 33 15.6 54 20 AAM83152 Rat orphan tyrosin  
807 33 15.6 54 21 AAY56439 Rat orphan tyrosin  
808 33 15.6 54 21 AAB34460 Saccharomyces cere  
809 33 15.6 54 22 ABB19870 Peptide #1966 enc  
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811 33 15.6 54 22 AAM55246 Human brain expres  
812 33 15.6 54 22 AAM55246 Human bone marrow  
813 33 15.6 54 22 AAM67641

814	33	15.6	54	22	AA015447	Peptide #1891 enco	887	67	22	AB023034	Protein #5033 enco
815	33	15.6	54	22	AA027935	Peptide #1972 enco	888	68	20	AA060176	Human endometrium
816	33	15.6	54	22	AB037216	Human peptide enco	889	68	20	AA060176	Propionibacterium
817	33	15.6	55	19	AA079143	Receptor protein t	890	69	17	AA056498	Mouse fas-associat
818	33	15.6	55	20	AA081400	Receptor protein t	891	69	21	AA051690	Arabidopsis thalia
819	33	15.6	55	22	AA090469	Human immune/haema	892	69	21	AA055737	Arabidopsis thalia
820	33	15.6	56	19	AA085999	S. pneumoniae deri	893	70	22	AA088583	Secreted protein e
821	33	15.6	56	21	AA045864	Arabidopsis thalia	894	70	22	AB031704	Peptide #4355 enco
822	33	15.6	56	21	AA001579	Human secreted pro	895	70	22	AB036922	Peptide #4428 enco
823	33	15.6	56	22	AA048066	Propionibacterium	896	70	22	AB050350	Human secreted pro
824	33	15.6	56	22	AB041901	Peptide #9407 enco	897	70	22	AB022244	Protein #4243 enco
825	33	15.6	56	22	AB025581	Protein #7580 enco	898	70	22	AA057663	Human brain expres
826	33	15.6	56	22	AA062780	Human bone marrow	899	70	22	AA070072	Human bone marrow
827	33	15.6	56	22	AA075596	Human ORFX protein	900	70	22	AA017896	Human peptide enco
828	33	15.6	56	22	AA035703	Peptide #9740 enco	901	70	22	AA030405	Peptide #4330 enco
829	33	15.6	56	22	AA045115	Human peptide enco	902	70	22	AA030405	Peptide #4442 enco
830	33	15.6	57	22	AA090372	Human immune/haema	903	70	22	AA055549	Peptide #4231 enco
831	33	15.6	57	22	AA023824	Human EST encoded	904	71	22	AB039703	Human peptide enco
832	33	15.6	57	22	AB045771	Human zalphaz2 epi	905	71	22	AA056615	Propionibacterium
833	33	15.6	57	22	AB029702	Human ORFX protein	906	71	22	AA061332	Propionibacterium
834	33	15.6	57	22	AB029617	Streptococcus poly	907	71	22	AB026181	Novel human diagno
835	33	15.6	58	20	AA011758	HLH domain of Myf-	908	71	23	AB080107	Human ORFX protein
836	33	15.6	58	22	AA044219	Propionibacterium	909	72	22	AB038418	Peptide #5924 enco
837	33	15.6	58	22	AA045997	Propionibacterium	910	72	22	AB023593	Protein #5592 enco
838	33	15.6	59	22	AA086450	Human immune/haema	911	72	22	AB023593	Human brain expres
839	33	15.6	60	20	AA088913	Polypeptide fragme	912	72	22	AA059028	Human bone marrow
840	33	15.6	60	21	AA027494	Arabidopsis thalia	913	72	22	AA017508	Peptide #5642 enco
841	33	15.6	60	22	AA047655	Propionibacterium	914	72	22	AA019208	Peptide #5893 enco
842	33	15.6	60	22	AB050982	Human secreted pro	915	72	23	AB041369	Human peptide enco
843	33	15.6	61	23	AB028702	Streptococcus poly	916	72	23	AB081332	Human ORFX protein
844	33	15.6	61	21	AA018542	zea mays protein f	917	73	21	AA015443	Arabidopsis thalia
845	33	15.6	61	22	AA019636	Arabidopsis thalia	918	73	21	AA049293	Arabidopsis thalia
846	33	15.6	62	22	AA066281	Human foetal prote	919	73	21	AB039762	Peptide #7268 enco
847	33	15.6	62	23	AB040348	Human peptide enco	920	73	22	AA060483	Human brain expres
848	33	15.6	62	23	AB070140	Human ORFX protein	921	73	22	AA073128	Human bone marrow
849	33	15.6	63	20	AA074327	Human prostate tum	922	73	22	AA033344	Peptide #7381 enco
850	33	15.6	63	21	AA035741	Human Mad3 homolog	923	73	23	AB042974	Human peptide enco
851	33	15.6	64	21	AA059872	Human normal uteri	924	73	23	AB054566	Human ORFX protein
852	33	15.6	64	21	AA020219	Arabidopsis thalia	925	74	22	AB054566	Propionibacterium
853	33	15.6	64	22	AB028437	Peptide #1288 enco	926	74	22	AA020692	Human novel foetal
854	33	15.6	64	22	AB029089	Peptide #1288 enco	927	74	22	AA020692	Human immune/haema
855	33	15.6	64	22	AB033921	Peptide #1327 enco	928	74	22	AA085343	Human zalphaz2 epi
856	33	15.6	64	22	AB034261	Peptide #1327 enco	929	74	22	AA003828	Human zalphaz2 epi
857	33	15.6	64	22	AB019263	Peptide #1767 enco	930	75	19	AA015770	H. pylori ORF 14ce
858	33	15.6	64	22	AB019695	Protein #1694 enco	931	75	19	AA060030	Streptococcus pneu
859	33	15.6	64	22	AA054387	Human brain expres	932	75	20	AA035806	Amino acid sequenc
860	33	15.6	64	22	AA055053	Human brain expres	933	75	21	AA060917	Arabidopsis thalia
861	33	15.6	64	22	AA066993	Human bone marrow	934	75	21	AA023011	Human secreted pro
862	33	15.6	64	22	AA067444	Human bone marrow	935	75	21	AA023011	Propionibacterium
863	33	15.6	64	22	AA014853	Peptide #1287 enco	936	75	21	AA054011	Arabidopsis thalia
864	33	15.6	64	22	AA015270	Peptide #1704 enco	937	76	21	AA054011	zea mays protein f
865	33	15.6	64	22	AA027280	Peptide #1317 enco	938	76	21	AA018541	Propionibacterium
866	33	15.6	64	22	AA027735	Peptide #1772 enco	939	76	22	AA051833	Propionibacterium
867	33	15.6	64	22	AA020278	Peptide #1260 enco	940	76	22	AA054295	Human polypeptide
868	33	15.6	64	22	AA030315	Peptide #1697 enco	941	76	22	AA012566	Human polypeptide
869	33	15.6	64	22	AB036650	Human peptide enco	942	77	21	AA013567	Arabidopsis thalia
870	33	15.6	64	23	AB037066	Human peptide enco	943	77	21	AA032681	zea mays protein f
871	33	15.6	64	23	AB032790	Human ORF1763 prot	944	78	22	AB022181	Novel human diagno
872	33	15.6	64	23	AB011249	Human ORFX protein	945	78	22	AA059277	Propionibacterium
873	33	15.6	65	21	AB053497	Human colon cancer	946	78	22	AA011222	Human polypeptide
874	33	15.6	65	22	AA061331	Propionibacterium	947	78	22	AA024142	Human ORFX protein
875	33	15.6	65	22	AB040031	Peptide #7537 enco	948	78	23	AB056444	Human EST encoded
876	33	15.6	65	22	AB024341	Protein #6540 enco	949	79	22	AB022403	Novel human diagno
877	33	15.6	65	22	AA060780	Human brain expres	950	79	22	AA063749	Human immune/haema
878	33	15.6	65	22	AA073454	Human bone marrow	951	80	22	AB012291	Novel human diagno
879	33	15.6	65	22	AA033652	Peptide #7689 enco	952	81	22	AA019328	Arabidopsis thalia
880	33	15.6	65	22	AB043313	Human peptide enco	953	81	22	AA021258	Human novel foetal
881	33	15.6	65	23	AB0206761	Human ORFX protein	954	82	22	AA094571	Human immune/haema
882	33	15.6	65	23	AB010351	Human ORFX protein	955	82	20	AA073888	Human prostate tum
883	33	15.6	66	23	AB040430	Human ORFX protein	956	83	20	AA004472	Human secreted pro
884	33	15.6	67	21	AA012018	Arabidopsis thalia	957	83	21	AA065309	Human 5' EST relat
885	33	15.6	67	21	AA080951	Human secreted pro	958	83	22	AA094630	Human reproductive
886	33	15.6	67	22	AB001579	Novel human diagno	959	84	21	AA060694	Arabidopsis thalia

960 33 15.6 84 21 AAG13566 Arabidopsis thalia  
 961 33 15.6 84 23 AAU97686 RNA3' terminal pho  
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 963 33 15.6 86 22 ABB30838 Peptide #3489 enco  
 964 33 15.6 86 22 ABB36016 Peptide #3522 enco  
 965 33 15.6 86 22 ABB21431 Protein #3420 enco  
 966 33 15.6 86 22 AAM56809 Human brain expres  
 967 33 15.6 86 22 AAM56918 Human bone marrow  
 968 33 15.6 86 22 AAM17022 Peptide #3456 enco  
 969 33 15.6 86 22 AAM29313 Peptide #3550 enco  
 970 33 15.6 86 22 AAM04730 Peptide #3412 enco  
 971 33 15.6 86 22 AAG35933 Human peptide enco  
 972 33 15.6 87 21 AAG35303 Zea mays protein f  
 973 33 15.6 87 22 AAU67508 Propionibacterium  
 974 33 15.6 88 19 AAW50153 Taranula venom pr  
 975 33 15.6 88 21 AAB11531 SEN virus protein  
 976 33 15.6 88 22 AAU67025 Propionibacterium  
 977 33 15.6 88 22 AAM88974 Human immune/haema  
 978 33 15.6 90 21 AAG14932 Arabidopsis thalia  
 979 33 15.6 90 21 AAG15442 Arabidopsis thalia  
 980 33 15.6 90 21 AAG26831 Zea mays protein f  
 981 33 15.6 90 21 AAG35425 Arabidopsis thalia  
 982 33 15.6 90 21 AAG49292 Propionibacterium  
 983 33 15.6 90 22 AAU53146 Human endocrine po  
 984 33 15.6 90 22 AAU18439 Human cardiovascular  
 985 32.5 15.3 42 22 AAU22114 Human polypeptide  
 986 32.5 15.3 43 22 AAO11974 Human polypeptide  
 987 32.5 15.3 45 13 AAR29176 Astrovirus serotyp  
 988 32.5 15.3 46 22 AAO10620 Human polypeptide  
 989 32.5 15.3 47 13 ABB53957 Lactococcus lactis  
 990 32.5 15.3 47 13 AAR20763 Peptide 13 based o  
 991 32.5 15.3 49 22 ABB44259 Peptide #11775 enc  
 992 32.5 15.3 49 22 ABB27136 Protein #9135 enco  
 993 32.5 15.3 49 22 AAM55305 Human bone marrow  
 994 32.5 15.3 49 22 AAM78004 Human bone marrow  
 995 32.5 15.3 49 22 AAM21894 Peptide #8328 enco  
 996 32.5 15.3 49 22 AAM38220 Peptide #12257 enc  
 997 32.5 15.3 49 23 ABG47017 Human peptide enco  
 998 32.5 15.3 50 5 AAP40503 Sequence of the CN  
 999 32.5 15.3 50 21 AAG55355 Arabidopsis thalia  
 1000 32.5 15.3 50 21 AAG55743 Arabidopsis thalia

# ALIGNMENTS

RESULT 1  
 ID AAB18941 standard; peptide; 43 AA.  
 AC AAB18941;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Homo sapiens.  
 PN WO200055634-A1  
 PD 21-SEP-2000.  
 PF 14-MAR-2000; 2000WO-FR00613.  
 PR 15-MAR-1999; 99FR-0003159.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Burnol A, Perdereau D, Kasus-Jacobi A, Berezat V, Girard J;

XX WPI; 2000-587566/55.  
 DR Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity  
 PT Claim 2; Page 25; 46pp; French.  
 PS B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX SQ Sequence 43 AA;

Query Match 100.0%; Score 212; DB 21; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-25;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PMRSISENSLVAMDFSGQSRVIENTEALSVAVEEGLAWKK 43  
 DB 1 PMRSISENSLVAMDFSGQSRVIENTEALSVAVEEGLAWKK 43

RESULT 2  
 AAB18942  
 ID AAB18942 standard; peptide; 84 AA.  
 AC AAB18942;  
 DT 08-FEB-2001 (first entry)  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 OS Homo sapiens.  
 PN WO200055634-A1.  
 PD 21-SEP-2000.  
 PF 14-MAR-2000; 2000WO-FR00613.  
 PR 15-MAR-1999; 99FR-0003159.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Burnol A, Perdereau D, Kasus-Jacobi A, Berezat V, Girard J;

XX WPI; 2000-587566/55.  
 DR Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity  
 PT Claim 2; Page 26; 46pp; French.  
 PS B18937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can

CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.

XX Sequence 84 AA;  
 XX Query Match 100.0%; Score 212; DB 21; Length 84  
 XX Best Local Similarity 100.0%; Pred. No. 2e-24; Indels 0; Gaps 0;  
 XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PMRSVSNLSVAMDFSGOKSRVIENTEALSVAVEEGLAWRKK 43  
 DB 13 PMRSVSNLSVAMDFSGOKSRVIENTEALSVAVEEGLAWRKK 55

RESULT 3  
 AAB18937  
 ID AAB18937 standard; peptide; 43 AA.

XX AAB18937;  
 XX 08-FEB-2001 (first entry)  
 XX Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 XX phosphorylated insulin receptor interacting region; Grb7 family protein;  
 XX insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 XX diabetes; obesity; polycystic ovarian syndrome; syndrome X.

XX Rattus sp.  
 XX WO2000055634-A1.  
 XX 21-SEP-2000.

XX 14-MAR-2000; 2000WO-FR00613.  
 XX 15-MAR-1999; 99FR-0003159.  
 XX (CNRS) CNRS CENT NAT RECH SCI.

XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPT; 2000-587566/55.

XX Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity

XX Claim 2; Page 23; 46pp; French.

XX BL937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.

XX Sequence 43 AA;  
 XX Query Match 96.7%; Score 205; DB 21; Length 43;  
 XX Best Local Similarity 93.0%; Pred. No. 9.2e-24; Indels 0; Gaps 0;  
 XX Matches 40; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 PMRSVSNLSVAMDFSGOKSRVIENTEALSVAVEEGLAWRKK 43

DB 1 PMRSVSNLSVAMDFSGOKSRVINDNTEALSVAVEEGLAWRKK 43

RESULT 4  
 AAB18938  
 ID AAB18938 standard; peptide; 84 AA.

XX AAB18938;  
 XX 08-FEB-2001 (first entry)  
 XX Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.

XX phosphorylated insulin receptor interacting region; Grb7 family protein;  
 XX insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 XX diabetes; obesity; polycystic ovarian syndrome; syndrome X.

XX Rattus sp.  
 XX WO2000055634-A1.

XX 21-SEP-2000.  
 XX 14-MAR-2000; 2000WO-FR00613.  
 XX 15-MAR-1999; 99FR-0003159.

XX (CNRS) CNRS CENT NAT RECH SCI.  
 XX Burnol A, Perdureau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPT; 2000-587566/55.

XX Fragments of Grb family proteins to identify compounds are useful in  
 XX treating insulin-associated diseases, particularly diabetes and obesity

XX Claim 2; Page 23-24; 46pp; French.

XX BL937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.

XX Sequence 84 AA;

XX Query Match 96.7%; Score 205; DB 21; Length 84;  
 XX Best Local Similarity 93.0%; Pred. No. 2.3e-23;  
 XX Matches 40; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 PMRSVSNLSVAMDFSGOKSRVIENTEALSVAVEEGLAWRKK 43  
 DB 13 PMRSVSNLSVAMDFSGOKSRVINDNTEALSVAVEEGLAWRKK 55

RESULT 5  
 AAB18949  
 ID AAB18949 standard; peptide; 43 AA.

XX AAB18949;  
 XX 08-FEB-2001 (first entry)  
 XX Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.

XX



```

) Sequence      80 AA;
Query Match      76.4%; Score 162; DB 21; Length 80;
Best Local Similarity 74.4%; Pred. No. 7.9e-17;

```

XX  
DT 08-FEB-2001 (first entry)



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XX DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
XX KW Phosphorylated insulin receptor interacting region; Grb7 family protein;
XX KW Insulin receptor; tyrosine kinase; insulin; insulin-associated disease;
XX KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.
XX OS Mus muris.
XX PN WO200055634-A1.
XX PD 21-SEP-2000.
XX PF 14-MAR-2000; 2000WO-FR00613.
XX PR 15-MAR-1999; 99FR-0003159.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Burnol A, Perdereau D, Kasus-Jacobi A, Berezat V, Girard J;
XX DR WPI; 2000-587566/55.
XX PT Fragments of Grb family proteins to identify compounds are useful in
XX PT treating insulin-associated diseases, particularly diabetes and obesity
XX PS Claim 2; Page 28; 46pp; French.
XX CC BI8937-64 represent the PIR (phosphorylated insulin receptor interacting
XX CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.
XX CC PIR is the actual binding region but its effect is about 10 times
XX CC greater in presence of SH2 (which by itself is inactive). Agents that
XX CC affect binding between the peptides and the insulin receptor can
XX CC stimulate or inhibit tyrosine kinase activity of the receptor. The
XX CC peptides are used for screening molecules for ability to treat diseases
XX CC in which insulin is implicated. The peptides are used to identify agents
XX CC that are potentially useful for treating insulin-associated diseases,
XX CC particularly diabetes and obesity but also polycystic ovarian syndrome
XX CC and syndrome X.
XX SQ Sequence 82 AA;
XX Query Match 75.0%; Score 161; DB 21; Length 82;
XX Best Local Similarity 78.0%; Pred. No. 1.2e-16;
XX Matches 32; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX QY 1 PWRISNSLVAMDFSGQKSRVIENTEALSVAVEEGLAWR 41
XX DB 13 PWRISNSLVAMDFSGQKSRVIENTEALSVAVEEGLAWR 53
XX RESULT 11
XX AAB18953
XX ID AAB18953 standard; peptide; 43 AA.
XX AC AAB18953;
XX XX 08-FEB-2001 (first entry)
XX DT Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
XX DE Phosphorylated insulin receptor interacting region; Grb7 family protein.
XX KW Phosphorylated insulin receptor interacting region; Grb7 family protein;
XX KW Insulin receptor; tyrosine kinase; insulin; insulin-associated disease;
XX KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.
XX OS Rattus sp.
XX PN WO200055634-A1.
XX PD 21-SEP-2000.
XX PF 14-MAR-2000; 2000WO-FR00613.

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XX PR 15-MAR-1999; 99FR-0003159.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Burnol A, Perdereau D, Kasus-Jacobi A, Berezat V, Girard J;
XX DR WPI; 2000-587566/55.
XX PT Fragments of Grb family proteins to identify compounds are useful in
XX PT treating insulin-associated diseases, particularly diabetes and obesity
XX PS Claim 2; Page 32; 46pp; French.
XX CC BI8937-64 represent the PIR (phosphorylated insulin receptor interacting
XX CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.
XX CC PIR is the actual binding region but its effect is about 10 times
XX CC greater in presence of SH2 (which by itself is inactive). Agents that
XX CC affect binding between the peptides and the insulin receptor can
XX CC stimulate or inhibit tyrosine kinase activity of the receptor. The
XX CC peptides are used for screening molecules for ability to treat diseases
XX CC in which insulin is implicated. The peptides are used to identify agents
XX CC that are potentially useful for treating insulin-associated diseases,
XX CC particularly diabetes and obesity but also polycystic ovarian syndrome
XX CC and syndrome X.
XX SQ Sequence 43 AA;
XX Query Match 75.0%; Score 159; DB 21; Length 43;
XX Best Local Similarity 69.8%; Pred. No. 9.6e-17;
XX Matches 30; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX QY 1 PWRISNSLVAMDFSGQKSRVIENTEALSVAVEEGLAWRKK 43
XX DB 1 PWRISNSLVAMDFSGQKSRVIENTEALSVAVEEGLAWRKK 43
XX RESULT 12
XX AAB18961
XX ID AAB18961 standard; peptide; 43 AA.
XX AC AAB18961;
XX XX 08-FEB-2001 (first entry)
XX DT Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
XX DE Phosphorylated insulin receptor interacting region; Grb7 family protein.
XX KW Phosphorylated insulin receptor interacting region; Grb7 family protein;
XX KW Insulin receptor; tyrosine kinase; insulin; insulin-associated disease;
XX KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.
XX OS Mus muris.
XX PN WO200055634-A1.
XX PD 21-SEP-2000.
XX PF 14-MAR-2000; 2000WO-FR00613.
XX PR 15-MAR-1999; 99FR-0003159.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Burnol A, Perdereau D, Kasus-Jacobi A, Berezat V, Girard J;
XX DR WPI; 2000-587566/55.
XX PT Fragments of Grb family proteins to identify compounds are useful in
XX PT treating insulin-associated diseases, particularly diabetes and obesity
XX PS Claim 2; Page 36; 46pp; French.

```

XX BI8937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.

XX Sequence 43 AA;  
 SQ  
 Query Match 75.0%; Score 159; DB 21; Length 43;  
 Best Local Similarity 69.8%; Pred. No. 9.6e-17;  
 Matches 30; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 PMSISENSLVAMDFSGKSRVIENTPEALSVAVEGLAWRK 43  
 I:||||:||||||| ||||| ||||| |||||  
 DB 1 PLRSVSDNTLVAMDFSGHAGRVINDNPREALSAAMEEAQAQRK 43

RESULT 13  
 AAB18954  
 ID AAB18954 standard; peptide; 80 AA.  
 XX  
 AC AAB18954;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 XX  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 XX  
 OS Rattus sp.

XX WO200055634-A1.  
 XX 21-SEP-2000.  
 XX  
 PF 14-MAR-2000; 2000WO-FR00613.  
 XX  
 PR 15-MAR-1999; 99FR-0003159.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI: 2000-587566/55.  
 XX  
 PT Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 PT and syndrome X.  
 PS Claim 2; Page 32; 46pp; French.

XX BI8937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX Sequence 80 AA;

Query Match 75.0%; Score 159; DB 21; Length 80;  
 Best Local Similarity 69.8%; Pred. No. 2.3e-16;  
 Matches 30; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 OY 1 PMSISENSLVAMDFSGKSRVIENTPEALSVAVEGLAWRK 43  
 I:||||:||||||| ||||| ||||| |||||  
 DB 13 PLRSVSDNTLVAMDFSGHAGRVINDNPREALSAAMEEAQAQRK 55

RESULT 14  
 AAB18962  
 ID AAB18962 standard; peptide; 80 AA.  
 XX  
 AC AAB18962;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.  
 XX  
 KW Phosphorylated insulin receptor interacting region; Grb7 family protein;  
 KW insulin receptor; tyrosine kinase; insulin; insulin-associated disease;  
 KW diabetes; obesity; polycystic ovarian syndrome; syndrome X.  
 XX  
 OS Mus mus.

XX WO200055634-A1.  
 XX 21-SEP-2000.  
 XX  
 PF 14-MAR-2000; 2000WO-FR00613.  
 XX  
 PR 15-MAR-1999; 99FR-0003159.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;  
 XX WPI: 2000-587566/55.  
 XX  
 PT Fragments of Grb family proteins to identify compounds are useful in  
 PT treating insulin-associated diseases, particularly diabetes and obesity  
 PT and syndrome X.  
 PS Claim 2; Page 37; 46pp; French.

XX BI8937-64 represent the PIR (phosphorylated insulin receptor interacting  
 CC region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein.  
 CC PIR is the actual binding region but its effect is about 10 times  
 CC greater in presence of SH2 (which by itself is inactive). Agents that  
 CC affect binding between the peptides and the insulin receptor can  
 CC stimulate or inhibit tyrosine kinase activity of the receptor. The  
 CC peptides are used for screening molecules for ability to treat diseases  
 CC in which insulin is implicated. The peptides are used to identify agents  
 CC that are potentially useful for treating insulin-associated diseases,  
 CC particularly diabetes and obesity but also polycystic ovarian syndrome  
 CC and syndrome X.  
 XX Sequence 80 AA;

Query Match 75.0%; Score 159; DB 21; Length 80;  
 Best Local Similarity 69.8%; Pred. No. 2.3e-16;  
 Matches 30; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 OY 1 PMSISENSLVAMDFSGKSRVIENTPEALSVAVEGLAWRK 43  
 I:||||:||||||| ||||| ||||| |||||  
 DB 13 PLRSVSDNTLVAMDFSGHAGRVINDNPREALSAAMEEAQAQRK 55

RESULT 15  
 AAB189708  
 ID AAB189708 standard; protein; 67 AA.  
 XX

DB 17 LGFSFGPKSRVLTSLHCPMPVEVLAEKHGGFOW 52.

RESULT 16  
AAU30892

TD AAU30892 standard; Protein; 72 AA.

XX  
AC AAU30892;

XX  
DT 18-DEC-2001 (first entry)

XX  
DE Novel human secreted protein #1383.

XX  
KW Human; vaccination; gene therapy; nutritional supplement;  
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX  
OS Homo sapiens.

XX  
PN WO200179449-A2.

XX  
PD 25-OCT-2001.

XX  
PF 16-APR-2001; 2001WO-US08656.

XX  
PR 18-APR-2000; 2000US-0552929.

XX  
PR 26-JAN-2001; 2001US-0770160.

XX  
PA (HYSE-) HYSEQ INC.

XX  
XX  
PI Tang YT, Liu C, Drmanac RT;

XX  
XX  
DR WPI; 2001-611725/70.

XX  
PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
PT vaccination, testing and therapy -

XX  
PS Claim 20; Page 366; 765pp; English.

XX  
CC The invention relates to novel human secreted polypeptides. The  
CC polypeptides and antibodies to the polypeptides are useful for  
CC determining the presence of or predisposition to a disease associated  
CC with altered levels of polypeptide. The polypeptides are also useful for  
CC identifying agents (agonists and antagonists) that bind to them. Cells  
CC expressing the proteins are useful for identifying a therapeutic agent  
CC for use in treatment of a pathology related to aberrant expression or  
CC physiological interactions of the polypeptide. Vectors comprising  
CC the nucleic acids encoding the polypeptides and cells genetically  
CC engineered to express them are also useful for producing the proteins.  
CC The proteins are useful in genetic vaccination, testing and  
CC therapy, and can be used as nutritional supplements. They may be used to  
CC increase stem cell proliferation; to regulate haematopoiesis; and in  
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;  
CC immune suppression and/or stimulation; as anti-inflammatory agents; and  
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid  
CC sequences of novel human secreted proteins of the invention.

XX  
SQ Sequence 72 AA;

```

      23.1%  Score 49;  DB 23;  Length 67;
      Local Similarity 33.3%;  Pred. No. 11;
      Gaps 12;  Conservative 3;  Mismatches 15;  Indels 6;  Gaps 1;
      11 VAMDFGSKSRVETN-----PTSLAVAVEGLAW 40
          : ||| ||||: |||: |||

```



AC ABC47266;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 36931.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00665.  
 XX  
 PR 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-060840R.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-234687P.  
 PR 27-SEP-2000; 2000US-236359P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 FA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI: 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 XX measure gene expression in human lung samples.  
 XX  
 PS Claim 27; SEQ ID NO 36931; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridize at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC in having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,

CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC and hyaline membrane disease, primary ciliary dyskinesia, pulmonary hypertension  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 84 AA;  
 Query Match 21.2%; Score 45; DB 23; Length 84;  
 Best Local Similarity 26.4%; Pred. No. 59;  
 Matches 14; Conservative 6; Mismatches 7; Indels 26; Gaps 2;  
 OY 17 GOKSRVIEPN-----TEALSVAV-----EEGLARRKK 43  
 DB 11 GOKARLLSRPLRGVSKHCLTFYHMYGGTGLLSVYLKKKEDESESLWRRR 63  
 RESULT 20  
 AAG03340  
 ID AAG03340 standard; Protein; 72 AA.  
 XX  
 AC AAG03340;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO: 7421.  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping.  
 XX  
 OS Homo sapiens.  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 DR WPI: 2000-500381/45.  
 DR N-PSDB; AAG03346.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 PS Claim 13; SEQ ID 7421; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
 CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer cDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length cDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.  
 XX  
 SQ Sequence 72 AA;

Query Match 21.0%; Score 44.5; DB 21; Length 72;  
 Best Local Similarity 50.0%; Pred No. 57;  
 Matches 10; Conservative 1; Gaps 1;

QY 21 RVIENTPALSVAVEGLAW 40  
 || :|||: ||| :| :|  
 Db 38 RVCPTSCSVA-QAGVQW 56

RESULT 21  
 AAU87164  
 ID AAU87164 standard; Protein; 74 AA.

XX AC AAU87164;

XX DT 05-JUN-2002 (first entry)

XX DE Novel central nervous system protein #74.

XX KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;  
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;  
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
 KW myocardial infarction; wound healing; cell proliferation; skin aging;  
 KW food additive; food preservative; gene therapy.

XX OS Homo sapiens.

XX PN WO200155318-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01332.

XX PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
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 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218250.  
 PR 26-JUL-2000; 2000US-0220963.  
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 PR 28-JUL-2000; 2000US-0224518.  
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 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225277.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
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 PR 22-AUG-2000; 2000US-0226688.  
 PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
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 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
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 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234323.  
 PR 21-SEP-2000; 2000US-0234327.  
 PR 23-SEP-2000; 2000US-0234597.  
 PR 23-SEP-2000; 2000US-0234598.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 29-SEP-2000; 2000US-0236327.  
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 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0238935.  
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 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
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 PR 08-NOV-2000; 2000US-0246525.  
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 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.



RESULT 23  
AAU41349  
ID AAU41349  
XX



AC	AAU41349;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	Propionibacterium acnes immunogenic protein #2245.
XX	
KW	SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW	uveitis; endophthalmitis; bone; joint; central nervous system; osteomyelitis;
KW	inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; ELISA;
XX	dermatological; osteopathic; neuroprotectant;
OS	Propionibacterium acnes.
XX	
PN	WO200181581-A2.
XX	
PD	01-NOV-2001.
XX	
PF	20-APR-2001; 2001WO-US12865.
XX	
PR	21-APR-2000; 2000US-199047P.
PR	02-JUN-2000; 2000US-208841P.
PR	07-JUL-2000; 2000US-216747P.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI	L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX	
DR	WPI: 2001-616774/71.
DR	N-PSDB; AAS59515.
XX	
PT	Propionibacterium acnes polypeptides and nucleic acids useful for
PT	vaccinating against and diagnosing infections,
PT	treating acne vulgaris -
PS	Example 1; SEQ ID No 2344; 1069pp; English.
XX	
CC	Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC	polypeptides. The proteins and their associated DNA sequences are used in
CC	the treatment, prevention and diagnosis of medical conditions caused by
CC	P. acnes. The disorders include SAPHO syndrome, osteomyelitis, acne,
CC	pustulosis, hypertosis and osteomyelitis), uveitis, synovitis, acne,
CC	P. acnes is also involved in infections of bone joints and the central
CC	nervous system, however it is particularly involved in the inflammatory
CC	lesions associated with acne vulgaris. A method for detecting the
CC	presence or absence of P. acnes in a patient comprises contacting a
CC	sample with a binding agent that binds to the proteins of the invention
CC	and determining the amount of bound protein in the sample. The
CC	polypeptides may be used as antigens in the production of antibodies
CC	specific for P. acnes proteins. These antibodies can be used to
CC	deregulate expression and activity of P. acnes polypeptides and
CC	therefore treat P. acnes infections. The antibodies may also be used as
CC	diagnostic agents for determining P. acnes presence, for example, by
CC	enzyme linked immunosorbent assay (ELISA).
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 79 AA;
Query Match	21.0%; Score 44.5; DB 22; Length 79;
Best Local Similarity	27.5%; Pred: No. 65;
Matches	11; Conservative 10; Mismatches 16; Indels 3; Gaps 1;
QY	4 SISENSLVAMPDFSGQSRVTENPTALSVAEEGLAWKK 43
	: :   :   :   :   :   :   :   :   :
Dd	28 SLVNSVPVTLSSREGPSNRV---PTRSLACATRHGVCSRER 64
RESULT 24	
AAU62249	ID
ID	AAU62249 standard; Protein: 90 AA

[illegible]

AC AAW94366;  
XX 21-NOV-2001 (first entry)  
XX Human reproductive system related antigen SEQ ID NO: 3024.  
XX Human reproductive system related antigen; reproductive system disorder;  
XX cancer; gene therapy.  
XX Homo sapiens.  
XX WO200155320-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US01339.  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
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XX 17-MAR-2000; 2000US-0190076.  
XX 18-APR-2000; 2000US-0198123.  
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XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
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XX 22-AUG-2000; 2000US-0226686.  
XX 22-AUG-2000; 2000US-0227182.  
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XX 01-SEP-2000; 2000US-0229287.  
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XX 06-SEP-2000; 2000US-0230437.  
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XX 08-SEP-2000; 2000US-0231414.  
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XX 12-SEP-2000; 2000US-0231968.  
XX 14-SEP-2000; 2000US-0232397.  
XX 14-SEP-2000; 2000US-0232398.  
XX 14-SEP-2000; 2000US-0232399.  
XX 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
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PR 21-SEP-2000; 2000US-0234274.  
PR 23-SEP-2000; 2000US-0234997.  
PR 23-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
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PR 29-SEP-2000; 2000US-0236327.  
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PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
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PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
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PR 01-DEC-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 05-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 06-DEC-2000; 2000US-0256719.  
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Search completed: March 28, 2003, 09:05:30  
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